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(54) Title: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

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BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

Field of the invention

5 The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

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Background to the invention

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively
15 expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with
20 complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses,
25 expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic,
30 or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular

35 target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X_L) or to the group of proteins promoting apoptosis (Bax, Bak) (Oltvai and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Sato *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996).

Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeier *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear.

It is an aim of the present invention to provide new *bax* sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (a) medicament(s) for treating said diseases.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

It is also an aim of the invention to provide methods for preventing infection with yeast or fungi.

It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

All the aims of the present invention have been met by the embodiments as set out below.

Summary of the invention

Since it has been discovered that the mammalian *bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *BAX* gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida spp.* homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of

SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

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626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660,
662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710,
712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional
15 equivalent, derivative or bioprecursor of said protein,

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70%
similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid sequences
as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44,
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(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70%

5 identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 10 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 15 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 20 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 25 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23,

25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 30 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 35 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,

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707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical,
more preferably more than 85%, or 90% or 95% identical and most preferably more than
15 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs
17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63,
65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109,
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615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649,
651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699,
701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means

10 the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly
15 employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between
20 two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more
25 nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence
30 of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,
37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85,
35 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713 and 715; from *Candida albicans* are defined in SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 718, 720, 722, 724, 726, 728, 730 and 732.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731

but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death. According to a more specific embodiment, these nucleic acid sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;

(e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,

615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and,

(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid corresponds to a mammal or human homologue of at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
10 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid
15 sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than
20 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and
- (g) the complement of any of the nucleic acids as specified in a) to f),
- 25 for the preparation of a medicament for treating diseases associated with yeast or fungi.

The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

- The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within
30 a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in

human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus *Candida*, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergilliosis, caused by members of the genus *Aspergillus*, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides immitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or

eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

- 5 According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising

- 10 to a human homologue of at least one yeast or candida nucleic acid described herein.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

- 15 The present invention also advantageously provides nucleic acid molecules of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention.

- 20 The probes will specifically amplify any of the nucleic acid molecules of the invention. The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

- 25 According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

- 30 Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,

56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1986). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50,

5 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 10 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714 and 716. Also according to the 15 invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 20 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and the use of human polypeptides as represented by SEQ ID NOs 676, 678, 25 680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 30 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 35 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 10 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 15 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 20 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 25 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 30 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and

(d) a functional fragment of any of said polypeptides as defined in a) to c).

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;

5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;

10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,

(d) a functional fragment of any of said polypeptides as defined in a) to c).

15 The invention also relates to the polypeptides of the invention and described above for use as a medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

20 The polypeptides described above or the human or mammal homologues thereof can also be used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian
25 homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

30 The present invention also relates to a vaccine for immunizing a mammal comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A “vaccine” is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions. When a vaccine is used for protecting individuals against certain infections or diseases, it is called a prophylactic vaccine. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

The term “therapeutic” refers to a composition capable of treating infections caused by yeast or fungi or capable of treating proliferative disorders.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the polypeptides or proteins of the invention. The polypeptides of the invention are represented in SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

The antibodies of the invention are capable of specifically binding to at least one of the yeast or candida polypeptides as defined earlier or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue. The invention also relates to the use of said antibodies in treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases. Said antibodies may also be used for the preparation of a medicament for and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi where the yeast or fungus is chosen from, but not restricted to *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response. According to another embodiment, the present invention provides a method of identifying compounds or polypeptides which selectively inhibit, induce or interfere with the

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

- 10 According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector
- 15 comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected
- 20 yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said
- 25 compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound .

- Alternative methods for identifying compounds which selectively modulate expression or
- 30 functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

- Another alternative to the above described method comprises (a) contacting a compound to be
- 35 tested with a genetically modified yeast or fungus in which modification results in the

overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound, (b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.

The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide

5 obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound.

According to another embodiment the invention relates to a method for identifying compounds

10 which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of

15 the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an

20 interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or

25 inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or

30 polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

5 This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or
10 said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene
15 product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the *GAL4* protein in yeast. Gal4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide
20 vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of Gal4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of Gal4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the
25 nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a *GAL4* transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent
30 protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In
35 addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relationship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,

band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation.

All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates

to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention.

Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

The invention further relates to a method for preparing pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

- 10 These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

- 15 According to yet another embodiment, the invention relates to a genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or
20 fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

- Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other
25 mammals.

- According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof,
30 which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

10 The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable pharmaceutically acceptable carrier.

15 The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *bax* gene which could be adequately expressed in this pathogenic organism.

Therefore, the present invention relates to an isolated nucleic acid representing a synthetic BAX-gene for expression in *Candida* spp. selected from the group of:

- 25 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90%
30 or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and
e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,

or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).

The synthetic *BAX* gene shows 73.7% identity with the gene coding for Bax- α . It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used
5 *Candida* spp. codons, are used instead of the choice made for the sequence represented in SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

10 According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the
15 proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic *BAX*, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion
20 partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic *BAX* gene and its fusion partner.

The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the
25 invention is a *Candida* spp. cell.

In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

30 The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death

According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic *BAX* gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

- 5 In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic *BAX* gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a
10 pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

- The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death
15 comprising the steps of:

- a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,
- b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide
20 encoded by said cDNA library, and,
- c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- a) providing a genetically modified organism as described above,
- 25 b) expressing a cDNA library in said genetically modified organism, and,
- c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

- 30 a) providing (a) genetically modified yeast or fungi as described above,
- b) treating said genetically modified yeast or fungi with a mutagen,
- c) isolating resistant yeast or fungal cells, and,
- d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

5

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 396 and SEQ ID NOs 691 to 716)

Figure 2. *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).

Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

YGL080W (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (330 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

YGR243W (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

YGR183C (QCR9) (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation. Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 399bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

YBR009C (SEQ ID NO 37), **YGR209C** (SEQ ID NO 187) and **YPR028W** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.

The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

Figure 4 Yeast cells with a disrupted **YGR183C** gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean \pm SD, n=3). SD bars are obscured by symbols.

- 5 **Figure 5.** Scheme for the synthesis of the synthetic *BAX* gene using *C. albicans* optimal codons.
- Figure 6.** DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans BAX* gene.
- 10 **Figure 7.** Representation of the expression constructs of the synthetic *CaBAX* gene (A) and the *yEGFP-synth CaBAX* fusion (B).
- Figure 8.** Growth of the *Candida Albicans* transformants: the individual transformants of *pGAL1P:synthCaBAX* and *pGAL1P:GFP-synthCaBAX* were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.
- 15 **Figure 9.** Growth kinetics of *GAL1P:synthCaBAX* (A) and *GAL1P:GFP-synthCaBAX* (B) on galactose containing minimal medium.
- Figure 10.** Immunoblot analysis of two independent transformants of *GAL1P:synthCaBAX* after 15 hours *Bax* induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the *Bax* protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal *Bax* antibody could be removed by the threatment with *S. cerevisiae* mannan.
- 20 **Figure 11.** Immunoblot analysis of the *GAL1P:GFP-synthCaBAX* strain on galactose containing minimal medium. The band appearing at 45kDa represents the *Gfp-Bax* fusion protein, while the band at 20kDa represents the *Gfp* protein alone.
- 25 **Figure 12.** FACS analysis of two independent *GAL1P:GFP-synthCaBAX* transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the *GFP-fluorescence* peak is not shaded.
- Figure 13.** Viability test *synthCaBAX* (A) and *GFP-synthCaBAX* transformants (B): Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.
- 30 **Table 1.** Oligonucleotides used for construction of the synthetic *CaBAXx* gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.
- 35

Tables 2- 6. Genes modulated by Bax expression in *S. cerevisiae*.

This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qt values were calculated using the Pathways™ software (Research Genetics).

Table 7. Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein expression. The Qt values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓ respectively in Tables 2-6).

Table 8. Codon usage for the synthetic *BAX* gene.

Table 9. Regulation of 23 selected "Bax-specific" functions.

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

- 5 Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YlpUTyL or YlpUTyLMuBax, after linearisation in the Ty
10 δ element (Zhu, 1986).

Cloning of mouse BAX cDNA

- Mouse *bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA polymerase (Stratagene®, Lo Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18
15 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3' (SEQ ID NO 690).

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

20

Plasmid constructions

- The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII* *GAL1* promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* *FLP* terminator fragment was inserted into
25 this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YlpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in the *KpnI-AatII*-opened and blunted YlpUT resulted in the plasmid YlpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-openend and blunted YlpUTy resulted in the plasmid YlpUTyL.

- Mouse *bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned
30 into the *XbaI-HindIII*-opened plasmid YlpUTyL, obtaining the final expression plasmid YlpUTyLMuBax.

The plasmid YlpUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results**Induction of Bax-expression in yeast cells**

A preculture of yeast strain INVSc1 containing YlpUTyLMuBax, wherein 5 Bax cassettes under the control of the *GAL1* promotor are integrated in the genome near Ty δ elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YlpUTyL as a control. The precultures were diluted in 100-ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

RNA isolation

Total RNA was isolated using RNAPure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells
5 were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA
10 pellet was resuspended in 50 µl RNase free dH₂O.

First strand cDNA synthesis in the presence of α -³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL yeast cells and incorporation of α -³³P
15 dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6 µl 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)
1 µl 0,1 M DTT
20 1 µl RNase Block (40 units/µl) (Stratagene)
1,5 µl 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)
1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
10 µl α -³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala,
25 Sweden),

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 5.10⁸ cpm/µg for both
30 the INVSc1YlpUTyL and the INVSc1 YlpUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α -³²P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during
5 hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5 µl polydA (1 µg/ml) and incubated for 24 hours at 42°C
10 whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0.5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a
15 PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50 µm using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

Example 2. Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time
20 point. An overview of the up and down regulated genes modulated in function of induction of Bax expression for several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

Example 3. Comparative gene expression analysis upon Bax-induced cell death and**H₂O₂-induced cell death****The oxidative H₂O₂-challenge**

A preculture of yeast strain INVSc1 containing YlpUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were
35 transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H₂O₂, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

First strand cDNA synthesis in the presence of α -³²P dCTP

- 5 RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YlpUTyL yeast cells.
- The specific activity of all probes was $5 \cdot 10^8$ cpm/ μ g.

10

Quantification of Hybridisation Signals

- Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics, 15 Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

Identification of Bax-responsive genes

- Pairwise comparisons of the normalised data obtained from INVSc1 YlpUTyLMuBax (B) and 20 INVSc1 YlpUTyL (C) revealed differentially expressed genes. To determine the -fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (*replacement*).

25 ***Identification of Bax-specific genes within the Bax-responsive pool***

- Pairwise comparisons of the normalised data obtained from INVSc1 YlpUTyLMuBax (B) and INVSc1 YlpUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background 30 value. The normalised data of the Bax-responsive genes were compared with data obtained from the H₂O₂-stressed INVSc1 YlpUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

Example 4. Search for homologues in *Candida albicans* and human

- 5 Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and
- 10 Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA). Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the
- 15 similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.
- The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

20 **Example 5. Screening for compounds modulating expression of polypeptides involved in Induction of cell death of *C. albicans***

- The method proposed is based on observations (Sandbakken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity
- 25 to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.
- Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbakken *et al.*, 1990). Such strains are more
- 30 sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 6. Assay for High Throughput screening for drugs

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (± 0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Example 7. Yeast cell viability assay upon induction of Bax expression

Materials and media

Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the *YGR183C* gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

Plasmid constructions

The Bax expression cassette, a *BsgI*(blunted)-*SapI*(blunted) fragment excised from YlpUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *Eco*136II-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD₆₀₀. Cells were pelleted by centrifugation and washed two times with sterile dH₂O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

Example 8. Bax Expression In Candida cells

Strains

The *Candida albicans* strain CAI4 (*ura3^Δ*) was used to perform the experiments (Fonzi and Irwin 1993).

E. coli transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (F' *mcrA* Δ (*mrr-hsdRMS-mcrBC*) Δ 80/*lacZ* Δ M15 Δ *lacX74* *deoR* *recA1* *araD139* Δ (*ara-leu*)7697 *galU* *galK* *rpsL* (Str^R) *endA1* *nupG*).

Media

Synthetic dextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CAI4), the media was supplemented with

50µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic *BAX* gene was performed using 2% galactose as carbon source.

Construction of the codon-optimised *BAX* gene

- 5 Construction of the synthetic *BAX* gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, et al. 1991; <http://alces.med.umn.edu/candida/codons.html>; <http://www.kazusa.or.jp/codon>). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic *BAX* gene.
 - 10 The synthCa*BAX* gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst* I site and a *Bgl* II site. The *Pst* I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl* II site served as a linker for a *yEGFP* fusion. Primer C2 introduced a *Sma* I site, suitable for cloning into the expression vector.
 - 15 Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO
 - 20 vector (Stratagene). All three fragments were sequenced to ensure that no mutation was introduced by the PCR.
- Subsequently, fragment A was digested with *Pst* I and *Taq* I, fragment B with *Taq* I and *Bam* HI and fragment C with *Bam* HI and *Sma* I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst* I and *Sma* I resulting in the plasmid pUC21:synthCandida*BAX*.
- 25 The sequence of the synthetic *BAX* gene is shown in Figure 6.

Construction of synthetic *BAX*- and *GFP*-synthetic *BAX* expression plasmids

- A *Pst* I-*Sma* I fragment containing the ORF of the synthetic *BAX* gene was cloned into the *Pst* I-*Stu* I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in
- 30 the expression construct pGAL1P:synthCa*BAX* (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position -3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.

- The yeast enhanced *GFP* gene *yEGFP*, (Cormack et al. 1997) was amplified by PCR using
- 35 primer 5'-AACTGCAGATGTCTAAAGGTGAAGAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGAAGATCTTCCTTTGTACAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the *yEGFP* gene into the pCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

- 5 The *yEGFP*-synth *Candida BAX* fusion was created by cloning a *Pst*I-*Bgl*II *yEGFP* fragment together with a *Bgl* II-*Sma* I synthetic *Candida BAX* fragment into the *Pst* I-*Stu* I digested expression vector pGAL1ACT1LUC. The obtained pGAL1P:*yEGFP*-synthCa*BAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

10 **Creation of the synthetic *BAX* expression strains**

Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.* 1992). The plasmids were linearised with *Bpu*1102 I to allow directed integration into the genome at the GAL1 promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different transformants was prepared using the Nucleon[®] extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The *BAX* probe used in the Southern blot was prepared by PCR. The PCR was performed using the pGAL1P:synthCa*BAX* plasmid as template, together with the sense primer 5'-ATGGATGGTTCTGGTGAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCCATTTTTCAGATG-3' (SEQ ID NO 14). Standard PCR conditions were used. For detection of the *yEGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

25

Western blot analysis

For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce *Bax* expression. Induction was performed for 15 hours. Yeast crude extracts were prepared as described before (Sambrook, Fritsch *et al.* 1989). Detection of the *Bax* protein was performed using a polyclonal rabbit anti-mouse /rat *Bax* antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.* 1999). Detection of the *Gfp* protein was done using an anti-*Gfp* monoclonal antibody (Molecular Probes, Eugene, OR, USA).

35

Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD₆₀₀ of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in microtitre plates using the Bioscreen C system (Labsystems).

Viability tests

Cells were pregrown in minimal dextrose medium to an OD₆₀₀ of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse Bax protein was placed under control of the *Candida albicans* GAL1 promoter allowing for conditional expression when cells are grown in galactose containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the yEGFP to allow screening for transformants with a high yEGFP-synthCaBAX expression level using FACS technology. The newly obtained plasmids pGAL1P:synthCaBAX and pGAL1:GFP-synthCaBAX were transformed into the *C. albicans* CAI4 strain. Transformants were selected on uridine-free minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on minimal galactose medium (inducing conditions). After two days incubation at 30°C all transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCaBAX gene had been integrated into the endogenous copy of the GAL1 promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently, cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was

observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCaBAX transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the GFP-synthCaBAX expressing strains. Here the fusion protein was detected at the expected molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the GFP-synthCaBAX expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCaBAX strain and the GFP-synthCaBAX strain. The synthCaBAX strain showed quite a rapid decrease in the amount of colony forming units during the first 6 hours of incubation on galactose containing media. Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

Oligo	Sequence 5' → 3'
A1	AACTGCAGGAAGATCTCCATGGATGGTTCTGGTGAACAATTGGGTTCTGGTGG TCCAACCTCTTCTGAACAATCATGAACCGTGCTTCTTGTTG (SEQ ID NO 3)
A2	TAGAAGCATCTTGTGGTGGTTGTTCCAAGTCAATTCTGGGTTTCAACGACC ATTCTACCAGCTCTATCTTGGATGAACCTTGCAACAAGAACACC (SEQ ID NO 4)
A3	GGAATTC7CGACATCAGCGATCATTCTTTGCAATTCATGTTAGAAATCCAATTC ATCACCGATTCTTCTCAAAACATTCAGACAATTTTTTGGTAGAAGCATCTTGTG (SEQ ID NO 5)
B1	GGAATTCGCTGATGTCGATACCGATTCTCCAAGAGAAGTCTTCTTCAGAGTCG CTGCTGATATGTTGCTGATGGTAACCTCAACTG (SEQ ID NO 6)
B2	AATTCTGGGACTTTGGTACACAAGCTTTCAAGACCAATTTAGAAGCGAAGTA GAACAAGCGACGACTCTACCCAGTTGAAGTTACCA (SEQ ID NO 7)
B3	CCACCTTGATCTTGGATCCAGACCAACAATCTTTCTCTCAAGAAATCCAAGGTC CAACCCATGATGGTTCTGATCAATTCTGGGACTTTG (SEQ ID NO 8)
C1	ATTGTTGGTCTGGATCCAAGATCAAGGTGGTTGGGAAGGTTTGTGTTACTT CGGTACCCCAACCTGGCAACCGTCA (SEQ ID NO 9)
C2	TCCCCGGGGGATTAAACCATTTTTCAGATGGTCAAGAAGCGGTCAAGAC ACCAGCGACGAAGATGGTGACGGTTTGCCAGGTTGGG (SEQ ID NO 10)

Table 2: Overview of the differentially expressed genes after 30 min Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Cell	Gene	Normalized expression	Log fold	P-value	
Cellular role : Cell cycle control					
YBR133C	HSL7	18932.54	37877.20	↑	2.00
Cellular role : Polymerase II transcription					
YDR253C	MET32	17661.13	45567.17	↑	2.58
YBR112C	SSN6	26698.87	65315.83	↑	2.45
YDR145W	TAF61	38697.96	73117.62	↑	1.89
YBR289W	SNF5	33111.77	72328.70	↑	2.18
YDR216W	ADR1	30127.45	8815.87	↓	3.42
YEL009C	GCN4	16533.76	3030.44	↓	5.48
YBR089C-A	NHP6B	22698.63	6297.49	↓	3.60
YMR043W	MCM1	39141.64	84180.45	↑	2.15
YKR092C	SRP40	5965.63	16105.82	↑	2.70
YMR273C	ZDS1	14899.61	35508.04	↑	2.42
YPL089C	RLM1	34922.91	67856.88	↑	1.94
YOR372C	NDD1	20285.12	44445.20	↑	2.19
YPL037C	EGD1	30833.33	5250.70	↓	5.83
Cellular role : Cell polarity					
YBL085W	BOI1	7693.29	18614.99	↑	2.42
Cellular role : Chromatine structure					
YBR009C	HHF1	16888.00	4178.80	↓	3.99
YNL030W	HHF2	49878.04	12566.96	↓	3.97
YDR224C	HTB1	67355.40	23156.82	↓	2.91
YBL002W	HTB2	25269.02	5383.97	↓	4.69
Cellular role: RNA processing					
YER112W	USS1	12776.74	31470.70	↑	2.46
YPL190C	NAB3	6381.36	17892.11	↑	2.80
YNL112W	DBP2	9956.84	28036.48	↑	2.82
Cellular role: Energy generation					
YPL078C	ATP4	26902.69	5980.38	↓	4.50
YDL004W	ATP16	36525.08	3004.34	↓	12.16
YDR377W	ATP17	14419.41	756.88	↓	19.05
YDR529C	QCR7	35346.95	5394.65	↓	6.55
YGR008C	STF2	13275.51	2276.27	↓	5.83
YEL039C	CYC7	13604.38	2689.66	↓	5.06
YKL150W	MCR1	105337.87	30743.75	↓	3.43
YLR038C	COX12	52687.73	5455.83	↓	9.66
YLR327C		113.986.77	54.014.65	↓	2.11
Cellular role: Carbohydrate metabolism					
YBR149W	ARA1	15149.55	4095.17	↓	3.70
YHR094C	HXT1	12528.90	785.73	↓	15.94
YDR345C	HXT3	36643.13	1632.48	↓	22.45
YDR343C	HXT6	77064.71	32060.05	↓	2.40
YDR342C	HXT7	76349.13	27615.15	↓	2.76
Cellular role: Signal transduction					
YER177W	BMH1	22856.29	44771.71	↑	1.96
YDR099W	BMH2	40127.38	74572.38	↑	1.86

YGR070W	ROM1	12055.28	28169.57	↑	2.34
YGR023W	MTL1	7354.78	19648.06	↑	2.67
<i>Cellular role: Protein synthesis</i>					
YGR034W	RPL26B	71942.48	74625.22	↑	1.04
<i>Cellular role: Protein folding</i>					
YLR216C	CPR6	9616.80	31126.02	↑	3.24
<i>Cellular role: Protein modification/degradation</i>					
YFR052W	RPN12	5583.57	14855.87	↑	2.66
YDL147W	RPN5	31932.20	52939.11	↑	1.66
YGR132C	PHB1	15429.56	5591.19	↓	2.76
YGR135W	PRE9	39921.63	5517.17	↓	7.24
YFR010W	UBP6	1892.76	828.94	↓	2.28
<i>Cellular role: Cell stress</i>					
YIR037W	GPX3	7869.22	21789.00	↑	2.77
YDR513W	TTR1	55988.32	33263.12	↓	1.68
YOL035C	GRX1	70248.30	10969.97	↓	6.40
YFL014W	HSP12	41689.29	18658.48	↓	2.23
YHR053C	CUP1A	72852.07	43488.52	↓	1.68
YHR055C	CUP1B	71934.03	56799.80	↓	2.77
YMR173W	DDR48	16670.70	5022.40	↓	3.32
YMR251W-A	HOR7	26879.95	417.36	↓	64.41
YLR043C	TRX1	58251.39	4435.79	↓	13.13
YBL064C	PRX1	21525.00	40969.00	↑	1.90
YOL151W	GRE2	2624.55	24152.03	↑	9.20
<i>Cellular role: Unknown</i>					
YBL081W		73834.11	74612.35	↑	1.01
YDR366C		39998.46	57428.80	↑	1.44
YCR004C	YCP4	6869.06	28115.73	↑	4.09
YCR013C		3988.55	15144.34	↑	3.80
YBR050C	REG2	4687.91	14408.20	↑	3.07
YBL109W		18744.60	35440.24	↑	1.89
YDR154C		19565.23	69428.03	↑	3.55
YEL071W	DLD3	22235.73	68790.83	↑	3.09
YHR095W		14426.76	34896.68	↑	2.42
YGR069W		43413.57	72420.39	↑	1.67
YDR544C		13567.00	27004.37	↑	1.99
YGR236C		24927.59	8032.35	↓	3.10
YIL057C		24246.39	773.56	↓	31.34
YGL080W		23425.00	3217.81	↓	7.28
YGL072C		16437.52	2652.80	↓	6.20
YHR056C	RSC30	72072.88	57446.85	↓	1.25
YKL054C	VID31	17990.49	38258.80	↑	2.13
YLR311C		7892.40	24164.87	↑	3.02
YJR115W		64690.89	102068.34	↑	1.58
YJL188C	BUD19	7580.28	22325.70	↑	2.95
YKR040C		50934.78	100733.41	↑	1.98
YLR053C		8117.66	20317.34	↑	2.50
YOR121C		59950.94	92470.43	↑	1.54
YNL143C		98911.28	110534.34	↑	1.12
YOR131C		7841.55	22353.72	↑	2.81
YNL338W		21800.45	38777.28	↑	1.78
YNL179C		13729.36	39516.53	↑	2.88
YOL150C		3408.74	60298.39	↑	17.69

YMR107W		65118.70	10042.48	↓	6.48
YKL065C	YET1	69556.19	12804.88	↓	5.43
YJR096W		21780.37	10655.13	↓	2.04
YJL161W		16468.73	2618.26	↓	6.29
YML128C	MSC1	80130.20	13785.84	↓	5.81
YMR251W		26879.95	417.38	↓	64.41
YMR173W-A		110104.98	61951.23	↓	1.78
YPL201C		17913.32	5018.97	↓	3.57
YOR285W		64074.73	28749.43	↓	2.15
YOR286W		13458.08	733.06	↓	18.38
<i>Cellular role: Cell wall maintenance</i>					
YKR076W	ECM4	2674.15	13040.04	↑	4.88
YLR390W	ECM19	5472.05	15145.85	↑	2.77
<i>Cellular role: Membrane fusion</i>					
YHR138C		19921.35	3707.57	↓	5.37
<i>Cellular role: Vesicular transport</i>					
YHR161C	YAP180A	13086.35	30160.90	↑	2.30
YPL085W	SEC18	6668.57	15208.49	↑	2.28
YKL196C	YKT6	18933.84	2890.07	↓	6.55
YPR028W	YIP2	25434.34	2049.47	↓	12.41
<i>Cellular role: DNA repair/recombination</i>					
YDL059C	RAD59	1948.61	13089.13	↑	6.72
<i>Cellular role: DNA synthesis</i>					
YEL032W	MCM3	23422.85	44327.48	↑	1.89
<i>Cellular role: Amino acid metabolism</i>					
YIL074C	SER33	3978.42	16702.66	↑	4.20
YGR155W	CYS4	4184.59	19270.89	↑	4.61
<i>Cellular role: Fatty acid metabolism</i>					
YHR179W	OYE2	2291.36	40274.02	↑	17.58
<i>Cellular role: Protein translocation</i>					
YNL131W	TOM22	16287.21	1679.78	↓	9.70
<i>Cellular role: Small molecule transport</i>					
YDR276C	SNA1	21148.48	1580.68	↓	13.38
YOR267C	HRK1	62689.30	110516.24	↑	1.76
YHR039-C	VMA10	60107.90	6490.93	↓	7.08
YOR382W	FIT2	6780.82	27236.15	↑	4.02

Table 3: Overview of the differentially expressed genes after 1h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Gene	Gene	Normalised YlpUTL	Normalised YlpUTyLB	Up/Down	Q value
Cellular role : Polymerase II transcription					
YDR145W	TAF61	20729.58	57376.27	↑	2.77
YDR216W	ADR1	5925.91	18459.00	↑	3.11
YBR112C	CYC8	50186.77	84511.50	↑	1.29
YMR043W	MCM1	21011.54	53700.49	↑	2.56
YPL089C	RLM1	23440.54	64284.32	↑	2.74
YOR372C	NDD1	26412.58	50804.99	↑	1.92
Cellular role : Cell cycle control					
YBR133C	HSL7	18761.64	53238.86	↑	2.84
Cellular role : Cell polarity					
YBL085W	BOI1	37895.40	57761.52	↑	1.52
Cellular role : Chromatine structure					
YDR224C	HTB1	13661.40	55656.34	↑	4.07
Cellular role: Energy generation					
YGR183C	QCR9	23181.54	81865.40	↑	3.53
YLR294C		5054.57	28994.72	↑	5.74
YKL150W	MCR1	43663.07	60593.16	↑	1.39
YMR256C	COX7	7606.58	28801.54	↑	3.79
YOL126C	MDH2	34144.81	65326.97	↑	1.91
YLR327C		97415.94	101651.17	↑	1.04
Cellular role: Vesicular transport					
YHR181C	YAP180A	11602.81	34695.20	↑	2.99
YLR206W	ENT2	14439.24	34621.70	↑	2.40
Cellular role: Carbohydrate metabolism					
YDR342C	HXT7	65273.56	22231.08	↓	2.94
YDR343C	HXT6	43572.28	6075.38	↓	7.17
YDR345C	HXT3	76352.52	40298.00	↓	1.89
YGR192C	TDH3	38472.30	14145.84	↓	2.72
YKR097W	PCK1	22919.81	38225.98	↑	1.67
YOR374W	ALD4	33711.37	2607.43	↓	12.93
Cellular role: Signal transduction					
YER177W	BMH1	16298.14	31748.91	↑	1.95
YDR099W	BMH2	50572.45	65123.58	↑	1.29
Cellular role: Cell wall maintenance					
YLR110C	CCW12	102525.29	11230.41	↓	9.13
Cellular role: Protein modification/degradation					
YOR261C	RPN8	12575.49	32568.47	↑	2.59
Cellular role: Cell stress					
YHR053C	CUP1A	32531.53	63579.94	↑	1.95
YHR055C	CUP1B	27939.92	65142.82	↑	2.33
YMR173W	DDR48	38338.83	60514.70	↑	1.58
YOR031W	CRS5	2922.32	23848.60	↑	8.16

YLR109W	AHP1	43067.08	6302.46	↓	6.83
Cellular role: Unknown					
YBL081W		82476.13	44279.86	↑	1.86
YBL109W		22998.63	63428.23	↑	2.76
YDR386C		14599.17	46494.73	↑	3.18
YDR154C		21298.57	56534.93	↑	2.65
YGR236C	SPG1	17717.80	64439.96	↑	3.64
YHR056C	RSC30	27020.16	65110.42	↑	2.41
YGR182C		8171.02	34669.96	↑	4.24
YDR544C		14797.70	37704.91	↑	2.55
YHR162W		13836.79	33381.64	↑	2.41
YGR243W		30829.68	59765.39	↑	1.94
YBR050C	REG2	14008.24	29603.16	↑	2.11
YEL071W	DLD3	19487.41	35273.39	↑	1.81
YDR133C		83074.54	62988.96	↓	1.32
YDR134C		83111.03	16839.53	↓	4.94
YHL021C		46028.06	8577.00	↓	5.37
YKL054C	VID31	28018.46	66537.91	↑	2.37
YLR311C		7803.52	31160.73	↑	3.99
YMR107W		13453.15	78850.98	↑	5.86
YKL066W		6751.84	24129.32	↑	2.76
YMR173W-A		38338.83	60514.70	↑	1.58
YML053C		23670.86	66254.48	↑	2.80
YOR121C		17039.58	58016.58	↑	3.40
YOL106W		19917.67	69853.66	↑	3.51
YNL338W		17864.90	49911.08	↑	2.79
YJR115W		84858.02	98161.71	↑	1.16
Cellular role: Small molecule transport					
YOR267C	HRK1	90123,84	96824,51	↑	1,07

Table 4: Overview of the differentially expressed genes after 2h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised intensities L	Normalised intensities VUB	Up/Down	Log value
Cellular role: Protein modification/degradation					
YCL052C	PBN1	5264.22	8175.70	↑	1.55
YDL147W	APN5	22386.40	47857.67	↑	2.14
YOR281C	APN8	27349.25	42198.05	↑	1.54
YGR132C	PHB1	5252.03	8459.53	↑	1.61
YBR139W		9458.26	3611.21	↓	2.62
Cellular role : Unknown					
YDR202C	RAV2	7483.71	10089.19	↑	1.35
YBR062C		4893.97	9894.82	↑	2.02
YDR366C		25468.2	59682.92	↑	2.34
YBL109W		24803.62	37444.64	↑	1.51
YDR154C		21168.26	33434.35	↑	1.58
YEL071W	DLD3	34153.85	44083.39	↑	1.29
YGR236C	SPG1	16978.52	31419.12	↑	1.85
YGR182C		30569.31	58805.05	↑	1.92
YDR544C		15937.14	24421.99	↑	1.53
YHR162W		26810.34	33794.73	↑	1.27
YHR056C	HSC30	33372.68	68425.24	↑	2.05
YDR133C		75520.99	62984.59	↓	1.20
YCR010C	ADY2	17240.59	11835.82	↓	1.46
YDR134C		72723.66	9776.23	↓	7.44
YGR069W		65418.73	53767.35	↓	1.22
YIL057C		16510.16	2198.04	↓	7.51
YGL072C		12209.68	6509.91	↓	1.88
YGL080W		22550.76	11525.24	↓	1.96
YLR311C		11095.31	24660.47	↑	2.22
YJR115W		74757.79	103422.48	↑	1.38
YMR099C		7057.15	11477.42	↑	1.63
YMR173W-A		31901.05	48886.91	↑	1.47
YML132W	COS3	24648.97	34895.33	↑	1.42
YKL066W		13581.94	25433.97	↑	1.87
YJL142C		7205.86	11920.21	↑	1.65
YLR346C		6447.57	11589.83	↑	1.79
YLR053C		41161.10	78636.82	↑	1.91
YMR110C		19410.64	29861.23	↑	1.53
YKR075C		19104.57	29948.72	↑	1.57
YOR121C		36492.56	59452.09	↑	1.63

Cellular role : Unknown					
YOL108W		31382.10	76664.72	↑	2.44
YNL338W		24117.93	38981.22	↑	1.62
YNL134C		9617.33	14613.60	↑	1.52
YKL065C	YET1	52422.65	33794.03	↓	1.55
YMR009W		20666.22	9519.29	↓	2.17
YJL144W		10316.92	3122.77	↓	3.30
YML128C	MSC1	584128.13	25434.11	↓	2.29
YNL179C		21938.96	10883.98	↓	2.02
YOL109W	ZEO1	22711.98	6581.11	↓	3.45
YNR002C	FUN34	18241.25	9752.25	↓	1.87
Cellular role: Chromatine structure					
YDR224C	HTB1	25356.73	30827.54	↑	1.22
YBL002W	HTB2	9241.68	14261.54	↑	1.54
YBL003C	HTA2	3453.55	6553.49	↑	1.90
YNL031C	HHT2	13376.02	2348.64	↓	5.69
Cellular role: Polymerase II transcription					
YBR289W	SNF5	59542.27	65885.13	↑	1.11
YDR073W	SNF11	12190.01	23088.03	↑	1.89
YMR043W	MCM1	66457.16	77022.05	↑	1.16
YPL089C	RLM1	49844.99	60624.28	↑	1.22
Cellular role : Signal transduction					
YDR099W	BMH2	55902.13	73874.51	↑	1.32
Cellular role: Cell stress					
YBL064C	PRX1	11203.87	14815.42	↑	1.32
YBR101C		25016.27	35781.64	↑	1.43
YLR043C	TRX1	10864.53	3912.03	↓	2.78
YGR209C	TRX2	30492.33	37829.20	↑	1.24
YER103W	SSA4	8763.38	15799.18	↑	1.80
YHR055C	CUP1B	18824.43	77613.05	↑	4.12
YHR053C	CUP1A	32726.82	63536.72	↑	1.94
YDR256C	CTA1	9614.29	4232.17	↓	2.27
YCR021C	HSP30	8090.05	3604.78	↓	2.24
YCL035C	GRX1	28437.57	12843.99	↓	2.21
YGR086C		36796.12	24272.57	↓	1.52
YFL014W	HSP12	61868.64	23288.19	↓	2.66
YOR031W	CRS5	6015.69	14519.12	↑	2.41
YMR251W-A	HOR7	17731.14	4231.39	↓	4.19
YOR120W	GCY1	114252.98	78052.05	↓	1.46
Cellular role: Protein synthesis					
YAL003W	EFB1	3044.80	5772.68	↑	1.90
YOL127W	RPL25	6266.96	12055.41	↑	1.92
YHR010W	RPL27	4057.16	10856.34	↑	2.68
YLR325C	RPL38	5401.85	12955.89	↑	2.40
YJL189W	RPL39	2044.64	8010.67	↑	3.92
YIL148W	RPL40A	5052.35	11595.54	↑	2.30
YKR094C	RPL40B	3994.57	10011.13	↑	2.54
YOL139C	CDC33	4132.18	8956.14	↑	2.17

Cellular role : Protein folding					
YLR216C	CPR6	20353.43	32713.37	↑	1.61
YKL117W	SBA1	11144.25	1500.56	↓	7.43
Cellular role: Vesicular transport					
YCR009C	RVS181	5350.32	9780.92	↑	1.83
YHR161C	YAP180A	25136.63	32481.67	↑	1.29
YBL078C	AUT7	18528.91	9843.25	↓	1.68
Cellular role : Carbohydrate metabolism					
YBL058W	SHP1	4626.50	8179.94	↑	1.77
YBR149W	ARA1	30706.41	9637.76	↓	3.19
YDR178W	SDH4	14880.91	6237.35	↓	2.39
YHR094C	HXT1	30389.99	18383.00	↓	1.65
YMR011W	HXT2	39524.90	21221.96	↓	1.86
YDR345C	HXT3	77025.40	58749.40	↓	1.36
YDR343C	HXT6	73149.70	8676.17	↓	8.43
YDR342C	HXT7	75331.76	27052.43	↓	2.78
YKL060C	FBA1	16273.54	21323.23	↑	1.31
Cellular role : Cell cycle control					
YBR133C	HSL7	32903	41984.32	↑	1.28
Cellular role : Energy generation					
YMR256C	COX7	18558.01	40422.91	↑	2.18
YML129C	COX14	11418.54	21798.88	↑	1.91
YFR033C	QCR6	9159.48	13398.67	↑	1.46
YDR529C	QCR7	24821.75	16556.87	↓	1.50
YJL166W	QCR8	15554.30	24509.26	↑	1.58
YHR001W-A	QCR10	12416.35	23465.31	↑	1.89
YBR039W	ATP3	11709.79	3088.19	↓	3.79
YPL078C	ATP4	11325.64	13769.72	↑	1.22
YPL271W	ATP15	3261.75	7839.05	↑	2.40
YLR327C		51742.90	128511.27	↑	2.48
YLR294C		15832.61	38544.44	↑	2.43
YAL060W	FUN49	11792.72	5778.91	↓	2.04
Cellular role: Small molecule transport					
YDR276C	SNA1	19337.39	12392.29	↓	1.56
YGR197C	SNG1	4766.18	10484.09	↑	2.20
YHR039C-B	VMA10	21190.93	10592.98	↓	2.00
YOR267C	HRK1	111849.17	101339.10	↓	1.10
Cellular role: RNA processing					
YGR250C		8709.92	17358.43	↑	1.99
Cellular role : Cell wall maintenance					
YER150W	SPI1	55592.73	22403.59	↓	2.48
YLR110C	OCW12	35147.41	5786.88	↓	6.07
Cellular role : Cell polarity					
YOR122C	PFY1	14459.45	20176.41	↑	1.40
Cellular role : Amino acid metabolism					
YPR035W	GLN1	20894.14	7522.05	↓	2.78

Table 5: Overview of the differentially expressed genes after 3h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Gene	Gene	Normalized Gene expression	Normalized Gene expression	Up/down	CR2/CR1
<i>Cellular role : Cell cycle control</i>					
YBR133C	HSL7	63562.10	43191.28	↓	1.47
<i>Cellular role : Cell polarity</i>					
YBL085W	BOI1	32734.79	23497.41	↓	1.39
<i>Cellular role : Chromatine structure</i>					
YDR545W	YRF1-1	20111.51	11479.67	↓	1.75
<i>Cellular role: Energy generation</i>					
YCR005C	CIT2	11882.42	25632.94	↑	2.16
YGR183C	QCR9	74474.20	11510.99	↓	6.47
YOL126C	MDH2	55984.88	17978.10	↓	3.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR019C	GAL10	3092.50	15697.54	↑	5.08
YDR345C	HXT3	14086.41	25657.66	↑	1.82
YKR097W	PCK1	50736.44	20858.02	↓	2.43
<i>Cellular role: Signal transduction</i>					
YDR099W	BMH2	63285.16	56028.91	↓	1.13
<i>Cellular role: Protein synthesis</i>					
YHR010W	RPL27A	23254.80	7217.14	↓	3.22
YLR325C	RPL38	26725.96	9121.29	↓	2.93
<i>Cellular role: Cell stress</i>					
YFL014W	HSP12	40848.44	69781.91	↑	1.71
YHR053C	CUP1A	20399.10	65037.14	↑	3.19
YHR055C	CUP1B	21763.09	64594.58	↑	2.97
YMR173W	DDR48	75407.16	36354.37	↓	2.07
YOL052C-A	DDR2	20479.72	33702.23	↑	1.65
<i>Cellular role: Unknown</i>					
YIL057C		7602.78	24104.02	↑	3.17
YHR056C	RSC30	41473.41	64809.08	↑	1.56
YDR544C		55075.67	29731.72	↓	1.85
YKR040C		48049.71	59849.47	↑	1.24
YNL338W		86107.91	30045.62	↓	2.87
YJR115W		74889.58	81238.98	↓	1.08
YBL109W		64754.79	57185.99	↓	1.13
YMR173W-A		75407.16	36354.37	↓	2.07

Table 6: Overview of the differentially expressed genes after 6h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

OFF	Gene	Normalised transcript	Yp	Up/down	Q-value
Cellular role: Cell stress					
YDR171W	HSP42	13484.04	27183.07	↑	2.02
YFL014W	HSP12	41197.12	29081.08	↓	1.42
YDR513W	TTR1	19985.22	12935.62	↓	1.54
YCL035C	GRX1	31735.39	12930.71	↓	2.45
YGR209C	TRX2	54455.65	47569.21	↓	1.14
YHR053C	CUP1A	81488.84	15289.39	↓	5.33
YHR055C	CUP1B	81278.95	20031.69	↓	4.06
YMR251W-A	HOR7	18824.54	5914.28	↓	3.18
Cellular role: Signal transduction					
YDR099W	BMH2	29412.99	58598.42	↑	1.99
Cellular role: Protein synthesis					
YGL147C	RPL9A	13655.66	1585.97	↓	8.61
YGR085C	RPL11B	27465.15	3791.35	↓	7.24
YDR418W	RPL12B	14417.77	1555.24	↓	9.27
YLR029C	RPL15A	37122.11	9321.81	↓	3.98
YOR312C	RPL20B	50334.94	5706.59	↓	8.82
YBR191W	RPL21A	21740.90	2571.30	↓	8.46
YPL079W	RPL21B	31059.43	5023.61	↓	6.18
YOL127W	RPL25	75971.72	11749.17	↓	6.47
YHR010W	RPL27A	45716.64	8096.40	↓	5.65
YDR471W	RPL27B	14636.79	2613.40	↓	5.60
YDL075W	RPL31A	11969.47	2611.53	↓	4.58
YBL092W	RPL32	7872.80	857.85	↓	9.18
YDL191W	RPL35A	28582.59	6048.25	↓	4.73
YDL136W	RPL35B	25433.49	5084.51	↓	5.02
YLR325C	RPL38	48051.23	8217.18	↓	5.85
YIL148W	RPL40A	47028.95	9543.65	↓	4.93
YKR094C	RPL40B	39900.50	5957.78	↓	6.70
YHR141C	RPL42B	10163.88	937.21	↓	10.84
YML063W	RPS1B	15916.48	1144.54	↓	13.91
YGL123W	RPS2	12505.56	2243.26	↓	5.57
YOR096W	RPS7A	24164.37	3223.60	↓	7.50
YBL072C	RPS8A	17198.50	3233.30	↓	5.32
YER102W	RPS8B	16234.83	1791.18	↓	9.06
YBR189W	RPS9B	10075.22	2150.89	↓	4.68
YOR293W	RPS10A	51787.23	12110.74	↓	4.28
YDR064W	RPS13	9736.57	1587.67	↓	6.13
YDR450W	RPS18A	37913.71	5674.60	↓	6.88
YML026C	RPS18B	14458.01	2027.28	↓	7.13
YKL156W	RPS27A	23725.18	11117.26	↓	2.13
YLR167W	RPS31	38648.54	2611.97	↓	14.80
YJL138C	TIF2	20154.61	7264.66	↓	2.77
Cellular role: Energy metabolism					
YGR183C	QCR9	57357.59	60447.53	↑	1.40
YDL004W	ATP16	25047.95	10988.85	↓	2.28
YKL150W	MCR1	50931.46	37076.83	↓	1.37

YLR038C	COX12	39506.08	29534.70	↓	1.34
<i>Cellular role: Unknown</i>					
YDR442W		14654.61	2242.42	↓	6.54
YDR134C		17025.59	10561.72	↓	1.61
YHR056C	RSC30	81350.52	31447.10	↓	2.59
YKR040C		48390.21	90125.88	↑	1.86
YLR414C		13463.40	8085.92	↓	1.67
YLR312C		25589.67	16184.57	↓	1.58
YJL188C	BUD19	22074.09	4528.39	↓	4.88
YOR285W		75099.98	61898.00	↓	1.21
YOL109W	ZEO1	66287.15	35502.43	↓	1.87
<i>Cellular role: Chromatine structure</i>					
YBR009C	HHF1	11173.15	5416.74	↓	2.06
YNL030W	HHF2	31366.74	20132.23	↓	1.56
<i>Cellular role: Nucleotide metabolism</i>					
YDR399W	HPT1	13339.03	5333.81	↓	2.50
<i>Cellular role: Polymerase II transcription</i>					
YEL009C	GCN4	34617.98	20798.63	↓	1.66
YPL037C	EGD1	17862.37	8229.01	↓	2.17
<i>Cellular role: Vesicular transport</i>					
YBL078C	AUT7	42661.70	32333.01	↓	1.32
YOR327C	SNC2	22716.56	13704.48	↓	1.66
<i>Cellular role : Small molecule transport</i>					
YHR039C-B	VMA10	44429.30	23826.51	↓	1.86
<i>Cellular role : Cell wall maintenance</i>					
YKL097W-A	CWP2	13529.93	1617.20	↓	8.37
<i>Cellular role: Carbohydrate metabolism</i>					
YKL060C	FBA1	33329.74	10367.82	↓	3.21

Table 7:

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 17	YAL003W	EFB1			1.90		
SEQ ID NO 19	YAL060W	FUN49			-2.00		
SEQ ID NO 21	YBL002W	HTB2	-4.69		1.54		
SEQ ID NO 23	YBL058W	SHP1			1.77		
SEQ ID NO 25	YBL064C	PRX1	1.90		1.32		
SEQ ID NO 27	YBL072C	RPS8A					-5.32
SEQ ID NO 29	YBL081W		1.01	1.88			
SEQ ID NO 31	YBL085W	BOI1	2.42	1.52		-1.39	
SEQ ID NO 33	YBL092W	RPL32			2.76		-9.18
SEQ ID NO 35	YBL109W		1.89	2.76	1.51	-1.13	
SEQ ID NO 37	YBR009C	HHF1	-3.99				-2.06
SEQ ID NO 39	YBR019C	GAL10				5.08	
SEQ ID NO 41	YBR039W	ATP3			-3.70		
SEQ ID NO 43	YBR050C	REG2	3.07	2.11			
SEQ ID NO 45	YBR062C				2.02		
SEQ ID NO 47	YBR089C-A	NHP6B	-3.60				
SEQ ID NO 49	YBR101C				1.43		
SEQ ID NO 51	YBR112C	SSN6	2.45	1.29			
SEQ ID NO 53	YBR133C	HSL7	2.00	2.84	1.28	-1.47	
SEQ ID NO 55	YBR139W				-2.60		
SEQ ID NO 57	YBR149W	ARA1	-3.70		-3.11		
SEQ ID NO 59	YBR189W	RPS9B					-4.68
SEQ ID NO 61	YBR191W	RPL21A					-8.46
SEQ ID NO 63	YBR289W	SNF5	2.18		1.11		
SEQ ID NO 65	YCL035C	GRX1	-8.40		-2.20		-2.45
SEQ ID NO 67	YCL052C	PBN1			1.55		
SEQ ID NO 69	YCR004C	YCP4	4.09				
SEQ ID NO 71	YCR005C	CIT2				2.16	
SEQ ID NO 73	YCR009C	RVS161			1.83		
SEQ ID NO 75	YCR010C				-1.40		
SEQ ID NO 77	YCR013C		3.80				
SEQ ID NO 79	YCR021C	HSP30			-2.20		
SEQ ID NO 81	YDL004W	ATP16	-12.16				-2.28
SEQ ID NO 83	YDL059C	RAD59	6.72				
SEQ ID NO 85	YDL075W	RPL31A					-4.58
SEQ ID NO 87	YDL147W	RPN5	1.66		2.14		
SEQ ID NO 89	YDR064W	RPS13					-6.13
SEQ ID NO 91	YDR073W	SNF11			1.89		
SEQ ID NO 93	YDR099W	BMH2	1.86	1.29	1.32	-1.13	1.99
SEQ ID NO 95	YDR133C			-1.32	-1.20		
SEQ ID NO 97	YDR134C			-4.94	-7.40		-1.61
SEQ ID NO 99	YDR145W	TAF61	1.89	2.77			
SEQ ID NO 101	YDR154C		3.55	2.65	1.58		
SEQ ID NO 103	YDR171W	HSP42					2.02
SEQ ID NO 105	YDR178W	SDH4			-2.30		
SEQ ID NO 107	YDR202C	RAV2			1.35		
SEQ ID NO 109	YDR216W	ADR1	-3.42	3.11			
SEQ ID NO 111	YDR224C	HTB1	-2.91	4.07	1.22		
SEQ ID NO 113	YDR253C	MET32	2.58				
SEQ ID NO 115	YDR256C	CTA1			-2.20		
SEQ ID NO 117	YDR276C	SNA1	-13.38		-1.50		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 119	YDR342C	HXT7	-2.76	-2.94	-2.70		
SEQ ID NO 121	YDR343C	HXT6	-2.40	-7.17	-8.40		
SEQ ID NO 123	YDR345C	HXT3	-22.45	-1.89	-1.30	1.82	
SEQ ID NO 125	YDR366C		1.44	3.18	2.34		
SEQ ID NO 127	YDR377W	ATP17	-19.05				
SEQ ID NO 129	YDR399W	HPT1					-2.50
SEQ ID NO 131	YDR418W	RPL12B					-9.27
SEQ ID NO 133	YDR513W	TTR1	-1.68				-1.54
SEQ ID NO 135	YDR544C		1.99	2.55	1.53	-1.85	
SEQ ID NO 137	YDR545W	YRF1-1				-1.75	
SEQ ID NO 139	YEL009C	GCN4	-5.46				-1.68
SEQ ID NO 697	YEL032W	MCM3	1.89				
SEQ ID NO 141	YEL039C	CYC7	-5.06				
SEQ ID NO 143	YEL071W	DLD3	3.09	1.81	1.29		
SEQ ID NO 145	YER103W	SSA4			1.80		
SEQ ID NO 147	YER112W	USS1	2.46				
SEQ ID NO 149	YER150W	SPI1			-2.40		
SEQ ID NO 151	YER177W	BMH1	1.98	1.95			
SEQ ID NO 153	YFR010W	UBP6	-2.28				
SEQ ID NO 155	YFR033C	QCR6			1.46		
SEQ ID NO 157	YFR052W	RPN12	2.66				
SEQ ID NO 159	YGL072C		-8.20		-1.80		
SEQ ID NO 161	YGL080W		-7.28		-1.90		
SEQ ID NO 163	YGL123W	RPS2					-5.57
SEQ ID NO 165	YGR008C	STF2	-5.83				
SEQ ID NO 167	YGR023W	MTL1	2.67				
SEQ ID NO 169	YGR034W	RPL26B	1.04				
SEQ ID NO 171	YGR069W		1.67		-1.20		
SEQ ID NO 173	YGR070W	ROM1	2.34				
SEQ ID NO 175	YGR086C				-1.50		
SEQ ID NO 177	YGR132C	PHB1	-2.76		1.81		
SEQ ID NO 179	YGR135W	PRE9	-7.24				
SEQ ID NO 181	YGR155W	CYS4	4.61				
SEQ ID NO 183	YGR192C	TDH3		-2.72			
SEQ ID NO 185	YGR197C	SNG1			2.20		
SEQ ID NO 187	YGR209C	TRX2			1.24		-1.14
SEQ ID NO 189	YGR243W			1.94			
SEQ ID NO 191	YGR250C				1.99		
SEQ ID NO 193	YHL021C			-5.37			
SEQ ID NO 195	YHR001W-A	QCR10			1.89		
SEQ ID NO 197	YHR039C-B	VMA10	-7.08		-2.00		-1.86
SEQ ID NO 199	YHR053C	CUP1A	-1.68	1.95	1.94	3.19	-5.33
SEQ ID NO 201	YHR055C	CUP1B	-2.77	2.33	4.12	2.97	-4.06
SEQ ID NO 203	YHR056C		-1.25	2.41	2.05	1.56	-2.59
SEQ ID NO 205	YHR094C	HXT1	-15.94		-1.60		
SEQ ID NO 207	YHR095W		2.42				
SEQ ID NO 209	YHR138C		-5.37				
SEQ ID NO 211	YHR161C	YAP180A	2.30	2.99	1.29		
SEQ ID NO 213	YHR162W			2.41	1.27		
SEQ ID NO 215	YHR179W	OYE2	17.58				
SEQ ID NO 217	YIL057C		-31.34		-7.50	3.17	
SEQ ID NO 219	YIL074C	SER33	4.20				
SEQ ID NO 221	YIR037W	GPX3	2.77				

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 223	YJL138C	TIF2					-2.77
SEQ ID NO 225	YJL142C				1.65		
SEQ ID NO 227	YJL144W				-3.30		
SEQ ID NO 229	YJL161W		-6.29				
SEQ ID NO 231	YJL166W	QCR8			1.58		
SEQ ID NO 233	YJR096W		-2.04				
SEQ ID NO 235	YJR115W		1.58	1.16	1.38	-1.08	
SEQ ID NO 237	YKL054C	VID31	2.13	2.37			
SEQ ID NO 239	YKL060C	FBA1			1.31		-3.21
SEQ ID NO 241	YKL065C	YET1	-5.43		-1.55		
SEQ ID NO 243	YKL068W			2.76	1.87		
SEQ ID NO 245	YKL097W-A	CWP2					-8.37
SEQ ID NO 247	YKL117W	SBA1			-7.43		
SEQ ID NO 249	YKL150W	MCR1	-3.43	1.39			-1.37
SEQ ID NO 251	YKL156W	RPS27A					-2.13
SEQ ID NO 253	YKL196C	YKT6	-6.55				
SEQ ID NO 255	YKR040C		1.98			1.24	1.86
SEQ ID NO 257	YKR075C				1.57		
SEQ ID NO 259	YKR076W	ECM4	4.88				
SEQ ID NO 261	YKR092C	SRP40	2.70				
SEQ ID NO 263	YKR097W	PCK1		1.67		-2.43	
SEQ ID NO 265	YLR029C	RPL15A					-3.98
SEQ ID NO 267	YLR038C	COX12	-9.66				-1.34
SEQ ID NO 269	YLR043C	TRX1	-13.13		-2.78		
SEQ ID NO 271	YLR053C		2.50		1.91		
SEQ ID NO 273	YLR109W	AHP1		-8.83			
SEQ ID NO 275	YLR110C			-9.13	-6.07		
SEQ ID NO 277	YLR206W	ENT2		2.40			
SEQ ID NO 279	YLR216C	CPR6	3.24		1.61		
SEQ ID NO 281	YLR294C			5.74	2.43		
SEQ ID NO 283	YLR311C		3.02	3.99	2.22		
SEQ ID NO 285	YLR312C						-1.58
SEQ ID NO 287	YLR327C		-2.10	1.04	2.48		
SEQ ID NO 289	YLR346C				1.79		
SEQ ID NO 291	YLR390W	ECM19	2.77				
SEQ ID NO 293	YLR414C						-1.67
SEQ ID NO 295	YML053C			2.80			
SEQ ID NO 297	YML129C	COX14			1.91		
SEQ ID NO 299	YML132W	COS3			1.42		
SEQ ID NO 301	YMR009W				-2.17		
SEQ ID NO 303	YMR011W	HXT2			-1.86		
SEQ ID NO 305	YMR043W	MCM1	2.15	2.56	1.16		
SEQ ID NO 307	YMR099C				1.63		
SEQ ID NO 309	YMR107W		-6.48	5.86			
SEQ ID NO 311	YMR110C				1.53		
SEQ ID NO 313	YMR173W	DDR48	-3.32	1.58		-2.07	
SEQ ID NO 691	YMR173W-A		-1.78	1.58	1.47	-2.07	
SEQ ID NO 315	YMR251W		-64.41				
SEQ ID NO 317	YMR251W-A	HOR7	-64.41		-4.19		-3.18
SEQ ID NO 319	YMR256C	COX7		3.79	2.18		
SEQ ID NO 321	YMR273C	ZDS1	2.42				
SEQ ID NO 323	YNL030W	HHF2	-3.97				-1.56
SEQ ID NO 325	YNL031C	HHT2			-5.69		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 327	YNL112W	DBP2	2.82				
SEQ ID NO 329	YNL131W	TOM22	-9.70				
SEQ ID NO 331	YNL134C				1.52		
SEQ ID NO 333	YNL143C		1.12				
SEQ ID NO 335	YNL179C		2.88		-2.02		
SEQ ID NO 337	YNL338W		1.78	2.79	1.62	-2.87	
SEQ ID NO 339	YNR002C	FUN34			-1.87		
SEQ ID NO 709	YOL052C-A	DDR2				1.65	
SEQ ID NO 341	YOL106W			3.51	2.44		
SEQ ID NO 343	YOL109W	ZEO1			-3.45		-1.87
SEQ ID NO 345	YOL126C	MDH2		1.91		-3.11	
SEQ ID NO 347	YOL139C	CDC33			2.17		
SEQ ID NO 349	YOL150C		17.69				
SEQ ID NO 351	YOL151W	GRE2	9.20				
SEQ ID NO 353	YOR120W	GCY1			-1.46		
SEQ ID NO 355	YOR121C		1.54	3.40	1.63		
SEQ ID NO 357	YOR122C	PFY1			1.40		
SEQ ID NO 359	YOR131C		2.81				
SEQ ID NO 361	YOR261C	APN8		2.59	1.54		
SEQ ID NO 363	YOR267C		1.78	1.07	-1.10		
SEQ ID NO 365	YOR285W		-2.15				-1.21
SEQ ID NO 367	YOR286W		-18.36				
SEQ ID NO 369	YOR327C	SNC2					-1.66
SEQ ID NO 371	YOR372C	NDD1	2.19	1.92			
SEQ ID NO 373	YOR374W	ALD4		-12.93			
SEQ ID NO 375	YOR382W		4.02				
SEQ ID NO 377	YPL037C	EGD1	-5.83				-2.17
SEQ ID NO 379	YPL078C	ATP4	-4.50		1.22		
SEQ ID NO 381	YPL079W	RPL21B					-6.18
SEQ ID NO 383	YPL085W	SEC16	2.28				
SEQ ID NO 385	YPL089C	RLM1	1.94	2.74	1.22		
SEQ ID NO 387	YPL190C	NAB3	2.80				
SEQ ID NO 389	YPL201C		-3.57				
SEQ ID NO 391	YPL271W	ATP15			2.40		
SEQ ID NO 393	YPR028W	YIP2	-12.41				
SEQ ID NO 395	YPR035W	GLN1			-2.78		

TABLE 8

TABLE 8							
C. albicans 522 CDS's				S. cerevisiae 11645 CDS's			
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Ala	GCU	30.7	8686	x	6	21.1	118595
	GCC	12.7	3582		4	12.6	70785
	GCA	15.4	4357		2	16.2	91018
	GCG	2	578		1	6.1	34546
Arg	CGU	5.9	1682		1	6.5	36518
	CGC	0.7	204		1	2.6	14571
	CGA	3.5	989		3	3	16957
	CGG	0.8	220		3	1.7	9801
	AGA	23.6	6673		1	21.3	119672
	AGG	2.7	769		2	9.3	52057
Asn	AAU	37.9	10731	x	1	36	202351
	AAC	18.7	5293		2	24.9	140194
Asp	GAU	43.6	12323	x	5	37.8	212658
	GAC	14.7	4152		7	20.4	114451
Cys	UGU	9.7	2757	x	1	8	44797
	UGC	1.7	493		1	4.7	26357
Gln	CAA	35.2	9964	x	1	27.5	154529
	CAG	6.9	1948		8	12.2	68463
Glu	GAA	49.5	14001	x	3	45.9	257930
	GAG	11.5	3252		10	19.1	107568

TABLE 8 - continued

C. albicans 522 CDS's					S. cerevisiae 11645 CDS's		
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Gly	GGU	33.5	9492	x	2	23.9	134515
	GGC	4.5	1281		7	9.7	54829
	GGA	13.7	3874		2	10.9	61481
His	GGG	7.7	2182		8	6	33627
	CAU	14	3964			13.7	77260
	CAC	5.8	1642			7.8	43878
Ile	AUU	39.9	11281	x	3	30.2	169795
	AUC	14.2	4005		7	17.1	98126
	AUA	12.3	3478			17.8	100027
Leu	UUA	1	295	x		26.3	148133
	UUG	36.1	10204			27.1	152590
	CUU	9.8	2777			12.2	68479
	CUC	2.5	694			5.4	30218
	CUA	4	1133			13.4	75414
Lys	AAA	48.6	13760	x		42.1	236746
	AAG	19.4	5477			30.8	173174
Met	AUG	18.4	5219	x	8	20.9	117410
Phe	UUU	28.6	8100	x		26	146355
	UUC	15.9	4486			18.2	102389

TABLE 8 - continued

aa	codons	C. albicans 522 CDS's				S. cerevisiae 11645 CDS's			
		frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number		
Pro	CCU	13.2	3722		1	13.6	76366		
	CCC	3.6	1027		5	6.8	38247		
	CCA	26.6	7531	x		18.2	102277		
	CCG	2.4	686		1	5.3	29758		
Ser	CUG	3.1	875		9	10.4	58583		
	UCU	23.3	6595	x	1	23.6	132608		
	UCC	10.3	2928		4	14.2	79928		
	UCA	24.6	6955			18.8	105570		
	UCG	6.5	1836		1	8.6	48186		
	AGU	23.6	6673			14.2	78649		
	AGC	4.5	1269		5	9.7	54330		
Thr	ACU	30.7	8689		1	20.2	113634		
	ACC	13.9	3928	x	8	12.6	70777		
	ACA	17.4	4928		5	17.7	99759		
	ACG	3.6	1019		1	8	44817		
Trp	UGG	11	3115	x	6	10.3	58092		
Tyr	UAU	24	6782			18.8	105489		
	UAC	11.6	3280	x	2	14.7	82483		
Val	GUU	33.2	9391		1	22	123726		
	GUC	10.3	2927	x	3	11.6	65203		
	GUA	8	2265			11.8	66100		
	GUG	10	2842		7	10.7	60033		

TABLE 9: Regulation of 23 selected "Bax-specific" functions

<i>Cellular role: Amino-acid metabolism</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YOR302W	YOR302W	11541.92	26808.35	8895.74	2.32
<i>Cellular role: Cell stress</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YML028W	TSA1	12889.91	2166.45	11327.36	0.17
<i>Cellular role: Chromatin/chromosome structure</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBR009C	HHF1	2149.69	8655.43	2909.14	4.03
YDR224C	HTB1	13661.40	55656.34	18829.27	4.07
YNL030W	HHF2	8676.99	19603.93	4732.39	2.26
<i>Cellular role: Energy generation</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBL099W	ATP1	2728.21	8786.71	1644.48	3.22
YGR183C	QCR9	23181.54	81865.40	24053.00	3.53
YJL166W	QCR8	5296.71	18093.93	5001.65	3.42
YLR038C	COX12	7336.65	19935.69	5118.43	2.72
<i>Cellular role: Signal transduction</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YHR135C	YCK1	3939.64	8358.11	3707.17	2.12
YOL100W	PKH2	2218.45	6088.96	2619.31	2.74
<i>Cellular role: Transcription factor</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR216W	ADR1	5925.91	18459.00	6434.43	3.11
<i>Cellular role: Unknown</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR504C	YDR504C	2741.47	6908.49	2839.62	2.52
YGR146C	YGR146C	2099.74	5616.94	1303.89	2.68
YGR236C	SPG1	17717.80	64439.96	24134.29	3.64
YHR138C	YHR138C	6218.30	14817.41	5220.50	2.38
YJL142C	YJL142C	6988.27	16006.02	6740.46	2.29
YKL123W	YKL123W	2826.82	5952.34	2766.04	2.11
YLR414C	YLR414C	4510.80	11867.69	3531.27	2.63
YMR107W	YMR107W	13453.15	78850.98	17417.00	5.86
YOL099C	YOL099C	3690.45	11604.72	5454.15	3.14
YPL201C	YPL201C	15960.14	33633.74	7449.66	2.11
YJL060W	YJL060W	8798.50	2406.39	6356.11	0.27

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CLAIMS

1. An isolated nucleic acid representing a synthetic *BAX*-gene selected from the group consisting of:
 - 5 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
 - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
 - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
 - d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by
10 SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and,
 - e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,
or a nucleic acid representing the complement of any of said nucleic acids as defined in (a)
15 to (d).
2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid
20 sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
- 25 7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
- 30 10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:

- a) providing (a) genetically modified yeast or fungi according to claim 11,
- 5 b) treating said genetically modified yeast or fungi with a mutagen,
- c) isolating resistant yeast or fungal cells, and,
- d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

10 14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.

15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:

- 15 a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,
- b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
- 20 c) identifying said *Candida* spp. polypeptide or cDNA.

16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- a) providing a genetically modified organism according to claim 10,
- b) expressing a cDNA library in said genetically modified organism, and,
- 25 c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.

30 18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.

19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,
- b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,
- e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and
- f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),
20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.
22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.
23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.
24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.

25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.
26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
- 5 27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.
28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.
29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 28.
30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.
- 10 31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:
- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs
- 15 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,
- 20 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a polypeptide having an amino acid sequence which is more than 70% similar to any of
- 25 the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540,
- 30 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and

(d) a functional fragment of any of said polypeptides as defined in a) to c).

32. A polypeptide according to claim 31 for use as a medicament.

33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.

34. An antibody according to claim 33 for use as a medicament.

35. A pharmaceutical composition comprising an antibody of claim 33 or 34.

36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

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- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,

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 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as
 represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41,
 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87,
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 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669,
 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717,
 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as
 specified in a) to e), and

(g) the complement of any of the nucleic acid molecule as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs

18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60,
5 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,
104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136,
138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,
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15 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,
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628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660,
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710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a
25 functional equivalent, derivative or bioprecursor of said protein,

(b) a polypeptide having an amino acid sequence which is more than 70% similar o any

of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24,
26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68,
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30 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142,
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178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210,
212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244,
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35 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302,

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634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,
668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714,
716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a polypeptide having an amino acid sequence which is more than 70% identical to

15 any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24,
26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68,
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110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142,
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25 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370,
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566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598,
600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,
634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c),
for the preparation of a medicament for treating diseases associated with yeast or fungi.

- 5 38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier diluent or excipient therefor.
39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in
10 a pharmaceutically acceptable carrier.
40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically
15 modified yeast or fungus.
41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:
- 20 (a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,
- (b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells; wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said
25 compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said
30 compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 5 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 10 (b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 15 (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

25 43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

- (a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,
- 30 (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,
- (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,
- (e) identifying the compound or protein.

5 44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

- (a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,
- 10 (b) interacting said compound with the complex formed by the expressed proteins as defined in a),
- (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,
- (d) identifying the compound.

15 45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- 20 (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,
- (c) identifying the compound.

25 46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

- (a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,
- 30 (b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide encoded by said cDNA library, and,
- (c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.
49. A compound or polypeptide according to claim 48 for use as a medicament.
50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.
51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.
52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.
53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.
54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.
55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.
56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.
- 5 59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.
- 10 60. A compound identifiable according to the method of claim 59.
61. A compound according to claim 60 for use as a medicament.
62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.
- 15 63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.
64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 25 66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.
- 30 67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 5 69. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 36 or a human homologue thereof or an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient
10 therefor.
70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.
- 15 71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 72. An expression vector comprising a human homologue of a nucleic acid as defined in claim 36.
73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.
- 25 75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.
76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.
77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.
- 30 78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.
79. A polypeptide encoded by a nucleic acid of claim 77.

Figure 1:

YBL002W, 896 bp, CDS: 501-896 (SEQ ID NO 21)

TGTTTGATATTAGTAGTCATGTTGTAATCTCTGGCCTAAGTATACGTAACGAAAATGGTA
GCACGTCGCGTTTATGGCCCCCAGGTTAATGTGTTCTCTGAAATTCGCATCACTTTGAGA
AATAATGGGAACACCTTACGCGTGAGCTGTGCCACCGCTTCGCCTAATAAAGCGGTGTT
CTCAAAATTTCTCCCCGTTTTCAGGATCACGAGCGCCATCTAGTTCTGGTAAAATCGCGC
TTACAAGAACAAAGAAAAGAAACATCGCGTAATGCAACAGTGAGACACTTGCCGTCATAT
ATAAGGTTTGGATCAGTAACCGTTATTTGAGCATAACACAGGTTTTTAAATATATTTAT
ATATATCATGGTATATGTGTAAATTTTTTGTGCTGACTGGTTTTGTATTATTTAGCT
TTTTAAAAATTTTACTTTCTTTCTTTGTTAATTTTTTCTGATTGCTCTATACTCAAACCAAC
AACCACTTACTCTACAACCTAATGTCTCTGCCGCCGAAAAGAAACCAGCTTCCAAAGCTC
CAGCTGAAAAGAAGCCAGCTGCCAAGAAAACATCAACCTCCGTCGATGGTAAGAAGAGAT
CTAAGGTTAGAAAGGAGACCTATTCCTCTTATATTTACAAAGTTTTGAAGCAAATCACC
CAGACACTGGTATTTCCAGAAAGTCTATGTCTATTTTGAAGTCTTTTCGTTAACGATATCT
TTGAAAGAATTGCTACTGAAGCTTCTAAATTGGCCGCTTATAACAAGAAATCCACTATTT
CTGCTAGAGAAATCCAAACAGCCGTTAGATTGATCTTACCTGGTGAATTGGCTAAACATG
CCGCTCCGAAGGTACTAGGGCTGTTACCAAATACTCCTCCTCTACTCAAGCCTAA

YBL002W, 131 aa (SEQ ID NO 22)

MSSAAEKKPASKAPAEKKPAKKTSTSVGKKRSKVRKETYSYIYKVLKQTHPDTGISQ
KSMILNSFVNDIFERATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTR
AVTKYSSSTQA

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)

TTGCCAACCTCAAAGAAGAATTATGGGCATATTGACCTTCTCCGGTTTTCCC'TCCCGC
GCTCTCGTATCCGTCGCAATTTGACCTCGAGCAAGCGCTCCACTATGTCTATATGTTTAC
CAGTAAACCTTCTTAACGTTTGTGATATTTTTTGAAC'TTCAACCACATTCAGTATGCGTG
TGTATATAAAGATATTCCTGATAGCACTATGTTTATCTTTATACAATATACAAAAGGTCA
CCCAGGACGAGCAGCGCGGCTATTTTTCTATCATTCCTGTAATAGCGACCAACGGTCGGC
GGCTATTTTTTTTTTTTGCATTTTTTTCGGGATGGGTTCCTCCGGCAAAGCTAGCCCCGGA
GATTTTTTAATTACGTAAAGAAACAAGGGGCCGGATGTTGCTGCTATTTGGTATATAAAGAG
AGAAGGAGAGATATAGAAAATTGTGCTTCTAGATTCTCGCAGTAGGATGAGATAAATTTTC
AAGAAGCAGGAAGCAAAGGATGTTTAGTAGAATTTGTAGCGCTCAATTAAAGAGGACGG
CATGGACCTTCTTAAGCAGGCTCACTTGCAATCACAGACGATTAACCAATTTGCCACAG
CACCTATTCGTGCAAACAATTCAAACAAAGTGATCAACCAAGACTAAGAATAAACTCTG
ATGCTCCTAATCTTGATGCTGACACAACGGTTGGTAAATCAATTTTTTACGACTACTTGG
GCGACTCTTGGGGGGTC'TTGT'TTCTCACCCAGCAGATTTACCCCTGTCTGCACCACCG
AAGTCAGCGCATTCGCCAAATTGAAGCCGGAATTCGACAAGAGAAATGTTAAATTGATCG
GGCTTTCAGTGGAAGATGTTGAGTCCACGAAAAATGGATTCAAGACATCAAGGAAATAG
CAAAGGTTAAAAATGTTGGTTTCCCAATAATTGGTGACATTTTAGAAACGTGGCATTCC
TATATGATATGGTAGATGCCGAAGGATTCAAAAATATCAATGATGGGTCAGTGAAGACCG
TGAGGTCGT'TTTCGTATCGATCCCAAGAAGAAGATTAGACTGATTTTTTACCTACCCCT
CCACCGTCGGAAGAAACACTTCTGAAGTGTTAAGGGTAATCGACGCC'TTGCAATTGACTG
ACAAGGAGGGCGTAGTAAC'TCCAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTC
CCTCTGTCTCCAATGATGAGGCGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCCCT
ATTTAAGATTCACCAAGTCGAAATAA

YBL064C, 261 aa (SEQ ID NO 26)

MFSRICSAQLKRTAWTLPKQAHLSQTIKTFATAPILCKQFKQSDQPRLRINSDAPNFDA
DTTVGKINFYDYLGDWSGVLFShPADFTPVCTTEVSFAFKLKPEFDKRNVLIGLSVEDV
ESHEKWIQDIKEIAKVKNVGFPIIGDTFRNVAFLYDMVDAEGFKNINDGSLKTVRSVFVI
DPKKKIRLIFTYPSTVGRNTSEVLRVIDALQLTDKEGVVTPINWQPADDVLIIPSVSNDE
AKAKFGQFNEIKPYLRF'TKSK

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YBR089C-A, 800 bp, CDS: 501-800 (SEQ ID NO 47)

TTTTTTAGGTGGCGCGCAACTATAAAGTACAGCAAGTGAGGTTGAGGCAATACTGGGAG
TTTACACTATGGGAGACAGCTCCTAACACCAAGCAGAAAAACGACTTTTTCGCAAAGTAT
GTAAGGCGCTGGGTGAGCCAGCGGACGAGGATGGGCTTAATAAGAACGTACAGTTTAGC
ACAGCTAGAACAGGATACAGCTAAGGGCAACTCTGCTTTTCGGGAGAAGTTAAAGAGGGG
TAGACAATGATGGTAACTTTATAAACCAGGCTACAATGAAGGTTGTAGCAGCAAGGAAGAT
GATATTTTAAATACGGTTCAGGTGAAATGAAATAGCCGCCCATACCGGCATGCTCAAGTTG
TAAGTCAGGACTCTAGCTTTCTACTGTAGTATCCTCTAAAGGACTGCTGTTCTGTGCACC
CCCTTCCTTTGTTTATCATAGCGCACGACAAGAGTACTAACTAATTAACTTAGAACATTA
ACATATATAAACTAGCGCTATGGCCGCAACTAAAGAAGCAAAGCAACCAAAGGAACCAA
AGAAGAGGACCACCAGGAGAAAGAAGGATCCTAACGCCCCTAAGAGGCGGTTGTACAGCTT
ATATGTTCTTTGCTAATGAAACAGAGACATTGTCCGTTCCGAGAATCCTGACGTAACCTT
TTGGCCAAGTAGGCAGAATATTGGGTGAGAGGTGGAAGGCCTTAACTGCTGAAGAAAAGC
AACCCTATGAATCTAAGGCTCAAGCAGACAAGAAGAGATACGAATCTGAAAAGGAATTGT
ACAATGCTACACGTGCTTGA

YBR089C-A, 99 aa (SEQ ID NO 48)

MAATKEAKQPKPKKRTTRRKDPNAPKRRLSAYMFFANENRDIVRSENPDVTFGQVGRI
LGERWKALTAEEKQPYESKAQADKKRYESEKELYNATRA

YBR149W, 1535 bp, CDS: 501-1535 (SEQ ID NO 57)

TTCGCAAACATCAACTTCTCCTTAATCGACCAACTGACAATGAACTTCAGGTTCTACGAG
AGATCTGCCAATTTCCAGAAGGAAACAATAGGTGGGTTAAGAATGATGCTACAAGATAAG
GATAACTATATCAAAAACACTGATGCAACATTTGAAGAAAAAAGAGAGTACAAAGTTGATA
AAAGACAGCAAGAATGGCGCCTCCACCTTAACATCTTAACAATTTTCGTTTACTGAAAATG
CTACTAGTATATAATCATTAAGTATCTAACTATCACTCAATAAAAAATATTATAGATCGCT
TAAAAACTCGTTTATTGCGGATTATAAATCCACCAAAAGCCGCTCTACCCTTACCTCCGC
CTGGAAAAATTATAATATATAAAGTGAGCCTCGTAATACAGGGGTAAAAAGGAAAGAGGG
GGATATCAAGCATCTGGACTTATTTGCACTATCTCCGCCTTCAATTGATAAAAGCGTCTT
GATTTTAACTCAACTGCTATCATGTCTTCTTCAGTAGCCTCAACCGAAAACATAGTCGAAA
ATATGTTGCATCCAAAGACTACAGAAATATACTTTTCACTCAACAATGGTGTTCGTATCC
CAGCACTGGGTTTGGGGACAGCAAATCCTCACGAAAAGTTAGCTGAAACAAAAACAAGCCG
TAAAAGCTGCAATCAAAGCTGGATACAGGCACATTGATACTGCTTGGGCCTACGAGACAG
AGCCATTTCGTAGGTGAAGCCATCAAGGAGTTATTAGAAGATGGATCTATCAAAAGGGAGG
ATCTTTTTCATAACCACAAAAGTGTGGCCGGTCTATGGGACGAAGTGGACAGATCATTGA
ATGAATCTTTGAAAGCTTTAGGCTTGGAATACGTCGACTTGCTCTTGCAACATTGGCCGC
TATGTTTGAAGATTAAAGGACCCTAAGGGGATCAGCGGACTGGTGAAGACTCCGGTTG
ATGATTCTGGA AAAACAATGTATGCTGCCGACGGTGACTATTTAGAACTTACAAGCAAT
TGGAAAAAATTTACCTTGATCCTAACGATCATCGTGTGAGAGCCATTGGTGTCTCAAATT
TTTCCATTGAGTATTTGGAACGTCTCATTAAAGGAATGCAGAGTTAAGCCAACGGTGAACC
AAGTGGAACTCACCTCACTTACCACAAATGGAATAAGAAAGTTCTGCTTTATGCACG
ACATTCTGTTAACAGCATACTCACCATTAGGTTCCCATGGCGCACCAAACTTGA AAAATCC
CACTAGTGAAAAAGCTTGCCGAAAAGTACAATGTCACAGGAAATGACTTGCTAATTTCTT
ACCATATTAGACAAGGCACTATCGTAATTCGAGATCCTTGAATCCAGTTAGGATTTCTT
CGAGTATTGAATTTCGCATCTTTGACAAAGGATGAATTACAAGAGTTGAACGACTTCGGTG
AAAAATACCCAGTGAGATTCATCGATGAGCCATTTGCAGCCATCCTTCCAGAGTTTACTG
GTAACGGACCAAACTTGGACAATTTAAAGTATTAA

YBR149W, 344 aa (SEQ ID NO 58)

MSSSVASTENIVENMLHPKTTTEIYFSLNNGVRIPALGLGTANPHEKLAETKQAVKAAIKA
GYRHIDTAWAYETEPFVGEAIKELLEDSIKREDLFITTKVWPVLWDEVDRSLNESLKAL
GLEIVDLLLQHWPLCFEKIKDPKGISGLVKTPVDDSGKTMYAADGDYLETYKQLEKIYLD
PNDHRVRAIGVSNFSIEYLERLIKECRVKPTVNQVETHPHLPQMELRKFCFMHDILLTAY
SPLGSHGAPNLKIPLVKKLAEKYNVTGNDLLISYHIRQGTIVIPRSLNPVRISSSIEFAS
LTKDELQELNDFGEKYPVRFIDEPFAAILPEFTGNGPNLDNLKY

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YBR289W, 3218 bp, CDS: 501-3218 (SEQ ID NO 63)

GATACGATCTATAGTCTCTAAAAAGGTAAAAACAATCAAGCGGGCCTTTTGACTTCGAAGT
GGAGGCTAAGCACCAATAATTGAGCTTATTTATAACTGAGAAATACTTATAGACCTCTAA
ATCTCTTCCAACCATTGAATGGTCTAAATAATCATCACTACTGCTATCTTCGAGCAATTG
AGGACATGTGGTACGAACGCGGGTCCACAGGTGCTTGAAGGAGGGAGCTGTTGCACCTAA
AAGATACTGGAATAAGTTTGTCTTTGTATCAGTGATATAGAATGACAAATACATCTA
TTTTGGTTGGGTGGTAAGGTTTACAGCCTCTGTTGTGCCCCAAGTCCTGTTATCGCCAA
CTTTAAATAAATCTCTTCTTGTCTTTGACCAAAAATTTTCATTTTTTCGTCGCATTTAAAA
GAAACTGAAATTTCAAACATAAACACCAAAACAAGCATCATCAAGGGAACATATAGTAA
AGAACTACACAAAAGCAACAATGAATAATCAGCCGCAGGGTACCAACAGCGTTCCAAATA
GTATTGGAAATATATTTAGCAACATTGGAACCTCCATCTTTTAACATGGCGCAAATTCGC
AACAGCTGTATCAGAGCCTCACACCACAACAATTGCAGATGATTTCAGCAACGACACCAAC
AGTTACTGAGGAGTCGTCTACAACAACAACAACAACAACAACAACAACCTTCACCGCCAC
CGCAAACGCATCAATCTCCACCCCTCCTCCGCAACAATCTCAACCCATTGCTAATCAAT
CAGCGACTTCTACCCCTCCTCCTCCTCCAGCACCACACAACCTTACATCCCCAAATTGGTC
AAGTGCCCTTAGCTCCAGCGCTATTAATTTGCCTCCACAAATTGCTCAGTTACCTTTGG
CTACACAGCAACAAGTTTGAACAAGTTGAGGCAGCAGGCCATAGCAAAAAATAATCCAC
AGGTTGTGAATGCAATTACTGTTGCACAACAACAAGTGCAACGCCAAATTGAGCAGCAAA
AGGGACAGCAACCGGCACAACTCAGCTAGAACAGCAGAGGCAATTGCTGGTTCAGCAGC
AACAGCAGCAGCAACTTAGAAACCAAATACAGCGACAACAGCAACAACAGTTTAGGCATC
ATGTGCAAAATACAACAGCAGCAACAAAAGCAACAACAACAGCAGCAGCAGCATCAGCAAC
AACAACAACAACAACAGCAACAGCAGCAACAGCAACAGCAACAGCAGCAGCAACAACAAC
AGCAACAACAACAACAACAGCAGCAGCAGCAGCAGCAGCAAGGACAAATACCGCAAT
CTCAGCAAGTTCTCAAGTTAGATCCATGAGTGGACAACCTCCCACCAATGTTTCAGCCCA
CTATTGGCCAACTTCTCAACTTCCAAAATTAAACTTACCCAAGTACCAAACTATTCAAT
ACGATCCACCAGAAACCAAGCTACCATATCCAACCTATTGGTCAGACAAAAAAGCAGATA
CGGATACTTTGTTGTACGAACAAATTATCCAGCGTGATAAAATTAACAAATATTCGCTAA
TAAGAGAAACCAATGGTTACGATCCGTTTACGATTTATGGATTAGTAATAAAGAGTATA
TTAGTAGACTGTGGCATACACTGAAGTATTATCAAGATTGAAGAACACTAGAATGAAAT
CTATCACAAGCACTTCTCAGAAGATTCTTTCGCAAGTATTTGGGGAAATGGTTACTCAG
GGTATGGTAATGGGATTACGAATACAACCTACCAGAGTTATTCCACAAGTAGAAGTTGGAA
ATAGGAAGCATTACCTAGAGGATAAATTAAGTCTATAAACAGGCCATGAATGAGACAT
CGGAACAGTTAGTTCCCATAGATTGGAGTTTCGATCAAGATCGTGACAGATTCTTCCTCA
GGGACACTTTGTTATGGAACAAAAATGACAAGCTTATTAAATTTGAAGACTTTGTGGACG
ACATGTTGCGAGATTACCGATTGAGGACGCTACGAGAGAGCAACACATTGATACTATTT
GTCAATCTATAAAGAGCAGATTTCAGGAGTTTCAAGGAAATCCATATATAGAGTTGAATC
AGGACCGTCTAGGCGGTGATGACTTGAGAATTAGAATCAAGCTGGATATTGTCGTGGGAC
AAAACCAAGTTAATCGATCAATTTGAGTGGGAGATCTCTAATAGTGATAACTGTCCAGAAG
AGTTTGCAGAGTCCATGTGTCAAGAAATPAGAACTACCAGGTGAGTTTGTGACTGCCATTG
CTCACTCCATAAGAGAGCAAGTTCATATGTATCATAAATCACTGGCACTGTTAGGTTACA
ATTTTGATGGATCAGCGATAGAAGATGATGACATTAGAAGCAGAATGCTCCCAACGATTA
CTCTTGATGATGTTTATAGGCCCTGCAGCGGAAAGCAAAATTTTACTCCAAACCTATTAC
AGATTTCACTGTCAGAGTTAGAGAGATTGGATAAAGATAAGGACAGAGACACAAGAAGGA
AAAGAAGACAAGGTAGATCTAATAGACGTGGTATGCTCGCATTTGTCGGGCACATCTGCAA
GTAATACATCTATGAACGGCGTTCACAACACAGTAGCAGCAGGAAATGCTTCATCGTTGC
CACCAGGAGAGATTTTACTGCCAGATATTGCAGATATTCCAAGAACTTTCAGGACTCCAG
TACCTAGCACTTTAATGCCCTGGTGGTGTGACGTAGGCCCTTCTGTGGAATCGTACGAAT
TGAGAAACACAACCACCTTATAAAAGCAGGCCAGATAGACCTAAGCCAGTTTCACCTCCTT
GTTATATTATTGACCATAATTCGGGTCAATTCGCTACTACTTTCTATTAAACTGCCTGGGA
AAGTTAATACAAAAGAAGAGTTTCGCAGCAGCGCCCAATGACACAAGTAGTGGCACCAATG
CAATGCTTCCGAGTCCAGAATCGCTGAAAACCTAAGCTGAATAGTAACATTCGCGCTGGTG
TGACGATACCTTCAATCCCAACCCGATTGCCAATCACACTGTTACTAATTCACCCAATC
CCCACTGCAGCCAGTAATCCCAGGTGGGGCAGCTAGTAAATCGGTACCTACACCTAGTC
TTCTTATAGCACTCCAGTAGCACCACATGATAGCGAAGCGACATTGTTGACTAATAGCA
ATAATGGTAGCAGTAACAATAACACACAGAATACATAG

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YBR289W, 905 aa (SEQ ID NO 64)

MNNQPQGTNSVPNSIGNIFSNIGTPSFNMAQIPQQLYQSLTPQQLQMIQQRHQQLLSRL
QQQQQQQQQTSPPPQTHQSPPPPPQSQPIANQSATSTPPPPPPAPHNLHPQIGQVPLAPA
PINLPPQIAQLPLATQQQVLNKLRRQQAIAKNNPQVVNAITVAQQQVQRQIEQQKGQQTAAQ
TQLEQQRQLLVQQQQQQQLRNQIQRQQQQQFRHHVQIQQQQQKQQQQQQHQQQQQQQQ
QQQQQQQQQQQQQQQQQQQQQQQQQQQQQIPQSQQVPQVRMSGQPPTNVQPTIGQLPQ
LPKLNLPKYQTIQYDPPETKLPYPTYWSDKKADTDLLYEQIIQRDKINKYSLIRETNGY
DPFSIYGFSNKEYISRLWHTLKYQDLKNTRMKSITSTSQKIPASIWNGNGYSGYNGGIT
NTTTRVIPQVEVGNRKHYLEDKLVYKQAMNETSEQLVPIRLEFDQDRDRFFLRDRTLWN
KNDKLIKIEDFVDDMLRDYRFEDATREQHIDTICQSIQEIQEFQGNPYIELNQDRLGGD
DLRIRIKLDIVVGQNQLIDQFEWEISNSDNCPEEFAESMCQELELPGEFVTAIAHSIREQ
VHMYHKSLLALGYNFDGSAIEDDDIRSRMLPTITLDDVYRPAAESKIFTNLLQISAAEL
ERLDKDKDRDTRRKRRQGRSNRRGMLALSGTSASNTSMNGVHNTVAAGNASSLPPEILL
PDIADIPRTFRTPVPSTLMPGGVDVGPSVESYELRNTTTYKSRPDRPKPVSPPCIIDHI
PGHSLLSIKLPKGVNTKEEFAAAPNDTSSGTNAMLSPESLTKLNSNIRAGVTIPSI
NPANHTVTNSPNPTLQPVIPGGAASKSVPTPSLPIAPPVAPHDSEATLLTNSNNGSSNN
NTQNT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

TTAAGAAAATGAACGTTACTATTTCTCTCTCGTTTTAGTTACATAAAATTTACTAATGG
TTGGAAAATTGCGGAAGCTATCACGCGATAACTAGGTACACACGCATTATTTTATAATC
CCATTATTAATAAATCCGTTATGACCTTTTAGTAATAACTTATTAAGAACCTCCGGGTA
AAATACTGTACTGCGGGGAAAGAAGGCGCTTCCCCTTCTTGGAACCTAATATAAATAATA
AATTTGCCTAAGGGCATTAGGCCTTACTGCCTTGCGCTAGCGTACTTATTTTCGATTACATC
AATTTGCACTATTCCGGCAGCTAGTTGATACTATAACATCCTACATTTTACTTGTTTTA
CGTTCATTTTTATTGTAAGTTTGTAACTTTATCAGAAAGAAAACAAGAAGAGGAAAGAAAG
GAAAAGAGGGGTCAAGTTAGTATCAATAAAAAAAGAGAGTAAACAAAACAATACAGAC
TCAATTGAAGCACTATAAGAATGGTAAAGATTGCGATAATTACTTACTCTACCTACGGGC
ACATAGACGTTTTAGCCCCAAGCTGTTAAGAAAGGTGTGGAGGCAGCTGGTGGTAAAGCTG
ATATATACAGGGTCGAGGAAACTTTACCTGATGAAGTCCTCACCAGATGAACGCTCCTC
AGAAACCTGAAGATATTCTGTGCTGACTGAGAAAACGTTGCTCGAATATGACGCTTTT
TGTTCCGGTGTTCCTCACTAGGTTTGGTAATTTGCCGGCTCAATGGTCCGCTTTTGGGATA
AAACCGGTGGATTATGGGCCAAGGGCTCTTTGAACGGCAAAGCTGCGGGGATATTCTGTTA
GTACTTCCAGTTACGGAGGTGGTCAAGAAAGTACCGTTAAAGCCTGTTTGTCTTATTTAG
CTCATCACGGAATTATCTTTTTACCCTGCGGTATAAGAATTCATTTGCTGAGTTAGCCA
GTATAGAAGAGGTACACGGTGGCTCTCCATGGGGTGGTGGTACCTTGCAGGACCTGACG
GCTCAAGAACTGCGTCTCCACTTGAATTGAGAATTGCTGAAATTCAGGTAAAAACATTCT
ACGAAACCGCCAAAAAACTTTTCCCTGCAAAAAGCAAGCCCTCCACTGAAAAGAAAGA
CCACTACTTCTGATGCGGCTAAGAGACAACTAAACCTGCAGCAGCTACAACCTGCAGAAA
AGAAGGAGGACAAAGGATTATTATCTGCTGTACTGTCATGTAA

YCR004C, 247 aa (SEQ ID NO 70)

MVKIAIITYSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLTGMNAPQKPEDIP
VATEKTLLEYDAFLFGVPTRFNLPAQWSAFWDKTGGLWAKGSLNGKAAGIFVSTSSYGG
GQESTVKACLSYLAHHGIIIFLPLGYKNSFAELASIEEVHGGSPWGAGTLAGPDGSRTASP
LELRIAEIQGKTFYETAKKLFPAKEAKPSTEKTTTSDAAKRQTKPAAATTAEEKKEDKGL
LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

TGAAAAATGATGAAGGCACATTGTTAATTGAAGAAGAAGAAGAAGAAGAAACAAAATTAA
AACCGATTGACCAATATATGTCTCTGAATGCCAAGGATGGAAATTATTGCAGAAGATTAG
ACTTTTTTTTGTGCAAGTGGGATGAGCTTGGAGCAGGAAGAATACACTATACTGGATCTA
AAGAGTACAATAGATGGATAAGAATATTGGCAGCGCAAAAAGGCTTCAAGCTTACACAAC
ACGGTTTATTTGCAAAATAATATCCTTCTCGAAAGCTTTAACGAACGCAGAAATTTTCGAGT
TATTAAACTTAAATACGCTGAACCCGAACATAGAAATATCGAATGGGAAAAAAAACCTG
CATAAAGGCATTAAAAGAGGAGCGAATTTTTTTTTTAATAAAAAATCTTAATAATCATTA

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AGATAAATAATAGTCTATATATACGTATATAAATAAAAAATATTCAAAAAATAAAATAAA
CTATTATTTTAGCGTAAAGGATGGGGAAAGAGAAAAAGAAAAAATTGATCTATCGATTTC
AATTCAATTCAATTTATTTCTTTTCGGATAAGAAAGCAACACCTGGCAATTCCTTACCTT
CCAATAATTCCAAAGAAGCACCACCACCAGTAGAGACATGGGAGATCTTGTCAGTGACAC
CGTACTTCTTAGCGACAGTGGCAGTGTCAACCACCACCAATGATGACGGTGTACCAGCAG
CAGAGCTCTTGACAACCTCGTCTAACAAAGCCTTAGTACCAGCAGCGAATTTTCGAATT
CGAAAACACCTGGTGGACCGTTCCAGACAATGGTCTTAGCCTTTGCAACAGTAGCAGCAA
ACAACCTTTCTAGATTCTGGACCATTGTCCAACCCCTTGCCAGCCAGCTGGAATACCTTCCCT
TGTCAGTGACAGTCTTGGTGTGGCATCAGCAGAGAAAGCATCAGCAATGATGAAGTCGA
CTGGCAAGACGACTTCGACACCCCTTGGCCCTTGGCCCTTTCCATCAACTTTGGAACGATTT
CAGCACCAGCCTTGTCTGAAGATGGAGTCACCGATTTTCAGTGTTTTCCAAAACCTTCTTGA
AGGTGAAAGCCATACCACCACCAATGATGATAGAGTCGACCTTGTCCAACAAGTTGTCAA
TCAATTGA

YCR013C, 215 aa (SEQ ID NO 78)

MGKEKRKKLIYRFQFNSIYFFSDKKATPGNSLPSNNSKEAPPPVETWEILSVTPYFLATV
AVSPPPMMTVLPAEELLTTSSNKALVPAANFSNSKTPGGPFQTMVLAFATVAANNFLDSG
PLSNPCQPAGIPSLSVTVLVLASA EKASAMMKSTGKTTSTPLALAFSINFGTISAPALSK
MESPISVFSKTFCLKVKAI PPPMMIESTLSNKL SIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)

AAAGTATCAAGTTCGCATAAATTTACTTCGAAGACAGAAGCCAGTAAATTTGTCTTCTTC
ATGGAAATAGTTTCCAAAAGTTCTTAGTAATTACCATATGTTCTTGTATGTGGCGCTGC
GAAAGAAAGGTTAGCCGACCGGCATCACCCATAATTGTATAATATAGCAATGAAGCAACT
TGTTGAAGTTTCTTTTAAAGTACTATAGTATTGAATAATATCATGTTCACTTGATAAAAT
TGGGTATTTTATTGACCATTATATCGCGTTGGACACTAATGTCTTTCAAGTTGGTGTAC
GTCACGTGCTTTTCAATGTACTGGGGCAAATTGATTAGAGGAAGCCACAGTTTGGCAAGG
GCAGATATGATAGGAAGCAGTAACGGCAAGGAAGGATAAGAACATCATTGAGGGAGTCTG
TGGCAGTTTAGCACATGCTTTGGACCATTAAAGGGTTACGTAGAGGAGAAGAGCATATTT
CAGGATAAACAGACAAAATAATGACGATACAAGCGAAGCCAGTTCGAGCATATCGTATG
ATTCGACTACATACGGCACAGCACCGGGCTTGGATATAAAAGAGTTCCAAATCATCGAAG
ATTGGAATGGAAGACCTGCCAGCGCTTGGTCCGTGCAGAGGATTGGGCTTCTACAGTCCA
AGATGGAAAGGTACACGTACAATATTTACCACAATAATAAATATGGGAAGCACAACCTTAT
CTAA⁶CTGATACCAGGGCATGCTCTCATTCACTTCGCTAATGAAACATTCCGGGTATGATG
GTTGGCGAATGGATGTTATAGATGTTGAGGCCCCGGGAGTGCCAGCCCTTCACCGCAGTAA
ATAATGGAGAAAACACCAACACTAGTGAGGTCAAGTATACAGTTGTGGCAGAAGCCCAAG
TAAAGGT¹TACCTTAAAGGATGGCACCAACACACAGTGTGGTGGGCTAGGTAGAATTACTT
TGTCCTCGAGAGGTGAATGTTATAACAGGTGCAAAAAAGAGGCTGTAGGCGATGCGTTAA
AGAAGGCGTTATTGAGCTTTGAAAAAATCATACTCGATTATGAGACTAAGATTACAAATA
ATTACTATGTCGATGGCTTGTATGGCTCAAAAAAATTAATAATGAAGCTAACACCAATT
ACAACCTTATTGTCAGCGACTAATAGCAAGCCGACTTTTATCAAATTGGAGGATGCTAAAG
GCACGCATATCAAATAA

YDL059C, 238 aa (SEQ ID NO 84)

MTIQAKPSSSISYDSTTYGTAPGLDIKEFQIIEDWNGRPASAWSVQRIGLLQSKIERYTY
NIYHNNKYGKHNLSKLIPGHALIQFANETFGYDGWRMDVIDVEARECQPFTAVNNGENTN
TSEVKYTVVAEQVKVTLKDGNTNTQCGGLGRITLSSRGECYNRSKKEAVGDALKKALLSF
EKIILDYETKITNNYYVDGLYGSKKIKNEANTNYNLLSATNSKPTFIKLEDAKGTHIK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)

ACTCTTCTCTGATTTTCAGCAATGGCCTTTTTTTTTCTTCACGATCATACTCCTTCGCTT
GTCTTTTGAATTTCTTTTATTCTTACTTTTGACGTTTGTGTTGACCTGTGAGTCCACGGG
CCTTCAAGGCGGCCTTTAAATTCCTTAAAGTTGTGAACCGGCCATGATTTGATCTTCCCTT
TTATTTGCTTCTCAACTGTACTATTTACAGTAATAATTAGTGCAACCTTCAGATGCTTCT
CGCTAAATGCTCATCTCTAAATTATCATTATTATTCCTAATAAATCCTAAATTTTTCAC
TCGTTCTGTACGGCTCATCGCCCCAATATTACCCGCTTGTATGTGATCTTTTGTACTTT

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TCGGTGGCAAAATGCAAAGGGGAATCCAAGGAAAAACCATAACAGGACACTACATCAGAG
ATAATCTTGAATTAAGAGAGTAGAGGAATATACTGCTGGGCTCACTACCATTTTGTGTC
TAGAGTAAACGTAGAGAAAGATGTCAAGAGATGCACCAATTAAGGCTGACAAGGATTATA
GCCAAATTTGAAGGAAGAGTTTCTTAAGATCGATTGCTCGCTCAAATGATTGTAAC
CTGCTTTAGACCAACTGTTAGTGTGGAGAAGAAAAACCAGACAAGCTTCAGATCTGGCCT
CCTCGAAAGAAGTTTGGCCAAGATTGTAGATCTGCTAGCATCAAGGAATAAGTGGGACG
ACCTAAATGAGCAATTGACTCTACTCTCAAAAAAGCATGGTCAGTTGAAATTGTCAATTC
AGTATATGATACAAAAGGTTATGGAATATTTGAAAAGCTCGAAATCTTTGGATTTAAACA
CCAGAATTAGTGTCAATTGAAACTATCAGGGTGGTTACAGAGAACAAAATATTTGTAGAAG
TGGAAAGAGCTAGGGTCACCAAGATTTGGTGGAAATTAAGAAAGAAGAGGGTAAGATTG
ATGAAGCTGCAGACATCTTGTGTGAGTTACAGGTTGAGACCTATGGCTCCATGGAAATGT
CTGAGAAAATTCAGTTTATATTAGAGCAAATGGAATTGAGTATATTAAGGTTGATTATT
CCCAAGCCACGGTGTCTTCAAGAAAAATTCGAAAAAACTTTTAAAAATCCAAAATACG
AGTCATTGAAGCTAGAATATTATAATCTTCTGGTAAAAATTAGTTTGCACAAGAGAGAAT
ACCTAGAAGTTGCGCAGTATCTGCAAGAAATTTATCAAACAGACGCCATTAAATCAGATG
AGGCTAAGTGGAAACCTGTTTATCGCACATTTGTATATTTCTTAGTCCTTTCACCTTACG
GCAATTTACAAAATGATTTAATTCACAAAATCCAGAATGATAACAACCTGAAAAAATTAG
AAAGCCAAGAATCTTTAGTAAAAATTGTTTACTACGAATGAGTTGATGAGATGGCCAAATG
TTCAAAAAACCTATGAGCCCGTCTTAAATGAGGATGATTTGGCATTGTTGGTGGAGAAGCTA
ATAAGCATCACTGGGAAGATTTACAAAAAAGGGTCATCGAGCACAATTTAAGAGTCATTT
CCGAATACTATTCCAGAATTACTTTACTAAGATTGAATGAATTGCTGGACCTAACGGAGA
GCCAGACGGAAACATACATCAGTGATTTGGTAAACCAGGGCATCATATACGCTAAAGTTA
ATCGCCAGCCAAAATCGTGAAATTTTGA AAAACCAAAAACTCAAGCCAATTATTGAACG
AATGGTCACATAATGTTGACGAACTATTAGAACATATAGAAACAATAGGCCATTTAATTA
CAAAAGAGGAAATCATGCACGGTTTGAAGCTAAATGA

YDL147W, 445 aa (SEQ ID NO 88)

MSRDAPIKADKDYSQLKEEFPKIDSLAQNDCNSALDQLLVLEKKTRQASDLASSKEVLA
KIVDLLASRNKWDLLNEQLTLLSKKHGQLKLSIQYMIQVM EYLKSSKSLDLNTRISVIE
TIRVVTENKIFVEVERARVTKDLVEIKKEEGKIDEAADILCELQVETYGSMEMSEKIQFI
LEQMELSILKGDYSQATVLSRKILKKTFFKNPKYESLKLEYNLLVKISLHKREYLEVAQY
LQEIYQTD AIKSDEAKWKPVLSHIVYFLVLSPLYGNLQNDLIHKIQNDNNLKKLESQESLV
KLFTTNELMRWPVIVQKTYEPVLNEDDLAFGG EANKHHWEDLQKRVIEHNL RVI SEYY SRI
TLRLNELLDL TESQTETYISDLVNQGIYAKVNRPAKIVNFEKPKNSSQLLNEW SHNVD
ELLEHIETIGHLITKEEIMHGLQAK

YDR253C, 1076 bp, CDS: 501-1076 (SEQ ID NO 113)

TTTCCCCGCTAAAATAACGCCAGATGCTTTCTATGCTTCTAATCTTTTACCATTTACCTT
TGTTTATTTCAATATAAACTTTAATTTACAGTCCCTATCTATTGCCCGACTGGACTAACA
TGCACGTGACATTTTGTGATGGTTTTTCGTCCCTTACTTAGTACGCTTAGTACGCCACAG
TTTATATTTTCTTGACAATAATAAAGAACCTGATTGTGGGTTAGAACTTGCTATACTTTT
AGTTTAAAATAAGCAGGAAATAATCTTGAGTTCTGTATCATTATTATAAATAAACTATA
TTTGTTCCTTTGTGCGCCCTCGGAACCTTCTCTCATTACATTGACGAGGTATATATAGATA
TAGTAGATATACATATCTATCCATGGTATATATGTATGCATCTGGATAATTGAATAGGGT
TTCATGTCATATGCCAAGAATTTGTTAATAATATAGTGGAAAAAGTCAAGAGGTATTAT
AAATTTCAAAAAAGTACCAAATGGAGGATCAGGATGCTGCATTTATCAAACAGGCTACAG
AAGCAATAGTGGATGTATCATTAAATATAGATAACATAGATCCTATAATAAAAGAGTTAT
TAGAAAGGGTAAGGAATAGGCAAAACAGGTTACAAAATAAAAAACCAGCACTCATACCGG
CAGAAAATGGTGTGATATAAATAGTCAAGGCGGTAACATAAAGGTTAAAAGGAAAACG
CATTACCAAAACCACCGAAGTCCAGCAAAAGCAAACCCCAAGATCGTAGAAATAGTACTG
GTGAAAAAAGATTTAAATGTGCGAAATGTTCTGTTGGAATTTTCAAGATCATCAGATTGGA
GAAGGCACGAAAAGACACACTTCGCCATATTGCCTAACATTTGTCTCAATGTGGCAAAG
GTTTTGCAAGGAAAGATGCATTGAAAAGACATTATGATACACTGACATGTAGGAGAAACA
GGACTAAATTACTAACTGCGGGTGGTGAGGGTATCAATGAATTACTGAAAAAAGTCAAGC
AATCCAACATCGTTTCATCGTCAAGATAACAACCACAATGGTAGCAGTAATGGCTGA

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YDR253c, 191 aa (SEQ ID NO 114)

MEDQDAAFIKQATEAIVDVSLNIDNIDPIIKELLERVNRQNRQLQNKKPALIPAENGVDI
NSQGGNIKVKKENALPKPPKSSSKPQDRRNSTGEKRFKCAKSLEFSRSSDLRRHEKTH
FAILPNICPQCGKGFARKDALKRHYDTLTCRRNRKLLTAGGEGINELLKKVKQSNIVHR
QDNNHNGSSNG

YDR276C, 668 bp, CDS: 501-668 (SEQ ID NO 117)

ACCTTTAGTTCTTAGCATCACCAATCGCAGACATCCAACGTATCCGTGCGCGTAATCCTT
CTCTTGGTAGTTGAGCACAGCATAACAGAAGAAGCCGCGCGCAAGCGGTAAATGCTTTTCC
TCCGGCCTTCTAACCAACCAAAACCGATCTCGGAACATGGGGGGGGAAGGTCTCTGAAT
CGAAAAACCCGAGACAGCGAGAGGGATTTTGCAGAAAATTACAAAGATCACTATTTACTG
CTCCCCCTCACTTCCGCGAGTCCCTAATAGCGGAAGATGCAATGGGTGTGGGCTCTGGGTG
CCCTTTAACACGCCCTCAAAAGGGGGTCTGGTTATTTTGCAGATGGGCGCTCTATAAA
TACAAAAGAGGAAGTGAGTGTTTTTGTGTTTGGGAAGAGGAAAGGAAAAAAGAAGAAAT
TTACTATCGGTGTGTGTTTTTCGCCAGTATAATACAAATGATTATACATTTTGAACATAA
CAGCACAGCACAATACAACAAATGGATTCTGCCAAGATCATTAAACATTATATTATCCCTTT
TCTTACCACCAAGTCGCCGTTTTTCTAGCCCGTGGGTGGGGTACTGACTGTATAGTGGATA
TCATTTTGACCATTTTGGCTTGGTTCCAGGTATGCTATATGCCTTGTACATTGTCTTAC
AAGATTAA

YDR276C, 55 aa (SEQ ID NO 118)

MDSAKIINIILSLFLPPVAVFLARGWGTDCIVDIILITILAWFPGMLYALYIVLQD

YDR377W, 806 bp, CDS: 501-806 (SEQ ID NO 127)

AATACAAGACTTGGTGGTCAGCGGAGCGCTATCCTTAGAGAATTCTATCGACCTCTCTAA
TATCAAGCACACCACATGGAAGGATTGGGAAAGAATCAACAAGAAGGAATTGCTTCGGGG
CAAAAAGGAACACAAAACTCGGTCAAAGTTTTTAACTTTTGAAGAGTTGTGGAACGGTGT
AGAAGGCATATAAAATAGATCGTTAATATATTTCTAACATCTTCTTGTAATGTAAATAT
TTTTAAAAGGGTTGATCTTATTACGGAGAGAACCAATCATATCGAAGGATTTCTCAATAGT
AAGTATCCCGCGCGTGGTCTCGGGGAAATAGAACGAGAACTTCAAGTACTTGATAGCA
AGAAAGTGAGTGCTTGGCTTCCCCATTTTGATTATAAAGAAAGGCATTATTTTCTAGGGC
AAGAAAAGACATTGTTGAAATTTGTTCCAGAAACTTTCATTTAAAGTCTTTCGTGAAAGGA
GTGGACGTCAAAAAGAAATAATGATTTTAAACGTGCAGTATCTACATTGATTCTCTCAA
AAGTTGTGTCTTCCAAGAATATAGGTTCCGGCACCAATGCCAAGCGCATTGCTAATGTTG
TTCATTTTTATAAGTCTTTTGCCCAAGGACCAGCACCAGCCATCAAGGCTAACACTAGAT
TGGCCAGATACAAAGCCAAGTACTTTGATGGGGATAATGCTAGTGGTAAACCATTGTGGC
ATTTTGTCTAGGTATAATTGCCTTTGGCTATTCCATGGAATATTATTTTCAATTTGAGAC
ATCATAAAGGTGCGGAAGAGCATTGA

YDR377W, 101 aa (SEQ ID NO 128)

MIFKRAVSTLIPPKVVSSKNIGSAPNAKRIANVVHFYKSLPQGPAPAIAKANTRLARYKAK
YFDGDNASGKPLWHFALGIIAFGYSMEYVFHLRHHKGAEH

YEL039C, 842 bp, CDS: 501-842 (SEQ ID NO 141)

AGTAATTGTCTCCCATTTTTGGTATACGAGCTAGCAGGACCTTTTGCCCAATGACCATTTC
CATATTCATCCCACTCACCACCGTCATCGTTGGTATTATTATTATCATTCCGCTTGAAGA
AAAAGAAACGAAAAAAGAAATGGATCAGCAGCCGGGTATAGCGCCCTTATTGAATTAT
TTTCCTTCTGTGCTTCTCTGAGAAGGGTCTGCAGTCCCCCGCGAGGGGTCTTTTCCCAC
CTTCTCAAAGCTAATAGCGATAATAGCGAGGGCATTATTCAAGTTCCAACACTATAAG
TGGCCGCAAGGGGCAAAGACAAAGGCACACAACATATATATATATCGTGTGTGAAGCTC
GAGAAGATTAGATCAGAATAGTTCTCTTTTTGTTGAGGTTGAAACAAAATCAAAGACTTA
TACAAGAAGATCACATACAAGCATTTATTACATTACTTTAAGTAAACTTCAGTAAACTA
CATTACATCATAAACAAAACATGGCTAAAGAAAGTACGGGATTCAAACCAGGCTCTGCAA
AAAAGGGTGCTACATTGTTTAAACGAGGTGTGTCAGCAGTGTACATAATAGAAGAGGGTG
GTCCTAACAAAGTTGGACCTAATTTACATGGTATTTTTGGTAGACATTTCAGGTCAAGTAA
AGGGTTATTCTTACACAGATGCAAACATCAACAAGAACGTCAAATGGGATGAGGATAGTA

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TGTCCGAGTACTTGACGAACCCAAAGAAATATATTCCTGGTACCAAGATGGCGTTTGCCG
GGTTGAAGAAGGAAAAGGACAGAAACGATTTAATTACTTATATGACAAAGGCTGCCAAAT
AG

YEL039C, 113 aa (SEQ ID NO 142)

MAKESTGFKPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTD
ANINKNVKWDEDSMSEYLTNPVKYIPGTMFAFAGLKKKKDRNDLITYMTKAAK

YER112W, 1064 bp, CDS: 501-1064 (SEQ ID NO 147)

TACTGAAGTCCCTCTAAACCTACTGCCTTTTATTTTATAGGCTCTAAAAATAACCATGGACA
ACGTGAATTGGGTAGCATCTTTTTTTTAAATAGATAGTTTATTATGTATAACAATAATTTA
AAGATATTCATAGTGATAAGTAATTTTAAATGAGTTTAAAGTACTACTTTTCCTTTACCG
CCAGTTTCCTGTACTATGAAAAAGGCAAATTCGCGATTGTAGCCGCCACACGCATTTTG
ATCATCAATTACGAAATTTGCCGCACACGTGTACGTGATAAGCACTCTTACTATCATGT
TTTACGGAGTAGCAATGATGTTCAATTATTGCAGCTTTCTTTTCGTGAAATCGTAGTATCA
TAGACCTTCCTAATGATGGAAGCGGTAAAGAAGGAAATCGTAAAAGTAAATTAACGAAGT
AGTATTAGTAAACAGAGTTGAAAACTGATAAATCTTCAACTCGAACTGAAAAGAAACA
CAATAGAAATATTTTTTCTCAATGCTACCTTTTATATCTTTTAAACAAATGCGAAGGGACAAC
AAATGCAAAATAGAATTGAAAAACGGTGAAATTTATACAAGGGATATTGACCAACGTAGATA
ACTGGATGAACCTTACTTTTATCTAATGTAACCGAATATAGTGAAGAAAGCGCAATTAATT
CAGAAGACAATGCTGAGAGCAGTAAAGCCGTAAAAATTGAACGAAATTTATATTAGAGGGA
CTTTTATCAAGTTTATCAAATTGCAAGATAATATAATTGACAAGGTCAAGCAGCAAATTA
ACTCCAACAATAACTCTAATAGTAACGGCCCTGGGCATAAAAGATACTACAACAATAGGG
ATTCAAAACAATAAGAGGTAAC TACAACAGAAGAAATAATAATAACGGCAACAGCAACC
GCCGTCCATCTCTCAAAACCGTCAATACAACAACAGCAACAGCAGTAACATTAAACAACA
GTATCAACAGTATCTAATAGCAACAACCAAAATATGAACAATGGTTTAGGTGGGTCCGTCC
AACATCATTTTAAACAGCTCTTCTCCACAAAAGGTGCAATTTTAA

>YER112W, 187 aa (SEQ ID NO 148)

MLPLYLLTNAKGQMQIELKNGEIIQGILTNVDNWMNLTLNVT EYSEESAINSEDNAES
SKAVKLENIYIRGTFIKFIKLQDNIIDKVKQQINSNNNSNSNGPGHKRYNNRDSNNNRG
NYNRRNNNNNGNSNRRPYSQNRQYNNSNSNINNSINSINSNNQNMNGLGGSVQHFNSS
SPQKVEF

>YFR010W, 2000 bp, CDS: 501-2000 (SEQ ID NO 153)

GAAAAATTTCAACGGTGGTGTCTTAATGGTTTCCCATGATATCTCTGTTATTGACTCTGT
TTGTAAAGAGATTTGGGTTTCAGAGCAAGGTACTGTCAAGAGGTTCGAAGGTACAATTTA
CGACTATAGAGATTACATCTTGCAGTCTGCTGATGCTGCAGGTGTGGTTAAAAAGCATTG
ATTATTTAGGAAGCACCTCAGAATATATTTCCATAGAAGCCTAAATTAAGTATGCATTC
ATAGCCCCATGATACTTTTTTTTTTGACTACTTGTATTGGAATCTAATTGACCTAATCGG
GCATTTCTGGGTCATTGGGTATATGTATCACTTTTTTACGTAAAAAAGTAGTGGCTAATATAA
AACATAAAATCTACAAGAAGGGTGAAGTGCTTTTTCGAATTTTGCCACTGCAAGTAATTGG
TGCAATTGAAATACGAGATTTTCGTTCTCTAAGAGGATATAAAAAATAAGGAAATTAGCCCT
ACCTATCCTTGTTGTTAAAAATATGAGCGGAGAAACGTTTGAGTTCAATATTAGACATTCTG
GTAAAGTTTACCCAATAACACTTTCCACTGATGCTACTTCAGCAGATTTGAAAAGCAAAG
CAGAGGAATTGACCCAAGTCCCAAGTGCCCGCCAAAAATACATGGTTAAAGGTGGCTTGT
CTGGCGAAGAGTCCATTAAAAATATATCCCTTAATCAAGCCAGGATCGACAGTAATGCTAT
TGGGGACTCCAGATGCTAACCTGATTTCTAAACCAGCCAAAAAGAATAATTTCAATTGAAG
ACCTTGCGCCTGAGCAACAAGTCCAACAATTTGCTCAATTGCCTGTTGGTTTCAAGAATA
TGGGCAACACCTGTTATCTGAATGCTACCCTACAGGCTTTATACAGAGTGAACGATTTAA
GGGATATGATTCTTAATTATAACCCTTCTCAAGGTGTGTCTAACAGTGGTGCACAAGATG
AAGAGATTCACAAACAAATCGTTATTGAAATGAAGCGTTGTTTTGAAAATTTACAGAATA
AAAGTTTCAAGAGTGTTTTGCCAATTGTGTTATTAAACACGCTAAGAAAGTGTTATCCAC
AATTTGCTGAACGTGATTCAACAAGGTGGGTTCTATAAACAGCAAGACGCTGAGGAGTTGT
TTACACAAC TATTCATAGTATGAGTATTGTTTTTGGTGACAAATTTTCCGAAGATTTCA
GGATTCAATTTAAACTACCATCAAAGACACAGCTAATGATAACGATATTACTGTTAAAG

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AAAATGAAAGCGATTCTAAATTACAATGTCATATTTCTGGTACTACAAATTTTCATGAGAA
ATGGGCTCCTGGAAGGTTTGAATGAGAAAATTGAAAAAGATCAGACTTGACTGGCGCCA
ATTCCATCTATAGCGTCGAAAAGAAAATATCAAGATTACCAAAGTTTTTAACGTTCAGT
ACGTTAGATTTTTCTGGAAAAGGTCAACCAACAAAAATCTAAATATTGCGTAAGGTCG
TTTTCCCATTTCAATTAGATGTTGCAGACATGCTTACCCCAGAATACGCAGCAGAGAAGG
TAAAAGTTCGTGACGAAC TGAGAAAAGTTGAAAAGGAGAAAAATGAAAAGGAAAGAGAGA
TCAAAAGGCGTAAATTTGACCCATCATCCAGTGAAAATGTCATGACACCAAGAGAACAAT
ATGAGACACAAGTGGCTCTTAACGAAAAGTGAAAAGATCAATGGCTCGAAGAGTATAAGA
AACATTTTCCTCCAAACTTGAAAAAGGTGAAAACCCATCTTGTGTTTATAACTTGATCG
GTGTCATTACACATCAAGGTGCCAATTCTGAGTCTGGACACTATCAAGCTTTCATAAGGG
ACGAAC TGAGCGAAAATAAATGGTACAAATTTAATGATGATAAAGTTAGCGTTGTTGAAA
AGGAAAAAATTGAATCTTTAGCCGGTGGGGGCGAAAGTGATAGTGCATGATCTTAATGT
ATAAAGGATTTGGTCTGTAA

>YFR010W, 499 aa (SEQ ID NO 154)

MSGETFEFNIRHSGKVYPITLSTDATSADLKSABELTQVPSARQKYMVKGGLSGEESIK
IYPLIKPGSTVMLLGTDPANLISKPAKNNFIEDLAPEQQVQQAQLPVGFKNMGNNTCYL
NATLQALYRVNDLRDMILNYPNSQGVNSGAQDEEIHQIVIEMKRCFENLQNKSPKSVL
PIVLLNLTLRKCYPQFAERDSQGGFYKQQDAEELFTQLFHSMSIVFGDKFSEDFRIQFKTT
IKDTANDNDITVKENESDKLQCHISGTTNFMNGLLEGLNEKIEKRSDLTGANSIYSVE
KKISRLPKFLTQYVRFVFKRSTNKKSKILRKVVFPFQLDVAADMLTPEYAAEKVKVRDEL
RKVEKEKNEKEREIKRRKFDPSSENVMTPREQYETQVALNESEKDQWLEEYKKHFPNLL
EKGENPSCVYNLIGVITHQGANSESGHYQAFIRDEL DENKWKFNDDKVSVEKEKIESL
AGGGESDSALILMYKGFL

>YFR052W, 1325 bp, CDS: 501-1325 (SEQ ID NO 157)

CAGAGACATGTTTTAATTCAAGTGATGAGGCGGAAACGTGCAAGATCCTAAATGAAGGAT
AAAAAGAGTTCTTAAAAAGGGAAGTAAGGAATAACAGAGTAGAAAAACCGAAAAGACAAC
TTAACAAATCGGCAACACTTTTATGGGGCCCCGCTCGCCTGTGTGCAAGTAGTATTCGAC
CTGGAACACGCACTTTACCACGAGAAGACAGCAATAGTCCGTACAACATTAATTAGTTTCG
ACAATTGCTCGCCTTTATAAGCCATGCTAGTAGCCCAATCAAACACTTTACTTGCCCTGAA
GTTCCCTTTTTTCGCTAGCCTGTAACCTAAATAAGCCATCTAACCTTTTTTTTCTAAAAAT
TTTCTTTATTACCCTGTGCGCTTATTTTCTATTCTACACATTATTTGCCACCCATTGAAA
TTGTAGCTTGTATTAATAGGGAAGCCGGAAGTATAACCGGTGGAAGTACTATTGAAG
TGAGATAAGAAGCCATCGTAATGCCCTCGTTAGCCGAATTGACCAAGTCGTTAAGCATAG
CCTTTGAAAACGGCGATTATGCCGCGTGTGAGAAGCTCTTGCCCCCTATCAAGATCGAAC
TTATCAAGAATAACCTTTTAATACCTGACTTATCCATTCAAATGACATCTATTTGAATG
ATTTGATGATTACTAAAAGGATCCTGGAAGTAGGTGCCCTTGCTAGCATCCAACTTTCA
ATTTTGACAGCTTCGAGAATTACTTCAACCAATTGAAGCCTTACTACTTTAGCAACAATC
ATAAATTATCTGAATCTGACAAGAAATCGAAGCTGATAAGTCTGTATTTGTTGAACTTAT
TGTCTCAGAATAACACAACCAAGTTTCACTCGGAATTGCAGTATCTAGATAAACATATCA
AGAACTTGGAAGACGATTCACTTTTGTCTTACCCTATCAAAC TAGACAGATGGCTCATGG
AAGGGTCGTACCAGAAAGCATGGGATCTTCTGCAATCTGGGTCGCAGAAATATATCAGAAT
TCGACTCTTTTACCGATATCCTAAAAATCAGCTATAAGAGACGAAATTGCTAAAAATACCG
AGCTATCCTACGACTTTCTCCCTCTCTCCAACATAAAGGCTTTGCTCTTTTCAACAACG
AAAAAGAACTGAAAAATTTGCACTAGAGAGAACTGGCCTATTGTCAACTCGAAAGTTT
ACTTCAATAACCAATCAAAGGAGAAAGCTGATTACGAAGATGAAATGATGCATGAAGAAG
ACCAAAAGACAAACATTATCGAAAAAGCAATGGATTATGCCATAAGTATTGAAAAATATTG
TGTA

>YFR052W, 274 aa (SEQ ID NO 158)

MPSLAELTKSLSIAFENGDYAAACEKLLPPIKIELIKNNLLIPDL SIQNDIYLNDLMITKR
ILEVGALASIQT FNFD SFENYFNQLKPYPSNNHKLSESDKSKLISLYLLNLLSQNNNTT
KEHSELQYLDKHIKNLEDDSLSYPIKLDRLMEGSYQKAWDLLQSGSQNISEFDSFTDI
LKSAIRDEIAKNTELSYDFLPLSNIKALLFFNNEKETEFALERNWPVIVNSKVYFNNQSK
EKADYEDEMMEEDQKTNIIEKAMDYAI SIENIV

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>YGL072C, 860 bp, CDS: 501-860 (SEQ ID NO 159)

ACTCTTTTGTCTAGGGAGTTTCGTGCTCGCTAAGAGGTTTGTCAATGACACCGAAAAGAGGAT
AATAGGTAATACTTTTTTGTAACTGTAAAGAATATTAAATCGTTTTTCACGGAATTGGCCCTC
TTCCCTATATTCATCCGAGGTTGTGTACTGTAGCGGTTTATACCTTCAACCTGTGAAAGT
TATGTAATATGCGAATTCGTTCGTCTGCTTGATAATCTGAAGAATATAGTCTCGAGCACGC
GATGGAGCAGAAAGGGGAGAAATGAATACTGATGAGCTTAACGATGAGGAGGCCGTTTCC
GTTTCTCTTGATTACCCCTTTCATCCAACAGTCAATATAAGTACGCCAACTTGCGTTAAAA
CGGCCAATGTGACACCAGTTCACCTCGGCAAGCCCTTCTCAGGCTCTCACTAGCTCGAATA
ACGAGAACTCTTCACGACTCATCTACTTGGCATTTCCTGGGTGCAGTTCAACCTCACTCG
CGTGGCGGGTGTGAGGTGCATGGGTGCCGGTATTTTTTTTAGTTTCGCTCTGCGCCTTAC
CGCATCAGCTTCGAGAACATACTATATTAAATGATTATATACGCTATTTAATGACCTTGC
CCTGTGTACTATTTCTTAGCTCGTTTGGGCAGGCGGTGATCGTTGTACTCTGTGCGGTCC
TGTATTTGACTATAGCCGGTTCGGGTATTTCTCCACAAATCTTTCTTAGCGTTCTCG
GGCGCCGTGTGCGCTGGGTGGAATAACTGTGGTCATTAAAGCTTGGCAGGTTATCACTC
ACTTTAGTGTTTTCACTGGCGCTGAACCTTTATATCGGGGACACCCTTGTACTTCCCTCA
CTAGTGTTATTGTCGTTTAG

>YGL072C, 119 aa (SEQ ID NO 160)

MGAGIFFSSLALRDQLREHTILNDYIRYLMTLPCVLFLLSSFGQAVIVVLCRVLYFDYSR
FRYFLHKSFLSVLGRRVGLGGITVVIKAWQVITHFSVFSGAELYIGGHPCTSLTSVIVV

>YGL080W, 893 bp, CDS: 501-893 (SEQ ID NO 161)

GAAGAAAAGAAGAAGGGGATGATGAGGAAGGAGAAATAGAACTTGAAATTATTAGAGTA
AAAAGAATAAAGGGCAGGACGAAGATAAAGAAGACGCTTACTTGCTTCTCGAAAAACAAG
AAAATTATTACCCCTCAGCACTCCAATAGTATGTGGTTACTACTAATAGTAATCTTGATT
TTTGACCGCTACTATCGAATTAAATATAATTTTATAACCCAGTTCTATATTGCTGGGTG
GTATTACCGCTTCACTAGGCTAGTCAATAAGTGGAGTTTTTGTCTCTGGACGTGGCCTGTA
AAGTTCTCTTTTGCGACGGCCCCCGCTTTAACCAGGGCGAAATGACAAGTGCTTTCTGG
CAAAGAAGGAATAGCCACTACAACCTGCGGTCTCCACCTTTCTCCACCGATAATCTATTT
AAACACTCACTTGCCAATCAGCAAACGTCAATACATCTACATATATACGTATAGATTTTA
TTGCACTGTGATCAAAAAGAATGTCTCAACCGGTTCAACGCGCTGCAGCACGCTCATTCC
TTCAAAAATACATCAATAAAGAACTTTGAAATATATTTTCAACACACTTCTGGGGTC
CCGTATCAAAATTTCCGTATCCCAATTGCTGCTATATATGATCTGAAAAAGACCCTACAC
TAATCTCTGGCCCAATGACTTTTGCTTTAGTTACCTATTACAGGTGTTTTTCATGAAGTATG
CTCTTTTCAGTATCACCCAAAACTACTTACTGTTTGGATGCCACCTTATTAATGAACTG
CGCAATTAGCTCAAGGCTATAGGTTTCTCAAATACACGTATTTCAACAGATGAGGAGA
AGAAAGCTCTAGATAAGGAATGGAAAGAGAAAGAAAAAACTGGTAAACAGTAA

>YGL080W, 130 aa (SEQ ID NO 162)

MSQPVQRAAARSFLQKYINKETLKYIFTTHFWGPVSNFGIPIAAIYDLKKDPTLISGPMT
FALVTYSGVFMKYALSVSPKNYLLFGCHLINETAQLAQGYRFLKYTYFTTDEEKKALDKE
WKEKEKTGKQ

>YGR008C, 755 bp, CDS: 501-755 (SEQ ID NO 165)

CGCAATAGTTATGAACCTTAACCGAGCTCAAATAATTTAAAGATAAAAAGATAAAAAGATAAA
AGATAAAAGACAAAAGAAAATTCATAGCCCATGTTGAAGTATCCAGCGGGAAATGTTGC
TATCCAACAGAAAGTACCAAGCCAGTTTCAAAAAGGTACAGAATTAAGTGATGCTATCCG
TCCCACAATAATTTTCTCCAGCGGAGGAAATATACGCGGAGGGGGGAGGAAAACCTCT
CAGTAAGCAATGAAGGGATAGATAATGGGGGCGCGCTGCCTAGCTTAGGCTAAGAACT
CCTTCGAAAACAGGGGGCTGCGAGCGCAGAAGCGAACACTTGTCAATTTGTATAAAAGGAC
TATTTATAAGTTTGCTTTTGTCACTCTCTTGGCCCTAATTACCCATACTATTGTAACAA
TTGTTGTGTAACTCAATTATACAAATAAACGAACAATCAACAGTAACAAACCGCTCAAG
TGTACAACCAATCAGAAAAAATGACGAGAACAACAAGTGACCGAACGTAAGGAAAGG
CTGATCCAAAGTACTTTTCGCACACTGGTAACTACGGTGAATCTCCAAATCACATCAAGA
AGCAAGGTTCCGGCAAGGGTAATTGGGGTAAGCCAGGCGATGAGATTGATGACTTAATG
ATAATGGTGAAATACCCCCAGTGTTCAAGAAAGATAGAAGAGGCTCAAATTTGCAATCGC

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ATGAACAAAAGTTTGAAAACGTCCAAAAGGAATGA

>YGR008C, 84 aa (SEQ ID NO 166)

MTRTNKWTTEREGKADPKYFSHTGNYGESPNHIKKQSGSGKNWGPDEIDDLIDNGEIPP
VFKKDRRGSNLQSHQKFENVQKE

>YGR023W, 2156 bp, CDS: 501-2156 (SEQ ID NO 167)

TTAGATCATGGCTAGGGGGATCTGGAAGTACAATGATGTGCTCTCCCCCTCTCAAACACA
ACACCAAGATGAACCTAAGGGCTCATCTCGAAAGTGAAGGTGCCTCATTAGGTTATTAG
TGGTGCCTGTTGTGTCTTCCATGAACAAGGAGCACTTAATTACTTGTGTGTCATGAGAT
ATCATTTTTTTTTTTCCCTCTTTCTTGGGGTCTTGACAGTCATCAAATCGAAGTTTTTAG
TTTTTCTTCTTCGGGAAGATCAATTTTAGGTAGAAAAGTGTAGATGAAAAACGAAGGATA
CTGCTATTTACTGTAAGTACTCTTCGGTCCATATTGGAAGACCAAGGCATAATAAGGATA
TATTCGAGGAGATAATTGGGATATAATCTCCATTGCTTCCGAAATTTGTTTAAACACT
TCTAGTTTCAATTCGGGTTGGTTCGATCTTCGTTTCCACTTTTAACTTACTCCAGTTAGT
ATAATATAAGTAGTTAAGGTATGGCAAGCTGCAATCCGACCAGGAAGAAGAGCTCTGCTT
CAAGCCTATCTATGTGGAGAACGATTCTCATGGCGTTAACAACACTACCGCTAAGTGTTC
TTTCGAGGAGTTGGTTCAGCTAATAGCACAAACATCGAGCACAGCTCCTTCCATCACTT
CGCTTTCCGCAGTTGAGTCATTTACGTCCAGTACCGATGCAACGAGCAGCGCAAGTTTAT
CAACGCCGAGTATAGCTTCAGTATCCTTTACTTCCCTTCCCACAAAGTTCTTCACTGCTTA
CTCTTTTCGTCAACATTATCTCAGAACTTTCCTCTTCGTCCATGCAAGTTTCGTCTCTT
CAACATCGTCGTCTTCTTCGGAGGTTACGTCATCATCGTCATCATCAATATCTCCTT
CCTCTTCATCATCAACAATAATATCATCGTCATCATCACTGCCGACATTCAGTGTGGCAT
CAACATCTTCGACAGTTGCCCTCCACACTTTCCACTAGCTCATCGTTGGTTATCTCTA
CGTCTTCGTCAACGTTTACGTTTACGTTTCGAAAGTTCAAGCTCTTTGATTTCTCTCAA
TTTCAACATCCGTTTCGACTTCTTCAGTGTACGTTCCCTCCTCTTCAACTTCATCTCCAC
CTTCGTCCCTCATCCGAATGACATCATCCTCGTACTCATCATCCTCATCCTCATCCACCC
TCTTTTCTTACTCCTCCTCATTTTCATCATCCTCATCCTCATCCTCATCATCCTCT
CATCCTCATCATCATCATCATCATCATCATCATCATATTTTACCCTCTCCACATCTTCTCTT
CATCCATATACTCGTCTTCGTTCATATCCTTTCATTTTCATCTTTCATCTTCTCTCAAACCTA
CCTCATCAATCACTTCTACATCCGCCCTCATCTTCTATTACTCCCGCTTCCGAATATFCCA
ATTTGGCAAAAACCATAACTAGTATAATAGAAGGCCAGACCATCCTCTCTAACTACTATA
CCACAATAACGTATTCACCGACAGCATCCGCATCTTCAGGAAAAAATTCACATCACTCAG
GCTTATCAAAAAAGAATCGTAATATTATCATCGGTTGTGTGGTTGGCATAGGTGCCCCC
TCATCCTAATTCTACTAATATTGATTTACATGTTTGTGTTTCAGCCTAAAAAACGGATT
TCATTGACTCTGACGGTAAAAATGTGCACAGCTTATCGTAGTAACATTTTACCAGAAATAT
GGTATTTCTTGCTGGGTAAAAAATTTGGTGAAACAGAAAGATTTCAGCTCAGATTCCCCCA
TCGGCAGCAATAATATTCAGAAATTTGGTGATATCGATCCAGAAGATATACTTAAACAATG
ACAACCCCTACACCCCTAAACACACTAATGTTGAAGGCTACGACGACGACGACGACGACG
ACGCTAATGATGAAAACCTATCATCCAACCTCCATAACAGAGGCATAGATGATCAATACT
CACCTACTAAATCTGCATCATATTCAATGTGGAATAGTAATAGTCAAGATTACAACGACG
CAGATGAAGTAATGCACGATGAAACATTCATCGTGTATTATGATGACAGCGAAGCTAGCA
TCGACGAGAATATTACACGAAACCAACACGGCTTAAATATCACGAATATTAA

>YGR023W, 551 aa (SEQ ID NO 168)

MASCNPTRKKSSASSLSMWRTILMALTTLPVLSQELVPANSTTSSTAPSITSLSAVES
FTSSTDATSSASLSTPSIASVSFTSFPQSSSLTLLSSTLSELSSSSMQVSSSSSTSSSS
EVTSSSSSSSISSSSSTIISSSSSLPTFTVASTSSTVASSTLSTSSSLVISTSSSTFT
FSSESSSSLISSSISTSVSTSSVVPSSSTSSPPSSSELSSSYSSSSSSSTLFSYSS
FSSSSSSSSSSSSSSSSSSSSSSSYFTLSTSSSSSIYSSSYSPSSSSSNPTSSITST
SASSSITPASEYSNLAKTITSIIEGQTILSNYYTTITYSPTASASSGKNSHHGLSKKNR
NIIIGCVVGIGAPLILILLILIYMFVQPKKTDFFIDSDGKIVTAYRSNIFTKIWFLLGK
KIGETERFSSDSPIGSNNIQNFQDIDPEDILNNDNPYTPKHTNVEGYDDDDDDANDENL
SSNFHNRGIDQYSPTKSASYSMSNSNSQDYNDADVMHDENIHRVYDDSEASIDENYYT
KPNNGLNITNY

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>YGR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2:
880-1244 (SEQ ID NO 169)

TATAAAAAAAAAATTCTGTAGACAATAAAATAAGAAATGCCCATTTTGTAACTTAGCGAAA
GATGCCCAGTACATCCCTTTTACACCCGTGCATTAAAGGTGTTTGGGTTTAATAGGAGCT
TTATCATATCTCTTTGATTTTTTTTCTGCTGTCCTCGGCTTGAGGGACTCACAGAGATCT
GGAAATTTTCAGATTGTCAGTGCTTAGGATGGGTGTGTCAGTAGACGGTGGCCGCCGTGGA
TGGGAAATCTCATACGTTTACACACATAGTGTTTGGAAATTAATAGTAGCAATAGCTATC
TGGCTACTGTTTTAAAGTATTAGCCCGTTCTCAGTGCTTCTTTTTTAAGGAATAACAACG
GCAAGACCAAAGATATATCAAATATGGCTAAGCAATCTCTAGGTATGTTTGGAGGATACG
AATAACGATAGAAAACATGAGTGAATTCCCGTCCACGAAAAAATGTTAACATAAAATGCA
AGAGAACAATTAAATCGAATAATGTTAAATTATTGTAAAACAATGTGTATGATGAGGAGGA
ATGTACCTAAGCCAAAAAAG
ATTCAATCCAGGCATAGGGCGACTATTAGCACTCAACGATTTTTTAAGCTTGTGTATTGC
TGACATAAATTCCGGCTTTAGAATCCAATATTGAAAAACGTGAGTACGCAGAGGAGATAG
AAGAAAAGTAGGAAGTTACCGTTTATATTGATTTGTGAAATGCATACTCCGTTGGATGTG
GGGCAACATAGATTTAAGTGTGGATGAAAATTATGTGCTCATTGTGAAAAAAAAGTTTTG
CTTTTACTAACAAATTTTTTTATTATTGTGTTTTCAATAGACGTTTCTCTGACAGAAGAA
AGGCCAGAAAGGCTTATTTCACTGCTCCATCCTCTGAACGTCGTGTTTGTATCTGCTC
CATTATCCAAGGAATTGAGAGCTCAATATGGTATCAAGGCTTTGCCAATCAGAAGAGACG
ATGAAGTCTTGTGTGTTCTGTTCCAAAGAGGGTCAAGAAGGTAAGATTTTCATCTGTTT
ACAGATTGAAGTTTGCTGTTCAAGTTGACAAGGTCACCAAGGAAAAGGTCAACGGTGCTT
CCGTTCCAATTAACTTGCACCCATCCAAGCTTGTATCACTAAGTTACACTTGGACAAGG
ACAGAAAGGCTTTGATCCAAAGAAAGGGTGGTAAATTGGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKTMYVSSDRRKARKAYFTAPSSERRVLLSAPLSKELRAQYGIKALPIRRDDEVLV
VRGSKKGQEGKISSVYRLKFAVQVDKVTKEKVGASVPINLHPSKLVITKLHLDKDRKAL
IQRKGGKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

TTCGAATTATTTTGTGAAAACAGGGCTCGAAAGTGATCTCTTGCTTAGAAATATTGCGT
TGCCCGCTGGTGTCCATATCTTGGTTGCTTGTAAGTGGACCGCTACTACTGTTATGTTGAT
TTTCCGCATTTTCCCCACCGACTAAAACATCCCTTTTGAAGAAACCAATAAGTTGTCCC
AATAGCATTCGAAAATCTTACGCTTTTCCCTTAACCTAGACTTGCCAACTACTGCTATTCT
TCTTATATCGGCCAACTTGCAAAAACCCAATTGAAATCTTCCCTACCAATCTCAGCGAAA
TTTTCTTCACTACGATCTCATTTTTCACTGAAATCACTAAGTTTCCCTGATAAAGGTATAG
ACGACAGTTCCAACGGTGACCCTTGGATCAAAATTATGTCTTGTACGGGGAGTTTATTC
TAATATCAAAATAACTTATTCTCTCTCTTTCTCTCTGCTCTGAATGCCACCGCTGCTAG
ATAGCGAACTAAGTGAACATGGTCTTGCTTACCCCTATTCTCGCCGAGAGCTGTACAA
GATATTTTTTACTTTTGCCATCTTATACTCATCCTAATCATCTGTTTCATTTTCTCTTA
TTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGTTTTTGAAGAACTGCCTTTTTA
GAATTGTAAAAGACGAAGTGAAGTATTCAGGAGTATATTATTACATACATACAAAGCAAG
ACAAAGAAACATTTTGTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCTCTTATAATA
AGAAAGACCTGCTGTTTAAATGTGGGAGTAATCCGTCCTTACTCGATCTTCAATAA

>YGR069W, 111 aa (SEQ ID NO 172)

MVLLHPILAESCTRYFLLLPSTHPNHLHFPSISFFFFFFFFFSSFRNCLFRIVKDEV
KYSGVYYYIHTKQDKETFLDLTFYFNCFCIPYNKKDLLFNVGIVIRPLDLQ

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTTAGATCTAACATTTTACTTCAATTGTTTTGTATTCCCTTATAATAAGA
AAGACCTGCTGTTTAAATGTGGGAGTAATCCGTCCTTACTCGATCTTCAATAAATTGTCA
TCTTGATATCTAAAGGAGCGCTCCAGTACTCCAATTAAGCACCACCTAGTGCGTCTAGTGT
CGATTTTTTTTTTACGCATACGTTTGTATGTTTCTTAAATTTCCCATGATTTTTTGTGTC
CAATGTCTATCTACAACTCTATACGAAAGTAAACGCACCTTCATCTTTTTTGCCCTAAA
ACGGCAATATTTAGACATATCATAAGGGGCCCAAGGGAGAATCGTTAATTTTAACTTTT

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CTTTGCTCTTGAATGAAAAAGTAAATAAAATAAACTAAATCAAAAAAAGAACGCCACGT
TTGAATTTTAAAGCAAAAATTTTGTGATTTAGTAATGATATAAAATAAAACCAAGTCGTT
GGTAAGAATTTGGTTAGGTTATGAATAGTAATGAACTGGATCTAAGAAATAAATATTTT
ATGAGATATTCGGTAAGAAAAGAAAATCAGATACTTCAACCCCTACTCAGTTGTTCTCCG
GCTCCAAAGTTCAGACAAACATCAATGAAATTTCTATCACTAACGATGAGGATGAAGATA
GTACTGAAGATGAAAATAAGGCTTCATTGAAGGATTATACACTAGGGCACGACACCGGTG
CACGGTATAGGATAGCACCCGACTGTTCTTCCACCAATTAAAGGCATCTCCTGTCCTAC
ATATTTCAACAAACCTTAATTCAAGTCCACAATCCTTCACAGGCGATCAGATTTACCTA
CTAATAAAAAAATTTCAATAAATGATTCGACCAGACAAGATAAAAGGTAACAGTTGCACTA
CCACTTCATCACCTTCTCAAAAAAGATCGAATGTTTTGCTTCTCCTACGTAAGAAAAACATT
CATCTCCTTCACTATTATCATTTTCCAAAAACAGTGGCAGTCATATGGGGGATCCAAACC
AGCTATCTACGCCTCCAACTCCAAAAAGTGCAGGTACACGATGGAGTTACACAGTTCAT
TCAATGGAAAACATAGTTCTTCTAGCACCTCTTCTTTATTTGCATTAGAGTCACTGAAAA
CCCAAAATAGACGCTCATCAAACTCTTCCAATCATTCTAGTCAATATCGACGCCATACTA
ATCAACACCAACGTCATCATTTCAAGGTCCAAATCAAGTCTGTCTCTCTGACGGAATAT
CCATGATCAAAGGCACGCCTTTGGTTTATCCTGCACTTTTATCACTAATAGCAATTAAT
TCAAACAGACCATCAAATTGAGCACGCATAAAAAGATGGGGTTACTTTACAGAGATTCCT
TTACAGGAAAACAAGCAATTGATACTTTATGCTTGATCATAGGAAGCTTAGATCGTAATT
TGGGCATGTTGATCGGAAAATCGCTGGAAGCTCAAAAAATGTTCCATGACGTACTTTATG
ACCATGGCGTAAGAGATTCTGTACTGGAGATTTACGAGTTATCTTCAGAATCAATTTTTA
TGGCACATCAGTCGAGAGTTCTACTTCAATTGCCAACACATTTTCTTCATCATCTTCTT
CAGTTAATTCGCTCCGTACTAAAACCTGAAATATATGGTGTTTTTGTCCCATTGACACATT
GTTATTCCTCTACATGCTCTCTGAAAAACTTTGCTACTCTATTTCTTGCCCCAATCGTT
TGCAACAACAGGCTAATTTACATTTAAAAATTAGGTGGTGGTCTTAAGAGAAATATTTCGT
TAGCACTCGATAAGGAGGATGATGAACGAATTTCTGGACAAATCTGTACCAAAGAGCG
TATGGGAATCATTATCCAAACAAACAAATCAAAAAGGCAGGAGCAATATATGAGTTGTTTA
CTACAGAAAAGAAGTTTGTAATAATCTTTGGAAATCATCCGAGATACTTTTCATGAAGAAAT
TATTAGAAAACGAATATTATTCATCTGATGTAAGGATAAAATTTTGTAAGCACGTTTTTCG
CACATATCAATGAAATATATTTCTGTCAATAGAGAATTTTTGAAGGCTTTAGCACAAAGGC
AATCATTAAGCCCAATTTGTCTGGAATTCGAGATATATTTTTGCAGTATCTTCCTTTTCT
TTGATCCTTTTCTGTACATACATAGCATCAAGACCATACGCAAAGTATCTAATTGAAACCC
AAAGATCAGTTAATCCCAATTTTGCTCGTTTTGACGATGAAGTGTCTAATTTCTTCCCTGA
GGCATGGGATCGATTCAATTCCTATCTCAGGGTGTTCAGACCTGGTAGATATTCACGTGT
TGGTAAGAGAAAATAATACACTTCTCGGACCCAGTAACAGACAAAGATGATCTACAAATGC
TAATGAAAAGTCCAAGATCTTTTAAAGGATCTAATGAAAAGGATTGATAGAGCAAGCGGTG
CAGCACAAAGATCGTTATGACGTTAAAGTGTTAAAGCAGAAAATTCATTTCAAAAATGAAT
ACGTTAATCTGGGTTTGAATAACGAAAAAAGGAAAATCAAGCATGAAGGTTTACTCTCAA
GGAAGGACGTGAACAAAACAGATGCGTCCTTTTTCAGGAGACATTCAATTTTACCTACTCG
ACAATATGCTATTATTTCTTGAAATCAAAAGCTGTAAACAAGTGGCACCACACACTGTAT
TTCAGAGACCAATTCCTACTCCCTTTACTGTTTTATTTGTCCGGCTGAGGATATGCCACCCA
TAAAAAGATATGTGACAGAAAACCCAAATTGCTCAGCGGTGTGCTCTTACCCCAATATC
AAACGAGCAATCCCAAGAAATGCTATTGTATTTCGCCTATTACGGTACGAAACAACAATATC
AAGTTACTTTGTACGCGCCGACGCCGGCGGATTACAGACATTAATAGAAAAGGTGAAAC
AAGAGCAAAAAAGGCTCCCTTGATGAAACATAACATATTACTTTTTAAGCAATGGTAGGTC
AATTCTTTCACTCATACATAAATACATAATCGCGTCAACGATGTCTAATCTGTATGCTG
GTAAAAATTTTATTGGTTGCAACAAATATGGGACTCTTTGTTCTTAATTTATGCTACATCGA
TCAATCAAAAAACAGTGCACCTTCTGCACAAAATATCAATTTACAGATCTCTGTATTGG
AAGAATATAAAGTTATGATTCTTCTAATTGACAAAAAAGTACGGCTGTCTTTAGACG
TAATCGACGATGCAGAAAATGCAGATTTTCTTTTCAGAAAAAATTCATAAGTGTTATTTA
AATATGTTGCAATGTTCAAAGACGGTTTCTGTAAATGGTAAAAGAATCATTATGATTGCAC
ATCATTTTTTGCACGCCGCACAATATTGATTGTTAATCCTTTGATATTTGATTTTAATA
GCGGTAAATTTTAAAAAAAACCTAAAGGCAGGCTTGGTAGATTTTAGCGTTGATTCTGAAC
CTCTGTCTCTTTCTTTTTTTGGAGAATAAGATCTGCATTGGTTGTAAAAAAAATATCAAAA
TATTAAACGTACCGGAAGTGTGTGATAAAAATGGATTTAAAATGAGGGAGCTTTTAAATC
TACATGATAACAAAGTTTATAGCGAACATGTATAAAGAGACGTTCAAAGTAGTTTCCATGT
TTCCGATAAAAAATTCACCTTTTGCATGTTTTCCAGAACTCTGCTTTTTTCTCAATAAGC

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AAGGGAAGAGGGAGGAGACAAAGGGATGTTTTTCATTGGGAGGGGGAACCAGAACAGTTTCG
CGTGTTCCTACCCCTTATATTGTGGCAATTAATAGTAACCTTATTGAAATTAGACATATAG
AAAATGGAGAACTTGTCCGCTGTGTACTTGGAAACAAGATACGTATGTTAAATCATATG
CCAAGAAGATCTTATATTGTTATGAGGATCCTCAAGGATTTGAAATTATCGAACTGTTAA
ATTTTTGA

>YGR070W, 1155 aa (SEQ ID NO 174)

MNSNELDLRNKYFYEIFGKKRKSDTSTPTQLFSGSKVQTNINEISITNDEDEDSTEDENK
ASLKDYTLGHD TGARYRIAPDCSSHLKASPV LHISTNLNSSPQSFTGDQISPTNKKISI
NDSTRQDKGNSCTTTSSPSQKRSNVLLPHVRKHSSPSLLSFSKNSGSHMGDPNQLSTPPT
PKSAGHTMELHSSFNKGHSSSSSTSLFALES LKTQNRSSNSSNHSSQYRRHTNQHQHH
SRKSSPVS LTEISMIKGTPLVYPALLSLIAIKFKQTIKLS THKKMGLLYRDSFTGKQAI
DTLCLIIIGSLDRNLGMLIGKSLEAQKLFHDVLYDHGVRDSVLEIYELSSSEIFMAHQSQS
STSIANTFSSSSSVNSLRKTETIYGVFVPLTHCYSSSTCSLEKLCYSISCPNRLQQQANL
HLKLGGLKRNISLALDKEDDERISWTNSVPKSVWESLSKQQIKRQEAIYELFTTEKKFV
KSLEIIRDTFMKLLETNIIPSDVRINFVKHVFHINEIYSVNREFLKALAQRLSPIC
PGIADIFLQYLPFFDPFLSYIASRPYAKYLIETQSVNPNFARFDEVSNSSLRHGIDSF
LSQGVSRPGRYSLLVREIHFSDPVTDKDDLQMLMKVQDLLKDLMKRIDRASGAAQDRYD
VKVLKQKILFKNEYVNLGLNNEKRKIKHEGLLSRKDVNKTDAFSGDIQFYLLDNMLLFL
KSKAVNKWHQHTVFRPIPLPLLFICPAEDMPPIKRYVTENPNC SAGVLLPQYQTSNPKN
AIVFAYYGTQYQVTLYAPQAPAGLQTLIEKVQEQRLLDETKHITFKQMVGFHFSYI
NTNRVNDVLICHAGKILLVATNMGLFVLNYATSINQKPVHLLHKISISQISVLEEYKVM
LLIDKKLYGCPDVDIDDAENADFLFRKNSKVLFKYVAMFKDGFNGKRIIMIAHHFLHAA
QLLIVNPLIFDFNSGNFKNLKAGLVDFSV DSEPLSFSFLENKICIGCKKNIKILNVPEV
CDKNGFKMRELLNLHDNKVLANMYKETFKVVSMPFIKNSTFACFPEL CFFLNKQKGREET
KGC FHWEGEPEQFACSYPIVAINSNFIEIRHIENGELVRCVLGNKIRMLKSYAKKILYC
YEDPQGFELIELLNF

>YGR132C, 1364 bp, CDS: 501-1364 (SEQ ID NO 177)

CATACATGTATCAGACGTATAGCTCCTACGATTCTCAAGAATCCAGAAGTTTGGCATATT
ATGTATAAAGGCGATGATTATGTATATTTTATGTTGTCTCCAGTAAGTGGCAGCATAACC
CGGCCAGTCTGCGCTGCATGCTGTGAAGCAGTAATATGCGATATATACCACATATATTCC
GCTTCCGTT CAGGATTTGAAAAGAGAACTTCAGTGAATGACTATGACTACATAGTTGG
AGTCTTAGACCATTGCAAATGAGTTATTCAAGTATGAGAGATCAACACTGATGAGAATAA
ACTCGTCTTCATGATGATACGGGTAACGCGAATGTATCGCATCAATAAATTT CAGGGAAA
GGGAGTTTGACGATCTCATGGATGCAACGGTTGAGGTATATAATATTAAGCAGAAAGAAG
AGGAAAAAATAAATCGGTAAACCAACCATCAACGGTACGAAACTTACATTCAAAATCA
ATAATTTACTTTAGAAAAGAATGTCTAATTTCTGCCAAACTTATCGATGTATCATCACCAGG
TGGCGTTGCCCATTGGTATAATTGCTAGCGGGATT CAGTACTCCATGTATGATGTGAAGG
GTGGTTCTCGTGGTGTTATTTTCGACAGAATCAATGGTGTAAGCAACAGGTTGTGGGTG
AAGGCACTCATTTCTTGGTGCTTGGCTACAGAAGGCGATCATATACGATGTGAGGACGA
AACCAAGAGCATTGCTACCAATACTGGTACGAAGGATTGCAAATGGTGT CATTGACCT
TGAGAGTCTTACATAGACCAGAGGCTTACAGCTACCGCAATATACCAAAATTTGGGTC
TCGATTACGACGAAAGAGTGTTACCATCTATCGGCAATGAGGTTTTAAAGTCTATAGTAG
CTCAATTTGATGCTGCTGAGTTAATTACTCAGAGAGAAATTATTTCTCAAAAAATCAGAA
AAGAGCTTTCTACGAGGGCCAACGAATTCGGTATTAAGTTGGAAGATGTCTCTATCACTC
ATATGACGTTTGGTCCCGAATTCACGAAAGCAGTTGAGCAGAAGCAGATTGCACAGCAAG
ATGCCGAAAGAGCCAAATTCCTTGTCGAAAAGGCAGAGCAAGAGAGACAAGCTTCTGTTA
TCAGAGCTGAAGGTGAAGCAGAAAGTGCTGAATTCATTTCAAAGCCTTAGCTAAAGTTG
GTGATGGTCTGTTATTGATTAGAAGATTAGAAGCTTCTAAGGACATCGCTCAAACATTAG
CAAACCTCATCTAACGTTGTCTATTTACCAAGTCAACATTCTGGTGGTGGTAACAGCGAGT
CTTCGGGATCACCAAAATTCCTTGCTTTTGAACATTGGCCGTAA

>YGR132C, 287 aa (SEQ ID NO 178)

MSNSAKLIDVITKVALPIGIIASGIQYSMDVKGSGRVIFDRINGVKQVVGEGTHFLV
PWLQKAIIDVVRTKPKSIATNTGT KDLQMVSLTLRVLHRPEVLQLPAIYQNLGLDYDERV

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LPSIGNEVLKSIVAQFDAAELITQREIISQKIRKELSTRANEFGIKLEDVSIHTMTFGPE
FTKAVEQKQIAQQDAERAKFLVEKAEQERQASVIRAEGEAESAEFISKALAKVGDGLLLI
RRLEASKDIAQTLANSNNVYLPSQHSGGNSESSGSPNSLLLNIGR

>YGR135W, 1277 bp, CDS: 501-1277 (SEQ ID NO 179)

TTCTGAACCTGAATCTGAAATTGTTAAACCTGTTTCCCTCAAAGCCTGCAAACAAAGACGA
TAGTTCCCTTATTAACACGTTGCGTAGTTTTATCGCTGATTACTCCTTCGACACCCAGGT
GAACCTCCAGGAAGAAGGGTGGTGTCTACGATGGTAAGATTTTGCCATTGCCCAAAGC
CGATAAGCCTATCCCACTTCATGAATATATAACACTCGCAGAGCTCGATGTTGGAGACAG
TGAGTGAGCAGTGAATTGCTCATGTTTTCTCTGCATCCTCATTTAATGACAATTAGCCAT
GTAATAACATCTTGAGGCAGTTAAATATTCTGTTACCTGTCAGGTGGCAAAAATTTATAG
AATAAAGCATAAAAAGATGGATATCTATGTAATAAGGAAACATTGGCAGAGCGAAGAGA
ACAGACTGCTTTCTATAAAAAGTTTTCGATCAGTCTCTATTTTAATAATTGATTATTGGA
TATAGTTAGTAGTGTTAAACATGGGTTCAGAAGATACGATTCCAGGACAACAATTTTCT
CCCCTGAGGGACGCTATATCAGGTTGAATACGCGCTAGAATCCATTTACATGCAGGTA
CCGCAATTGGGATTATGGCATCTGATGGGATTGTTCTTGACAGCAGAACGCAAAGTCACAA
GTACTTTACTAGAACAAGACACCTCTACCGAAAACTTTATAAGTTAAACGATAAAATTG
CGGTTGCCGTTGCTGGACTGACTGCAGATGCAGAAATTTCTAATAAATACGGCTAGAATTC
ACGCTCAAAATTACCTTAAAACCTATAATGAAGATATACCAGTAGAAATTTTGGTGAGAA
GGCTAAGTGATATAAAACAAGGTTACACGCAACATGGTGGTTTAAGACCATTGTGGTGTGT
CCTTTATCTACGCCGGTTATGACGATAGATACGGTTACCAATTGTATACATCTAATCCAT
CGGGAACTATACAGGGTGAAGGCTATTAGTGTTGGCGCTAACACATCAGCAGCACAAA
CCCTACTTCAATGGACTACAAGGATGATATGAAAGTCGATGATGCCATTGAACTGGCTT
TAAAAACGTTATCCAAACTACCGACAGTAGCGCGCTGACTTATGACAGGTTGGAATTTG
CTACTATCAGAAAGGGTGCTAATGACGGAGAAGTGTATCAGAAGATTTTCAAGCCTCAAG
AGATAAAGGATATATTGGTAAAGACTGGTATTACCAAGAAGGATGAAGACGAAGAAGCTG
ATGAAGATATGAAATAA

>YGR135W, 258 aa (SEQ ID NO 180)

MGSRRYDSRTTIFSPTEGRLYQVEYALESHAGTAIGIMASDGIVLAAERKVTSTLLEQD
TSTEKLYKLNDKIAVAVAGLTADAEILINTARIHAQNYLKTYNEDIPEILVRRLSDIKQ
GYTQHGGRLRPFVGSFIYAGYDDRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLLQMDY
KDDMKVDDAIELALKTLSTTDSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILV
KTGITKKDEDEEADMK

>YGR155W, 2024 bp, CDS: 501-2024 (SEQ ID NO 181)

GTGTTCTCATCCGACCCTCTGATTCATTTGGTGGCCATTACATTTTCCCTCAATGACACA
TTCCCTTATTTTCATAACTGATTAAAAATGGTAATGGCACGTGATAGTAGTGGCTCACAAAA
CAAAATTTTCTTTCTCAGCGCTGACAAAGCTTCATTTGCATTCTAACCTTATCACAAACA
CTTCAACTTCACCCAAGTAAGGATAATCAGCTCTGTCTGACTGATAAATGCTATATCCG
GCATATGCAGTCCACACGGCATTACCGTTTCACTAATTTATTGCCATCTTCTCCACAGT
TTTGACCCGAAAGGAAAAAAGAAACCAACACCGAAAAATTTTTTCTCCTAAAGGTTAAA
GTAAACGCAAGGCACCTTACCAGGCTTGATATATAAATGTCGTGATGCTTCTATGCCAA
AGTAAAAGGCAACACTTGAAGATTTCTGTTGAGGCCACTTGCTCAAAGGACATCTAGATA
AATACGACGTAAGAATAAAAAATGACTAAATCTGAGCAGCAAGCCGATTCAAGACATAACG
TTATCGACTTAGTTGGTAACACCCCAATTGATCGCACTGAAAAAATTGCCTAAGGCTTTGG
GTATCAAACCACAAATTTATGCTAAGCTGGAACATATACAATCCAGGTGGTTCATCAAAG
ACAGAATTGCCAAGTCTATGGTGAAGAAGCTGAAGCTTCCGGTAGAATTCATCCTTCCA
GATCTACTCTGATCGAACCTACTTCTGGTAACACCGGTATCGGTCTAGCTTTAATCGGCG
CCATCAAAGGTTACAGAACTATCATCACCTTGCCGAAAAAATGTCTAACGAGAAAGTTT
CTGTCTAAAGGCTCTGGGTGCTGAAATCATCAGAACTCCAAGTGTGCTGCTTGGGATT
CTCCAGAATCACATATTGGTGTGCTAAGAAGTTGGAAAAAGAGATTCCTGGTGCTGTATA
TACTTGACCAATATAACAATATGATGAACCCAGAAGCTCATTACTTTGGTACTGGTCGCG
AAATCCAAAGACAGCTAGAAGACTTGAATTTATTGATAATCTACGCGCTGTTGTTGCTG
GTGCTGGTACTGGTGGGACTATTAGCGGTATTTCCAAGTACTTGAAAGAACAGAATGATA
AGATCCAAATCGTTGGTGCTGACCCATTCTGGTTCAATTTTAGCCCAACCTGAAAACCTGA

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ATAAGACTGATATCACTGACTACAAAGTTGAGGGTATTGGTTATGATTTTGTTCCTCAGG
TTTTGGACAGAAAATTAATTGATGTTTGGTATAAGACAGACGACAAGCCTTCTTTCAAAT
ACGCCAGACAATTGATTTCTAACGAAGGTGCTTGGTGGGTGGTTCTTCCGGTTCTGCCT
TCACTGCGGTTGTGAAATACTGTGAAGACCACCTGAACCTGACTGAAGATGATGTCATTG
TTGCCATATTTCCAGATTCCATCAGGTGCTACCTAACCAAATTCGTCGATGACGAATGGT
TGAAAAAGAACAATTTGTGGGATGATGACGTGTTGGCCCGTTTGGACTCTTCAAAGCTGG
AGGCTTCGACGACAAAATACGCTGATGTGTTTGGTAACGCTACTGTAAAGGATCTTCACT
TGAAACCGGTTGTTTCCGTTAAGGAAACCGCTAAGGTCCTGATGTTATCAAGATATTAA
AAGACAATGGCTTTGACCAATTGCCTGTGTTGACTGAAGACGGCAAGTTGTCTGGTTTAG
TTACTCTCTCTGAGCTTCTAAGAAAATCAATCAATAATTCAAACAACGACAACACTA
TAAAGGGTAAATACTTGGACTTCAAGAAATTAAACAATTTCAATGATGTTTCTCTTTACA
ACGAAAATAAATCCGGTAAGAAGAAGTTTATTAAATTCGATGAAAACCTCAAAGCTATCTG
ACTTGAATCGTTTCTTTGAAAAAACTCATCTGCCGTTATCACTGATGGCTTGAAACCAA
TCCATATCGTTACTAAGATGGATTTACTGAGCTACTTAGCATAA

>YGR155W, 507 aa (SEQ ID NO 182)

MTKSEQQADSRHNVIDLVGNTPLIALKKLPKALGIKPIYAKLELYNPGGSIKDRIAKSM
VEEAEASGRIHPSRSTLIEPTSGNTGIGLALIGAIGYRTIITLPEKMSNEKVSVLKALG
AEIIRTPTAAAWDSPESHIGVAKKLEKEIPGAVILDQYNNMMNPEAHYFGTGREIQRQLE
DLNLFNLRVAVAGAGTGGTISGISKYLKEQNDKIQIVGADPFGSILAQPENLNKTDITD
YKVEGIGYDFVPQVLDRLKIDVWYKTDDKPSFKYARQLISNEGVLVGSSSGSAFTAVVKY
CEDHPELTEDDVIVAIFPDSIRSULTKFDVDEWLKNNLWDDDLARFDDSKLEASTTKY
ADVFGNATVKDLHLKPVVSVKETAKVTDVIKILKDNFQDLPVLTEDGKLSGLVTLSELL
RKLSINNSNNDNTIKGKYLDPKKLNFNNDVSSYNENKSGKKKFIKFDENSKLSDLNRFFE
KNSSAVITDGLKPIHIVTKMDLLSYLA

>YHR095W, 935 bp, CDS: 501-935 (SEQ ID NO 207)

GACACCTTTTCCGGTGTGTTGGAGGGGCAACGGCGGGTGCACCTTGACTTTCACTTAAGTT
GTCGTGAAAACCTTTCATTTTACCTTCTGGAGTATTCATGGCCTTTGAACGACCAGATTC
CAATTGATGATGTTGGATGAATTTGATTTCTGAGGAGATATTAGATCGGGAGTTGAAT
CATGATTTTACGTATATCAACTAGTTGACGATTATGATATCTTTATAGATTTTAAGGTGG
GGAAAGAACATGAGACCCAGATGGAATTGATTATGGGACATTGTTGCCCTTTATATATA
ATTTCAATATACTAATTCAAATGATTAAAAACGTGAGGGGGACACGCAACTTCGGGTGTT
AAGAAATATTTTGCTACATTAGATAATGGTGGAGTTTCTGGCTTGTGCGATAAAAGCCA
TCAAATGTGCGCAGCAGCTCATGTTTACGTTTGTCTTCTGCCCACGTCATATGAGTGG
TATTCTTCTATCAGCACTTGATGAATATCTTTTCTCATATATCTGAAAGACAAAAGAT
CGGCACGGCAATGCCCTGCAGCATTTCTTCTAGTTTTCGGAATTTCCATTACGTATTG
GATCTTGTGCGCATATTTGTGAGTCTTTCACGGAAGAAAAAGAGCACTGGGTCACTT
CGGAAAAAATTTTGACTCAATGCAACAGTGTCAATCCTTTGCGCTGTCTCTTTGAAGA
AAAATCAGGAGTGCAAGATATCGATTAAATTCCTTGGAAGTTATGATGGTTAGTCTTAGTT
TAACTCTCTTGAAGAAGGGTFTTTTTCAGTTGGTCAACACTCTTTAGAGGTAAAAAAGAG
AAAAAAGAGAAATTCCTCATGTAATTTACCATGATTCTACGTTTGTGCAAG
CAAAAATGAAGATAATCCGAGCGCATGCGAAGTAG

>YHR095W, 144 aa (SEQ ID NO 208)

MNILFLIYLKDKRSARQCPAFLPSFSEPLRIGSCAHICQSFTTEKKKEHWVTSEKLLTQ
CNSVILCAVSLKKNQECKISINSLEVMMVSLSLTLKKGFFSWSTLFRGKKKKKKKKR
ILHVIYHDSFTLQAKMKIIRAHAK

>YHR138C, 845 bp, CDS: 501-845 (SEQ ID NO 209)

CTACGAAAATAAGCAAAAAATAAATAAAAAACAAAAACAAAAACAAAAAC
AAAAACAAAAACAAAAACACATATTGTTATGATGACTGGACGAAAGAAAGATCGTCGT
CTTTCTTAATTGTTTGTCTTTCAGTACAGTTATTATCAGTGTCTCTTTCTTTTATGTT
ACTATGTGATGTTACTGATACATCACGCGCTTCTTTATGTTTCTTTTATGTTTCGT
TACAGGATTTATAGTTTTCAGTATATTGACTTCAATAATTTCTAATATTCAGTTCCCTA
TTAAATTTGATTATTCGGATTAGATCGGTGCGCGCTACCAAAAAGAGCGAAGAAAGAG

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GAAAACGCAAGTGGATAAAGGGGTGGGGGGCAAAGTATTTAAGAAAAAGCGATGCGATG
GAGAGAACAAATGGATAAGTTGCGTTTCCTCGTTATATTACAACATTTAAATCTATTGTG
TAACAGACTATAGCATATATATGAAGGCCAGTTACTTAGTTTTGATTTTCATTAGCATAT
TCTCCATGGCACAGGCATCTTCCTTATCATCATACATCGTAACTTTCCCAAGACGGATA
ATATGGCTACGGACCAGAATAGCATTATTGAAGATGTCAAAAAATATGTGGTGGACATAG
GGGTAAAAATAACACACGAATATAGCTTGATAAAGGGCTTTACAGTGGACTTACCTGATA
CGACCAAATTTTGGACGGTCTGAAAGAACGTTTGAGCTATATTGAAAGCGAGTACGGTG
CTAAATGCAATTTGGAAAAGGATTGAGAAGTTCATGCTCTAAACCGTGACCATTTAGTTG
CTTAG

>YHR138C, 114 aa (SEQ ID NO 210)

MKASYLVLFISIFSMAQASSLSSYIVTFPKTDNMATDQNSIIEDVKKYVVDIGGKI THE
YSLIKGFTVDLPDSQILDGLKERLSYIESEYGAKCNLEKDSEVHALNRDHLVA

>YHR179W, 1703 bp, CDS: 501-1703 (SEQ ID NO 215)

ATATCTTACGTAATGAACTTCCGTAATGAACTTCCGTAATTCAGATCTCTTAGCATCTC
TTGTTCAATCTTCAGACTCTACTAAGTGTCTTACCAACCATTGGATGCTCATTACAAAT
GAATGAATATATTGCACGGAACGGAAGCGGCATGCTTTTTCCGTCTCGTGTGCTTAGTAA
AGCAAAACGGAGTAGAATCGGTAAGAACTTCCTTTTTGGGTGGAAAATCATTGCCATTG
TTTGACACCTTTCTTTTTCCGTATTGTTTCGAGCACCGCGTTCTTTTTGGGTACTTGAT
GAGGTAGCAGATTCCCTGGAACGTGCTTTCTCTCGAGGTAACCTGCCTTGTTTCTCCTGGT
GACTTTCTAAAATATAAAAGGAAAAGCATATCTCTAGTTTCGAGTTTTTTCTTCATACTT
TATTTCTTATGTTAAACGGTCCAGATATAGAATAAATCATCATATTAAGCTAAATATAG
ACGATAATATAGTATCGATAATGCCATTTGTTAAGGACTTTAAGCCACAAGCTTTGGGTG
ACACCAACTTATTCAAACCAATCAAATTTGGTAACAATGAACTTCTACACCGTGCTGTCA
TTCCTCCATTGACTAGAAATGAGAGCCCAACATCCAGGTAATATTCCAAACAGAGACTGGG
CCGTTGAATACTACGCTCAACGTGCTCAAAGACCAGGAACCTTGATTATCACTGAAGGTA
CCTTTCCCTCTCCACAATCTGGGGGTACGACAATGCTCCAGGTATCTGGTCCGAAGAAC
AAATTAAGAATGGACCAAGATTTTCAAGGCTATTTCATGAGAATAAATCGTTCCGATGGG
TCCAATTATGGGTCTAGGTTGGGCTGCTTTCCAGACACCCTTGCTAGGGATGGTTTGC
GTTACGACTCCGCTTCTGACAACGTGTATATGAATGCAGAACAAGAAGAAAAGGCTAAGA
AGGCTAACACCCACAACACAGTATAACAAAGGATGAAATTAAGCAATACGTCAAAGAAT
ACGTCCAAGCTGCCAAAACCTCCATTGCTGCTGGTGCCGATGGTGTGAAATCCACAGCG
CTAACGGTTACTTGTTGAACCAGTTCTTGGACCCACACTCCAATAACAGAACCGATGAGT
ATGGTGGATCCATCGAAAACAGAGCCCGTTTACCTTGGAAAGTGGTTGATGCAGTTGTCTG
ATGCTATTGGCCCTGAAAAAGTCGGTTTGAGATTGTCTCCATATGGTGTCTTCAACAGTA
TGTCTGGTGGTGTGTAACCGGTATTGTTGCTCAATATGCTTATGTCTTAGGTGAACTAG
AAAGAAGAGCTAAAGCTGGCAAGCGTTTGGCTTTTCGTCATCTAGTTGAACCTCGTGTC
CCAACCCATTTTTAACTGAAGGTGAAGGTGAATACAATGGAGGTAGCAACAAATTTGCTT
ATTCTATCTGGAAGGGCCCAATTATTAGAGCTGGTAACTTTGCTCTGCACCCAGAAGTTG
TCAGAGAAGAGGTGAAGGATCCTAGAACATTGATCGGTTACGGTAGATTTTTTATCTCTA
ATCCAGATTTGGTTGATCGTTTGGAAAAAGGGTTACCATTAAACAAATATGACAGAGACA
CTTTCTACAAATGTGAGCTGAGGGATACATTGACTACCCTACGTACGAAGAAGCTCTAA
AACTCGGTTGGGACAAAAATTAA

>YHR179W, 400 aa (SEQ ID NO 216)

MPFVKDFKPQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRAQHPGNIPNRDWAWEYYAQ
RAQRPGTLIITEGTFPSPQSGGYDNAPGIWSEEQIKWTKIFKAIHENKSFAWVQLWVLG
WAAF PDTLARDGLRYDSASDNVYMNAEQEEKAKKANNPQHSITKDEIKQYVKEYVQAANK
SIAAGADGVEIHSANGYLLNQFLDPHSNNRTDEYGGSIENRARFTLEVVDVAVDAIGPEK
VGLRLSPYGVFNMSGGAETGIVAQYAYVLGELERRAKAGKRLAFVHLVEPRVTNPFLTE
GEGEYNGGSNKFAYSIIWKGP IIRAGNFALHPEVVREEVKDPRTLIGYGRFFISNPDLVDR
LEKGLPLNKYDRDTFYKMSAEGYIDYPTYEEALKLGWDKN

>YIL074C, 1910 bp, CDS: 501-1910 (SEQ ID NO 219)

TGGGAGTCTTTAGCAAGTTCGGCAAAATATCGATATCAATAGTATTGCTAAATAAACCTTT

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TTTATTCCATTACTGTCGTTTATACTGGCTGACCCCTTAATTCCTTAGCAATCTTTGCCCT
GCACCCGTACCAGGAAGCGTGATAGAATCGGTAGCTACAAAATTTTATAGCATAGTTAATA
AGTGCTATTGTTTTCATAATGTCACGTGCACTATCAATAATTACACTCTTGTTCTTG
CCAAATATACAAAAATGCCACATTTTTTCTTTACACCGAAGAAATTTGGCCGTCAGCCG
GACAGCGCTCAGATTAAATGTGGGGCTAGATTCTTCACGCTGGAAACGAGTCACCGTTATG
AAACTAATGGAATCTCCCAGGTTTAATACATAAGAAGGTTACGAGCTACTACATTAAAA
AATACTTTGTCGTGTTTAGCTGTAGATTATTGTAACATTAAAAAGTAACAAACACTGATT
TCGGGTATTTCTCCCTAACATGTCTTATTACGCTGCCGATAATTTACAAGATTCATTCC
AACGTGCCATGAACTTTCTGGCTCTCCTGGTGCAGTCTCAACCTCACCAACTCAGTCAT
TTATGAACACACTACCTCGTCGTGTAAGCATTACAAAGCAACCAAGGCTTTAAACCTT
TTTCTACTGGTGACATGAATATTCTACTGTTGGAAAATGTCAATGCAACTGCAATCAAAA
TCTTCAAGGATCAGGGTTACCAAGTAGAGTTCCACAAGTCTTCTCTACCTGAGGATGAAT
TGATTGAAAAAATCAAAGACGTACACGCTATCGGTATAAGATCCAAAAC TAGATTGACTG
AAAAAATACTACAGCATGCCAGGAATCTAGTTTGTATTGGTTGTTTTTGCATAGGTACCA
ATCAAGTAGACCTAAAATATGCCGCTAGTAAAGGTATTGCTGTTTTCAATTGCCATTCT
CCAATTCAAGATCCGTAGCAGAATTGGTAATTGGTGAGATCATTAGTTTAGCAAGACAAT
TAGGTGATAGATCCATTGAACTGCATACAGGTACATGGAATAAAGTCGCTGCTAGGTGTT
GGGAAGTAAGAGGAAAAACTCTCGGTATTATTGGGTATGGTCACATTGGTTTCGCAATTAT
CAGTTCTTGCAAGCTATGGGCCTGCATGTGCTATACTATGATATCGTGACAATTATGG
CCTTAGGTACTGCCAGACAAGTTTCTACATTAGATGAATTGTTGAATAAATCTGATTTTG
TAACACTACATGTACCAGCTACTCCAGAACTGAAAAAATGTTATCTGCTCCACAATTCTG
CTGCTATGAAGGACGGGGCTTATGTTATTAATGCCTCAAGAGGTACTGTGCTGGACATTC
CATCTCTGATCCAAGCCGTCAAGGCCAACAAAATTCAGGTGCTGCTTTAGATGTTTATC
CACATGAACCAGCTAAGAACGGTGAAGGTTCAATTTAACGATGAACCTAACAGCTGGACTT
CTGAGTTGGTTTCATTACCAAATATAATCCTGACACCACATATTGGTGGCTCTACAGAAG
AAGCTCAAAGTTCAATCGGTATTGAGGTGGCTACTGCATTGTCCAAATACATCAATGAAG
GTAACCTCTGTCGGTCTGTGAACTTCCCAGAAGTCAGTTTGAAGTCTTTGGACTACGATC
AAGAGAACACAGTACGTGCTTGTATATTTCATCGTAACGTTCTGTTGTTTGAAGACCG
TTAATGATATCTTATCCGATCATAATATCGAGAAACAGTTTCTGATTCTCACGGCGAGA
TCGCTTATCTAATGGCAGACATCTCTTCTGTTAATCAAAGTGAAATCAAGGATATATATG
AAAAGTTGAACCAAACTTCTGCCAAAGTTTCCATCAGGTATTATACTAA

>YIL074C, 469 aa (SEQ ID NO 220)

MSYSAADNLQDSFQRAMNFSGSPGAVSTSPTQSFMTLPRRVSITKQPKALKPFSTGDMN
ILLLENVNATAIKIFKDQGYQVEFHKSSLPEDELIEKIKDVHAIGIRSKTRLTEKILQHA
RNLVCIGCFICIGNQVDLKYAASKGIAVFNSPFSNSRSVAELVIGEIIISLARQLGDRSIE
LHTGTWNKVAARCEVRGKTLGIIGYGHIGSQLSVLAEAMGLHVLYYDIVTIMALGTARQ
VSTLDELLENKSDFVTLHVPATPETEKMLSAPQFAAMKDGAYVINASRGTVVDIPSLIQAV
KANKIAGAALDVYPHEPAKNGEGSFNDELNSWTSSELVSLPNIILTPHIGGSTEEAQSSIG
IEVATALSKYINEGNSVGSVNFPEVSLKSLDYDQENTVRVLYIHRNVPGVLKTVNDILSD
HNIEKQFSDSHGEIAYLMADISSVNQSEIKDIYEKLNQTSAKVSIRLLY

>YIR037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)

GTTTTCCATGCTTTTGGCCGATTTCTTCCACCAACGCTTCCATTTCGAGACCTGTCCGTGA
TGTCGAGGACACGATAGACAAAATTTGTCTGCACCGTATTCTCTTTGCAAAGACTGCAGAC
CAGCTTCCGTTCTTGCTACGCCGTAGACGATGCATTCATCGTCTCTTCGATAACAGTTT
TCACCAATTGCAGGCCAATCCCACGGGAGGCACCTGTAATCAAAAATAACCTTGCCCATAT
CCCTTCTTTGACAGATTATAAGTTGTTTCTCTTGTGTTGCTGTTTCGCGACAGCCCTTATTTC
CTGTATTCTTCTTCTTTTCTGCAATTATCGTTTTTATGCCACTTTACGAAAAAGGTCAAA
AAGTGAAAAAAGAGGGAAAAAACCATGAGGAACAGTATGCTCCCTTAATATCGGAAAAG
CAATAGTAATAAAAACAGCATCAGAGCTTTCCACGTCTCTCTCTTCCAAGCTGTCATCTC
GTAAAGTATTCAAGTTTATCATGTCAGAATTCTATAAGCTAGCACCTGTTGACAAGAAAG
GCCAACCATTCCCTTCGACCAATTAAAGGGAAAAGTGGTGCTTATCGTTAATGTTGCCCT
CCAAATGTGGATTCACTCCTCAATACAAAGAACTAGAGGCCTTGACAAACGTTATAAGG
ACGAAGGATTTACCATCATCGGGTTCCCATGCAACCAGTTTGGCCACCAAGAACCTGGCT
CTGATGAAGAAATTGCCAGTTCTGCCAACTGAAGTATGGCGTGACTTTCCCATTTATGA

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AAAAAATTGACGTTAATGGTGGCAATGAGGACCCCTGTTTACAAGTTTTTGAAGAGCCAAA
AATCCGGTATGTTGGGCTTGAGAGGTATCAAATGGAATTTTGAAAAATCTTAGTCGATA
AAAAGGGTAAAGTGTAACGAAAGATACTCTTCACTAACCAACCTTCTTCGTTGTCCGAAA
CCATCGAAGAACTTTTGAAAGAGGTGGAATAG

>YIR037W, 163 aa (SEQ ID NO 222)

MSEFYKLAPVDKKGQPFPPFDQLKGKVVLI NVASKCGFTPQYKELEALYKRYKDEGFTII
GFPCNQFGHQEPGSDEEIAQFCQLNYGVTFPIIMKKIDVNGGNEP VYKFLKSQKSGMLGL
RGIKWNFEKFLVDKKGKVYERYSSLT KPSSLSETIEELLKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)

TCATAAAGTCTGGCGCGTATTCCCTGCACAATTTTCATATCTTCCCATATGAATACCTG
TTAGTCCGTATCACCAAGTGTAAGTCTTTTACAATGAGAACATCTAGAGTCTTTCTG
ATATGCGTAACTTCTGCCTCATTAATTTAAAAATTTCTTCATAGTAAATAGCTTATTTGC
TTGGAGCAGATGATCGACATGTATTTTTAGGAACATAAACTGCCTAAATATAATAGATCA
GCCTAAAAATAAGAATGCCAATCAACAAAGTTGTATTTCTATCTTCCGATATTCCGAGT
CCACCATTCAAGACCTCTGGTGAGATAGTTTGCTGCTTTTGCTCCCTTCCAAAGTGCTGA
TAAAAACCTCCGTGATTTTTTGAATACTCCCTGAATGTCTATTTTAAGTATATTATAAA
ATTAGTTTAAGTTGGTGCGGATAACGAAAACCTTGATGCAAGGTAAATAAATCAAGTATAT
CATAGAGTCTTTTCATTCATATGCTATACACAAGGTTGTTACGTCACAACCTCACAATTCA
CCAAGTTTTCAGGCACATCGCCCAATCTTGGCTCAAAAACCTTTATTTTTCGAAGGGTAATT
TGTAAGTCTTTTAGTGACAACACTGTATGGGACAGGTCTGGCATGCCATATATCTAG
AATCAAAATAGCTTGAATAAGTCCAAAGAGCAAGAAGATCCCCATGCCATCGCAGAAGACG
ACATTGTAAATATAGTCCATGACGCTCCCAATAGAATATTCAAGCCAGCACTTGATACCT
ATCAAGAGAAAGAGCTTGACTTACAAAAGAGTGACCTCCATAAAGTACTTCATCTTTGA
CGTACAGTGATGTCTCTCAATTTTCGATTGTTTGGGGGTTTCTCATTCAACTTTTCGAGCC
TAATAGGCAATTCCACCTTAGGCAAAAAATCCATCTTTATAAGGGAAGTGTCGTTAGTG
TTTATAGGTTTCCACCTTGATTATATGGCACTTAAACTTAGGATGAAACAGCTGGAAA
AAGCTGGAGTGCGCTTTGAGTAA

>YJL161W, 180 aa (SEQ ID NO 230)

MLYTRLLRHNSQFTKFSGTSPNLGSKPLFSKGNLYTSLLVTTLYGTGLACLYLESNSLNK
SKEQEDPHAIAEDDIVNIVHDAPNRIFKPALDITYQEKELDLQKSDLHKVLHSLTYSDVSQ
FSIVWGFLIQLSSLIGNSTLGKKSILYKGSVSVLGFPLIYMALKLRMKQLEKAGVRFE

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)

GTATATTCAAGAAGATGACACACCAAAGCCAAAGCCATTAAAGTAGATGATGAACAATG
GGACTACAAAATGAAATAAAGAAAAAATAGAAATAGGCTAGAAGATCAATTATTAAATCGC
CCTATTCTTCCCTTATTACCTACACAAAATAAAGCAGCAACATAAGAAACAAAAACAAAAT
GAAAACAAACCAATAAATCTATGTAAGCATACTCATTTCAATTTGATATTCAATTACTTG
ACTTTTTTTGTCCTTATTTGAGGCTCCATAAGCGCGCCATTTTCCCTACTCCCTTTTTTC
GTAAATAGTAATAATGTGCTGAAAAGAACAATGAAGTAGTTATCATACATATTCCGTCGT
GTCGATATGAGGGGAGGTGTCTCTTTCTTTTCATCCCTTGTGCGCAACCTCCAATATATAAG
AGCATAAGCAACTGATCTTACTTTAGTAATTAACCTTAGCATACCTAGCCCGAAGGAAGAA
AAAAAATTCACCTCAACAACATGGTTCCTAAGTTTTACAAAACCTTTCAAACGGCTTCAAAA
TCCCAAGCATTGCTTTGGGAACCTACGATATTCCAAGATCGCAAACAGCCGAAATTGTGT
ATGAAGGTGTCAAGTGCGGCTACCGTCATTTGATACCTGCTGTTCTTTATGGTAATGAGA
AGGAAGTTGGCGATGGTATCATTAATGGTTGAACGAAGATCCAGGGAACCATAAACGTG
AGGAAATCTTCTACACTACTAAATTATGGAATTCGCAAAACGGATATAAAAGAGCTAAAG
CTGCCATTCCGGCAATGTTTGAATGAAGTCTCGGGCTTGCAATACATCGATCTTCTTTTGA
TTCATTCCGCCACTGGAAGGTTCTAAATTAAGGTTGGAAACTTGGCGCGCCATGCAAGAAG
CGGTTGATGAAGGATTGGTTAAGTCTATAGGGGTTTCCAACATATGGGAAAAAGCACATTG
ATGAACTTTTGAAGTGGCCAGAAGTGAAGCACAAAGCCAGTGGTCAACCAAAATCGAGATAT
CACCTTGGATTATGAGACAAGAATTAGCAGATTACTGTAAATCTAAAGGTCTCGTCGTCG
AAGCCTTTGCCCCATTGTGTACGGCTACAAAATGACTAATCCAGATTTATTAAAAGGTTT
GCAAAGAGGTGGACCGTAATCCAGGTCAAGTTTTGATTCTGGTCTTTACAACACGGTT

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ATTTACCACTACCGAAGACTAAACTGTGAAGAGGTTAGAAAGGTAACCTTGCAGCCTACA
ACTTTGAACTGTCAGACGAACAGATGAAATTTCTTGATCATCCTGATGCTTATGAGCCTA
CCGATTGGGAATGCACAGACGCCATAA

>YJR096W, 282 aa (SEQ ID NO 234)

MVPKFYKLSNGFKIPSIALGTYDIPRSQTAEIVYEGVKCYRHFDTAVLYGNEKEVGDGI
IKWLNEPDGNHKBREEIFYTTKLWNSQNGYKRAKAIRQCLNEVSGLQYIDLLLIHSPLEG
SKLRLETWRAMQEAVDEGLVKSIGVSNYGKKHIDELLNWPELKHKPVVNQIEISPWIMRQ
ELADYCKSKGLVVEAFAPLCHGYKMTNPDLLKVCKEVDNRNPGQVLRWSLQHGYPPLPKT
KTVKRLEGNLAAYNFELSDEQMKFLDHPDAYEPTDWECTDAP

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)

CTGGGCTAGGTTTCACATATCAAAAAGAAGTTATGGCTTATGTGCTCTTTCTAAGTTTGA
CTTTATGCCAAAAATTTCTCCGTAGATCGCCGCCCGTTGAAGCAGCAGAATATTTTAAGT
GCGCCATAAAAACCTAGATAGAAAAGAAGGGAGAGAACATAAACGCAGAACACCACTACT
TTTAAGGCGTACGCAAACTGTTGGGCTTATCTATATTGTACTATCTACCTACTTGCAACG
TCTTTTACCTCCTCGATACGTACTGCTTATGCCCTGAACAATTTACATGTAACCCGCGAGC
TGCATGCTATATCACAGGATACGTTAACATAAAGGGGGCGCTACTAAACCCCTCTGGCGCA
GTGCAAAAATAGAAATATATGCCAAGTGGGACCTTGTATAGTTTCTGGTTTAAAGCTATT
CGTTCATTGCAACGCTCCTTTCTGCTATCCTTTTCGCAAAGTGGCAAGTACTGAAAACCGA
GAAGAATAAATAATATTGCGATGAGTTTATACTTTACGACATTATTTTATTGCTCACTG
TTGAGGTGGTAATGCTCTTCATCTTCGTTTTGCCTTTGCCATTCCGGATCCGTAGGGGTA
TTTTTAGCACCTATAACCAATTGACAGCGAAGCAGCAAATAAAAACTATAATCTTTATAA
CGGGTTGTCTTGTGGCCTGTTGTTTATTGATTTCATGGAAAAGGTCTCAAATTCGTGTTT
CATTATACCACAACGACAACAGTGGCTCAATCGGGTCATCTGCTGTAACCTCAATACAGC
CACTAGCATCAAGAGCGTACAATCAAAGAAATATGTATATTTCCGGGTTTCATATTGTACT
TTTCTATCTGTATCCCAACTGTCATGTCTATTGTCAAGAGACTGGTGAAATACCAAGGCT
TAATCAACGAACAAGAAAAGCAAAAATTGAACAAACCTTCCTCAAACAGCAAGAAAAGACT
CAAATGAAGCTGATTCCACCAAACCTCAAGAGGAACTAAGGAAAAGCAAATTTCTCTGG
AGGGCCTACAAAAGCAAGTCAAAAACCTGGAGAAATATTTTGATGAGAAGAATCAACCTG
GAAATGTAGCAGCTGCTGAAGCTTCCAAGAAAGGAACTAA

>YKL065C, 206 aa (SEQ ID NO 242)

MSLYFTTLFLLLTVFVVMLEFIFVLPFPFRIRRGIFSTYNQLTAKQQIKTIIFITGCLVGL
LFIDSWKRSQIRVSLYHNDNSGSIGSSAVTPIQALASRAYNQNRNMYISGFILYFSICIPT
VMSIVKRLVKYQGLINEQEKKLNKPSSNSKKDSNEADSTKLQEELRKKQISLEGLQKQV
KNLEKYFDEKNQPGNVAAAEASKKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)

AAAGAGGCTTCCATTAGGAGCAATAAAATATAAAGCACCAGCCATAGAAAGAATCCCCA
TTATAAAGCCCCGCTGTTTTTCCGTGATTGGAGTTCTACCGAACTGAGGGGAGGACGCCA
TGAGACGTCTTGTGTTGGTGTCCGCATAACCCCCCTTGCCACTTGAATTGACGGCCTGTTTC
TGCACGCATTCTTGACGACTAAGTTGCGAAGCATTTTACTGATAATATACACTCTTTGGA
TCGAGCCTACTTCCAGTTGGTAATTGGTGTCCACAATTTGAGCATTATATGTTTTTAA
CCAAAATTGCGCTCCTTTTCCCCTTTTTTTCTTATTGGGTGGCGTGCCGTACAGAACGATT
GGCTTGGTGTGAAATCAAGAGCAAGCACAATAGATATCAACATGAACAATATACAAAAGT
CTCTGGCACAGTTTGAAGTGGTGTAGACAGGCTAGGGCATTCTGAAGCTTTACGTATCA
CTAGAGAAGTTATTTTGGCAATGAGAATCTACTACATCGGTGTATTTGCTCTGGAGGAG
AAAAGGCTCTAGAGTTGAGTGAAGTTAAAGACTTGTCACAATTTGGTTCTTTGAAAGGT
CTAGTGTGTCAGTTTATGACTTTTTTTGCTGAAACGGTTCGCTCTAGAACTGGTGCAG
GACAAAGACAAAGTATAGAGAAGGCAACTATATTGGCCACGTTTATGCCAGGAGTGAGG
GCATATGTGGTGTGTTTGTATCACCAGCAAGAAATATCCTGTGACAGCAGCATACACACTAT
TAAACAAAATATTGGATGAATATTTAGTCGCACATCCTAAGGAAGAGTGGGCAGATGTGA
CTGAGACCAATGATGCATTGAAAAAGCAACTGGACACTTACATTAGCAAATATCAAG
ATCCTTTCACAGGCTGACGCTATCATGAAAGTTCAACAAGAACTGGATGAGACGAAAATCG
TTTTGCACAAAACGATTGAGAATGTTTTACAAAGAGGTGAAAAGTTGGATAATTTGGTGG

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ACAAATCGGAGTCATTAACGGCAAGTTCCAAAATGTTTATAAGCAAGCTAAAAAATCCA
ATTTCGTGTTGCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)

MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSSVGQFMFFAETVASRTGAGQRQSIE
EGNYIGHVYARSEIGCVLITDKEYPVRPAYTLNKLDEYLVHPKEEWADVTEINDAL
KMKQLDITYISKYQDPSQADAIMKVQQELDETKIVLHKTIENVLQRGEKLDNLVDKSESLT
ASSKMFYKQAKKSNSCCIIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEQ ID NO 259)

TAAATAGTTGAGGCTTTTCCCTGCATTCTGTCAAGAAGGGTATGTGTATGAACATGCAAAT
GACACTGTAAATGATTTCATTACCCGTATTATGGAGTGATTTCTTTCCCTTTTTTTTTTTT
ACATTTAGTTTCATTATTATGCAAATTAGAGGGTATACAGTTGAGATTTTAACACTTTGA
ATTAAAAAGTGTTACAGAGGAAACCGACGCAAAAGGCTTGGTGACGCAAACTTTTCCATC
TTTATTTTACCTCTTCAGACGGTCCTAAGACCTTTTGAACGTATCAATATAGTTTATCA
TCTGTTCTCTGTGTTCTCCGTTACTAAGATATTAGTCAGCTCTTGAAATTTACACCCC
TATTTATTTGTCTTAGCGTCCAACCCCTCTCAACCTTTTCCATTTCTTGTATAAAGGTA
GTTAATTAGGTAACGCTGCTCTTACCATCACTACAGTGCTTACGAGAATTTACCCAAACC
CTGCGCAAGATAAATAAGAAATGTCGAAACAGTGGGCGAGTGGTACAAACGGAGCTTTCA
AAAGACAGGTTTCGTCCTTCAGAGAAACAATCTCTAAGCAACACCCAATTTATAAGCCAG
CAAAGGGAAGATATTGGTTGTATGTTTCACTTGTCATGCCCATGGGCCCATAGAACAATAA
TTACGAGGGCTTTGAAGGGATTAACTCTGTTATAGGATGTAGCGTAGTCCATTGGCACC
TTGACGAGAAAGGATGGAGATTTTGGACATGGAAAAGCAATTGGAGGACAGTGAAGATT
TTTTGGAACATTGGCACGATGTTGACAGGTGGTATTAGAAGTGCATAAGAGGATTCCAGCA
AGAGCTTCGCCGAGATCAAGAATGACAGTCAAAGATTATGGTTGATGCTACCAATGAGC
CTCACATATGGATACAAGAGAATCAGTGACTTATATTACAAGAGCGATCCTCAATACTCGG
CAAGGTTACCCGTCCCAGTCCCTGTGGGACTTAGAAACCCAAACAATTGTTAACAACGAAA
GTAGCGAAATTATAAGGATTTTGAAGTCTAGTGCGTTTCGATGAATTTGTCGACGACGATC
ACAAGAAAACGGACCTTGTTCCCTGCTCAGTTGAAAACACAGATCGATGACTTCAATTCTT
GGGTTTACGACAGCATCAACAATGGTGTATACAAGACCGGATTTCGAGAGAAAGCAGAAG
TTTACGAAAGTGAAGTCAACAACGTATTTGAACATTTGGACAAAGTGGAGAAAATCCTGA
GTGACAAATATTCCAAATTGAAGGCCAAATACGGTGAAGAAGATAGACAAAAAATCTTGG
GTGAGTTCTTCACTGTGGGTGATCAATTAACAGAAGCTGACATTAGATTGTATACTACCG
TCATAAGATTCGATCCTGTGTACGTCCAACATTTCAAATGCAATTTTACCTCTATTAGAG
CCGGATATCCATTTATTCATTTGTGGGTAAGAAATTTATACTGGAATTATGATGCCTTCA
GGTACACAACAGATTTTGACCATATCAAGTTACACTACACGCGTTCCACACAAGGATCA
ACCCCTTGGAATTACGCCCCCTGGGACCCAAGCCAGATATTTCGTCCTTTATAA

>YKR076W, 370 aa (SEQ ID NO 260)

MSKQWASGTNGAFKRQVSSFRETIKQHPYKPAKGRYWLIVSLACPWahrTLITRALKG
LTSVIGCSVWHHLDEKGRFLDMEKQLEDSEDFLEHWHDVAGGIRTAKEDSSKSFAEIK
NDSQRFMVDATNEPHYGYKRISDLYYKSDPQYSARFTVPVLWDLETQTIWNNESSIIRI
LNSSAFDEFVDDHKKTDLPVPAQLKTQIDDFNSWVYDSINNGVYKTGFAEKADEVYSEVN
NVFEHLDKVEKILSDKYSKLKAKYGEEDRQKILGEFFTVGDQLTEADIRLYTTVIRFPV
YVQHFKCNFTSIRAGYPFIHLWVRNLYWNYDAFRYTTDFDHIKLHYTRSHTRINPLGITP
LGPKPDIRPL

>YKR092C, 1721 bp, CDS: 501-1721 (SEQ ID NO 261)

TCAAGGATACCTGGTTGATTCTACGTCGTCCTCTTCACTTTGGTTAATTCACCTTTGCCC
TTCACCTTGTGGTGTGCGGGTGTGTCAGTCATTAATGTTCTTTATCGCGAGAGGGGGTCT
ACATAATCTTGTTTTTTCACTCCAATAAGGCAGTTATAGTGAATTTGTTTTATTACAGAA
GGTGTACCCTTCGTTTCGAGTTATTTTACTCTTGTTTTGTAGTTTGTACATCTCTTTATGT
CTGGATCAAAACGATAATTGCAAGCTTATTGCAATTTAGTTCTCTTACCCATTTCTTTAC
AACGGGCCGAGAAAAAGTGGAGTTGGTCCGAGGAAGCTTTGAACGGGAAGAGGAAAAAAC
CTTCCCATCGCTCGAGCATACAATTTTTTTTTTTTCAATGCAGGCTGAAAAAATAAT
CACTTGATGATTGAACTCATCGCACTTTTATACAAAGCAAGAAAGAAACCCAAGTCGAG

• *Wissenschaftliche Grundlagen der Betriebswirtschaftslehre*

>YKR092C, 406 aa (SEQ ID NO 262)

>YLR043C, 812 bp, CDS: 501-812 (SEQ ID NO 269)

>YLR043C, 103 aa (SEQ ID NO 270)

>YLR053C, 827 bp, CDS: 501-827 (SEQ ID NO 271)

AACACTGGGGATATTTTGAGATTTACCACTAGTAGATACGGTGGTGTAGATACGTATGAT
TCCATCTTGAGGGACCAATCCACGATCATGGAACTTTTAGATAAACGGTGTGCCTATTCA
CCTCCAGTACTGTTTCGATAATGAGGCTAAAGAACGTGATCATGATCGCGATTGTTATCAA
GATTACAATCACGACCACCGGAGTCATTAATATTAATAAAAAAAAAAATGTGATTGTTAATA

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AGGGGTGGGATGCGCGAAATTCATGCGCTACAGTAGAAAGCGGTTGTTGCACAAATGATT
AAATCTTTTATCTCCAACTCACAATACTATCGCGATAGATGCATAATATGTGCAGCTTCTA
AACAGCACGGAGTGATGATAAATACGCATATATGTATATATATATGTATGTGCATATGCA
CGTCCCTTTTAAAACTCAAAATACAACATTCCTTAGTAAATCCTTTTGTGACACACGTCGG
AACAACTCAGGACGGAGTTAATGGATATGCTTCATAATAATGTAGTGATGCTATCAAAA
GCACCTCCAATAGCAATTTGAGTAATGAGGTAGACAAACAAAAATTGCAATACGATGACC
TCGGGAACACCGGATTTTCTGAACATTTGAGATGGAATCTCAAGATAATAATGATAGCA
TAGAGGATTTCTTGTCTTAAATATAAAATTTAACCACGAGGTTGAGTTTCGAGAACCAAA
GACAATATGAGCACAGAAAAAGACAAAGCATAACCCATTCATGTACCGTCAGAGG
TAGTGCGAGAGATGGTCAAGAAACACGCATTGAATGGCAGAATATAG

>YLR053C, 108 aa (SEQ ID NO 272)

MDMLHNKCSDAIKSTSNSNLSNEVDKQKLQYDDLGNITGFSELFEMESQDNNSIEDFLFF
NINLTQEVEFENQRQYEHTKKTKKHNPFYVPSEVVREMVKKHALNGRI

>YLR390W, 839 bp, CDS: 501-839 (SEQ ID NO 291)

GTGAAATTGAGACTGATAGGTGAGAGGTGAACCAATTGAGTGAGGAGTGGTTTAGTTACA
AATGCAGAAGAAGAAGCTAAAAGAGATACGCCCATACAGAGCAATATCAAAATGAGCAAG
AATGAGGTCTTCCGAATGGTTGGTTCTGACTTACTATTTGATTTCACTTTCTCTGATTCA
TTCAGGAAGAAAAGGGCGAAGTCCTCGAAATGAAAATTTCAACATCATTAACAGACCGGC
GCGCGCCTTTACAATTTAGTATGTACGCCACCAATAAAAGCTGCTTAAACAATAAGCTAG
AAAGCCCAAGGGTGTAAATAGTACAGCGAACCCCTTCAGCAACGGTACATCAACAACCC
CTTGAAGAAGATAGAGACAATACAGCTACAGTCATCCCCTTCTCTTGTATTTTGGCCAC
AATTGATTGTATTACATCATATTTTGCCTGTGCGCTTCTTCTATCTTTTCCGCATAAACT
AGGGGAAACGCGATGAAGAAATGGATTGGCTGAAAAATACAACAATTGTAGTGTATTCA
GTTCACTCACTGACAAAAGTAACAACACAAGAAACGTCAAGTCCAGTGCAATATGCGAA
AGAACACTTTAGATATGGTCACTATAGGTATCGCATGCCTTGTGGGAGTCTACACGGGCA
CGAGATTTTTCGAGCCCATTTGTTATCGATAGATTGCGTAAGGATGGAAACTTGAGAACGG
ACATTCCCATCCCAGAATACGACGAGGACGGAAATCTGTTAAAGGTCACGCCGCTTTTAT
CATCCACACCAGCTGCACCACCTACACCACCTACACCTCCTACTCCACCACAACAGTAA

>YLR390W, 112 aa (SEQ ID NO 292)

MDWLKNTTIVVLFSSHSTDKSNKHKKRQVQCNMNRKNTLDMVTIGIACLVGVYTGTRFFPEI
VIDRLRKDGNLRDIPPEYDEDNLLKVTPSLSSPTAAPPTPPTPPTPPQQ

>YMR251W, 1601 bp, CDS: 501-1601 (SEQ ID NO 315)

ACTCCAGAGCGCAAGAGTTCGTTTCATCTACGAAATGTTGCTGGCATTGGCATCTCCACAA
GATGACATCCCAACGCCGGATGAAATCGAAAAGAAAAATAAGCTAAAGGAAACAACAACG
AGAACTATAGAGGAACATGTTGAGTTGAAAAGGTCATCCAATATACCGCCCCCTATATG
TATGTACCTTTACCTTTTATTTAAGTACTAGTGCTGTTTAGTTAGGTTATGTGAAGGCAC
GGGTTTTGTCTTTTTTTTTTTTTTTTTTTTACTATTACTTTCTTTTTTCAAGCTTTTAAAGCG
CCGAAATGATATTTAAGGGAAGATGACTAAAGGGACAGCGACGAGGATTCAGCCTGGACA
GTGATAGAAAAGTTATGCGGGAATACGTATATATAGTTGTATAAAATGTGGTTATAGAAC
ATCGCAGCGCCTTTAAATATATTGTCTTTTATTTCAATCTTATTCCATCTCTCTCTTGCA
ACCACGGCAAAGCTGGAGCTATGTCTGAAAAATCAGCTAGCAATAACAAGCTGAATTCA
AAAGGCAGTCATCGCCATTTCAGAGAAATCATCTCTGCGGATCACCCAATTTATAAACCTG
CTAAGGGAAGGTACTGGCTGTATGTGGCGCTACCATGCCCATGGGCACAAAGAACCTTGA
TCACCAGGGCCCTGAAAGGGCTAGCGCCTATAATCGGGTGCAGTGATAGCGCATTTGGCACC
TGGATGACAAAGGCTGGCGATTCTTGAAGAAGGAGATGGGAAAACCAATGAAAGGCACT
GGTTTGACATTGCAGGCGGAATFAGCTCAGTAAATTTAAATACCAGTACTCCTGTGGCTA
ACATACCCAATAACGCGCATCGGTTGTTGGTTCGACGGAACAGATGAACCGCATTACGGGT
ACAAGAGACTAAGCGACTTCTATTTCAAAACAAAGCCAGACTATAAGGGAAGATTCACCG
TACCTGTTCTTTGGGACTTGGAAACATGCACTATAGTAAACAATGAAAGCAGTGATATCA
TCGGAATTATGAATTCCGCTGCGTTTGATGAGTTTGTGCGGCGAAGAATACCGTCAAGTCC
GTCTGGTACCTCGGTCTCTAGAGGCACAGATTACAGAGTTCAACTCTTGGGTGTACGATA
AAATCAACAACGGTGTATACAAGGCCGGTTTTGCAGAATGTGCAGAGGTATACGAGAGGG

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AGGTAACAAGCCTTTTTCAATATCTTGACAAATTGGAAAATCTTCTGGACAAGAAGTACA
CAGATTTGGAGGCGGAGTATGGTAAGAACAACAAGGACAAGATACTAGATCGCTACTTTG
CCATCGGAGACACTCTGACCGAGGCGGACGTGAGACTCTACCCAACGATAGTAAGGTTCCG
ACGTGGTATACCATCAACACTTCAAATGCAATCTGGCCACCATCAGAGATGATTATTTCC
GTATACACACGTGGCTCAAGAATATATACTGGCGCCACGAAGCCTTCCAGCGCACAAACGG
ACTTTACCCACATAAACTCGGATATACTCGCTCGCAGCCACGGGTCAACCCGATTGGGA
TCACCCCACTGGGGCCCAAGCCTGATATCCGACCTCCATGA

>YMR251W, 366 aa (SEQ ID NO 316)

MSEKSASNNKAEFKRQSSPFREIISADHPIYKPAKGRYWLYVALPCPWAQRTLITRALKG
LAPIIGCSVAHWLDDKGWRFL EEGDGKTNERHWF DIAGGISSVNLNTSTPVANIPNNAH
RLLDV DGTDEPHYGYKRLSDFYFKTKPDYKGRFTVPVLWDLETCTIVNNESSDIIGIMNSA
AFDEFVGE EYRQVRLVPRSLEAQITEFNSWVYDKINNGVYKAGFAECAEVYEREVTSLFQ
YLDKLENLLDKKYTDLEAEYGKNKDKILDRYFAIGDTL TEADVRLYPTIVRFDVVYHQH
FKCNLATIRDDYSRIHTWLKNIYWRHEAFQRTTDFTHIKLGYTRSQPRVNPIGITPLGPK
PDIRPP

>YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)

AAATTGGTCTCAATCTGGAATAAGTGCTACTTCGCACTGCTGGTCCTTGGATTAATATCC
CTGAAGGATACCTTACAACTCTGGTAGGAACTCTGGTTATAGAATAACCCCTTAGCCT
TTTTTACGTACTTGTATACCGTTTAAAATTTCCATGTACTATAACCTTTTTTCACTACT
ATTATGGAATCTATCGAGCGACCGGGCTTTTGTACCGAAGAGTGAAAAAATCGAGTTT
TGGTGTTTTGGTGAAAGAAATTTGGAGGACTATAAAGTACCTATACCTTTGTATTACGGACT
CAATAACAAGTCGTTCTGTGTCAGTGGTATTGAAGTTGTCAGATCTAAGAGTAGAGAGAAG
GTGGCATCTAATAGGTTTCGACGTTTTTCTTTTTTTAAGGTTTTATTGTGGTCTCCTAGA
ATTTAAGGTCCTTAGTTAGTTTTGGTTTTGTTTTGTGGTTACATATTTTCAATTCAAAGGA
GAATTTAGCTGTCTTTTATAATGTCCAATAGAGATAACGAGAGCATGCTGCGTACTACAT
CAAGCGATAAGGCGATCGCTAGTCAAAGGGATAAAACGGAAGTCTGAAGTTTTGATTGCTG
CACAGTCCCTTGGCAATGAAATCCGCAGCGTAAAAAACCTAAAAAGATTGTGATTTGGGT
CAATGGATTTACTTATTGATCCAGAATTAGATATAAAATTCGGTGGGGAATCTAGTGGGA
GACGATCATGGTCTGGCACGACATCCAGTTCTGCGTCAATGCCAAGTGACACAACCACCG
TTAATAACACACGATATAGCGATCCAATCCGCTAGAGAACTTGCATGGGAGGGGTAAC
CAGGGATAGAATCCTCCAATAAGACTAAACAAGGTAACCTTAGGTATAAAAAAGGTG
TTCACCTCTCCATCCAGGAATTAATGCTAACGTATTAAAGAAAACTTATTATGGGTTC
CCGCCAATCAACACCCCTAACGTTAAGCCTGATAATTTCTTAGAGCTTGTACAAGATACTT
TACAAAATATACAAC TAAGCGACAATGGTGAAGATAATGATGGGAATAGCAATGAAAATA
ACGATATTGAGGATAATGGGGAGGATAAAGAATCACAATCATATGAAAATAAGGAGAACA
ACACTATCAACTTGAACAGGGGGCTGTCAAGGCATGGAAACGCGTCACTAATACGAAGGC
CTTCAACATTGCGGAGGT CATATACAGAGTTTGATGATAACGAAGATGACGATAATAAGG
GAGACAGTGCCTCTGAAACAGTAAATAAAGTCAAGAAAGAATCTCCAAAATAAAAGAGA
GACCAGTGTGCTTAAGAGATATAACTGAAGAACTGACAAAGATCTCAAATAGTGCAGGAC
TAACCGACAATGATGCCATTACATTAGCCAGAACTCTTAGTATGGCTGGTTCATATTCAG
ATAAAAAAGATCAACCACAACCGGAAGGGCATTATGATGAAGGAGATATTGGTTTTTCAA
CTTCACAAGCGAATACTTTGGATGATGGTGAATTTGCCTCCAATATGCCCATCAATAATA
CGATGACATGGCCTGAACGATCGTCACTGAGAAGGAGTAGATTCAACACTTATCGAATCA
GGTCACAAGAGCAAGAAAAAGAAGTAGAACAAAGTGTGGATGAAATGAAAAACGACGACG
AAGAACGTCTAAAATTGACCAAGAATACAATAAAGGTGGAATAGATCCGCACAAATCCC
CTTTTAGACAGCAAGATGAGGATTCTGAGAATATGAGTTTCGCCTGGGTCAATTGGTGATT
TTCAAGACATTTATAATCATTACAGACAGTCTAGTGGCGAGTGGGAACAAGAAATGGGAA
TAGAGAAAGAAGCCGAAGAGGTACCCGTCGAAGTTTGAATGACACAGTAGAACAAGACT
TAGAGTTAAGAGAGGGAACAACAGACATGGTAAAGCCAAGCGCAACGGATGACAACAAAG
AAACGAAGCGACATCGTCGAAGAAACGGATGGACATGGTTGAACAATAAAATGAGCAGAG
AAGACGATAACGAAGAAAACCAAGGGGACGATGAAAATGAAGAAAACGTGGATTACAAA
GAATGGAGCTCGACAATTTCAAAAAACATTATATTTCTCTATTTAATGGCGGTGAGAAGA
CGGAGGTGTCAAATAAAGAAGAAATGAACAATTCAAGTACTTCCACCGCCACATCACAGA
CAAGACAGAAAATCGAGAAAACCTTTTGGCAACCTATTCAAGAAGAAAGCCACACCACAAGC

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ATGATGCATCATCATCACCCCTCGTCGTCACCATCATCGTCACCATCAATACCAAATAACG
ATGCCGTGCACGTTTCGCGTGAGGAAAAAGCAAAAAGCTTGGTAACAAAAGTGGAAGGGAGC
CGGTTGAACCCATTGTGTTGCGCAATCGCCCTCGTCTCACCGTCACCATCACAGCCGTC
ATGGTTCCCAAAAAATAAGCGTAAAAACCCCTTAAAGATTCTCAGCCGAGCAGCAGATAC
CATTACAACCACAATTGGAAGGCGCAATAGAGATAGAAAAGAAAGAGGAAAGCGATTCCG
AGAGCTTGCCCCAACTACAGCCGGCCGTTAGTGTAAGTAGTACCAAAAGTAACTCTAGAG
ACAGAGAAGAAGAGGAGGCAAGAAAAAGAACAAAGAGGAGCAATACGACAGAAAATTT
CCAACCAACAACACTCCAAACACGTCCAAAAGGAGAATACCGATGAGCAAAAAGCTCAAC
TACAAGCTCCAGCTCAAGAACAAGTCCAAACTTCAGTCCAGTTCAAGCTTCAGCCCCAG
TCCAAAATTTCAGCCCCAGTCCAAACTTCAGCCCCAGTTGAAGCTTCAGCTCAAACTCAGG
CTCCAGCGGCACCACCATTTGAAACATACCTCCATATTGCCCCCAAGAAAGCTTACATTTG
CAGACGTCAAAAAACCTGACAAACCAAACTCCCCGGTTCAATTCACAGACAGTGCCTTTG
GGTTCCTACGTGCTTTTGTGACAGTGTCTACGGTTATCATGTTTCGACCACCGTCTACCAA
TTAAGCTCGAAAGGGCCATATACCGGCTGAGTCACTTGAATTTGAGCAATTCGAAGAGGG
GACTGCGCGAGCAGGTATTACTAAGTAACCTCATGTATGCTTATCTGAACCTTGGTTAATC
ACACTCTGTACATGGAGCAGGTAGCCACGACAAAGAACAACAACAACAACAACAACAAC
AACCTGA

>YMR273C, 915 aa (SEQ ID NO 322)

MSNRDNESMLRTTSSDKAIASQRDKRKSEVLIAAQSLDNEIRSVKNLKRLSIGSMDLLID
PELDIKFGGESSGRRSWSGTTSSSASMPSTTTTVNNTRYSDPTPLENLHGRGNSGIESN
KTKQGNLYLGIKGVHSPSRKLNANVLKKNLLWVPANQHPNVKPDNLFELVQDTLQNIQLS
DNGEDNDGNSNENNDIEDNGEDKESQSYENKENNTINLNRGLSRHGNASLIRPSTLRRS
YTEFDDNEDDDNKGDASSETVNKVEERISKIKERPVSRLDITEELTKISNSAGLTDNDAI
TLARTLSMAGSYSDKKDQPPPEGHYDEGDIGFSTSQANTLDDGEFASNMPINNTMTWPER
SSLRRSRFNTYRIRSQEQEKEVEQSVDEMKNDDERLKLTKNTIKVEIDPHKSPFRQODE
DSENMSPPSGSDFQDIYNHYRQSSGEWEQEMGIEKEAEVVPVKVRNDTVEQDLELREGT
TDMVKPSATDDNKETKRHRRRNGWTWLNKMSREDDNEENQGDDENEENVDSQRMELDNS
KKHYISLFGGEKTEVSNKEEMNSSTSTATSQTRQKIEKTFANLFRRKPHHKHDASSP
SSSPSSSPSIPNNDVHVRVRKSKKLGNKSGREPVEPIVLRNRPRPHRHHSRHGSQKIS
VKTLKDSQPQQQIPLQPQLEGAIEIEKKEESDSESLPQLQPAVSVSSTKSNRDRREEEA
KKKNKKRSNTTEISNQQHSKHVQKENTDEQKAQLQAPAEQVQTSVPVQASAPVQNSAPV
QTSAPVEASAQTQAPAAPLKHTSILPPRKLTFADVKKPKPNSPVQFTDSAFGFPLPLL
TVSTVIMFDHRLPINVERAIYRLSHLKLNSKRGLREQVLLSNFMYAYLNLVNHTLYMEQ
VAHDKEQQQQQQQP

>YNL112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)

CTTGATGGATTTATGTGACGTTGTAGAATCTAAGTTTACTGAAAAATCAAGAGCATGTA
GATGTTACGGATCGACTCAAAGACCCTCTGTCACTCTGAAATTTCTAATAATTATGCACA
CCACGCTAGTATAGATACAGCTTGATTGTGTATCCCGTTTATAGTCGTGCTATTTAAAA
TCTATGTATAATATAACCAGATAAAAAATACACCTTCGTACAAGGTGCTAATAATGTTGAG
AATTCGAAATTCCTTTTTTAAAGGCGTATTCCGTATTGAATGATTGAAAAATTTATTTCTT
TTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGCCGATGCTCATCGCAGAAAAT
TTTTCTTTCAGTTTATTTGTCTTATAAAAAGACTGTCCTACGCTCAAATAACTTATACTT
TTCTGTATCTCATTCAAATTATTTCTTGTCAACAACCTGTAACAGAATTAAGCACTATT
AAGGCAAATTTAGAGCAAATATGACTTACGGTGGTAGAGATCAGCAATATAACAAGACTA
ACTACAAGTCTAGAGGTGGCGACTTCCGCGGTGGAAGAACTCTGATAGAACTCTTACA
ATGACAGACCACAAGGCGGTAACCTACCGTGGTGGTTTCGGTGGTTCGTTCCAATTACAACC
AACCCAGGAATTGATCAAACCAAACTGGGATGAAGAATTACCCAAATTGCCAACTTTCG
AAAAGAATTTCTATGTTGAACACGAAAGTGTTCGCGACAGATCGGACAGTGAGATTGCTC
AGTTCAGAAAGGAAAAATGAAATGACTATTTCCGGACACGATATTCCAAAGCCAATCACCA
CTTTCGATGAAGCTGGTTTCCAGACTACGTTTGAATGAAGTGAAGGCTGAAGGATTG
ACAAACCAACTGGCATTCAATGTCAGGGTTGGCCAATGGCTTTATCTGGTAGGGACATGG
TTGGTATTGCTGCCACTGGTTCCGGTAAGACTTTGTCTTATTGTTTACCAGGTATTGTTT
ATATCAACGCTCAACCATTATTGGCTCCAGGCGATGGACCAATTGTTTTGGTTTTGGCTC

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AGTGAGTAACTTTTGGAGTAATACGAAGTAACCAAAGAGGTCAAAACGGAAGCTATATACC
CCAAAATAAGCATCATTCAAATGGTCGAATTAACCTGAAATTAAGACGATGTCGTTCAAT
TAGACGAACCACAATTTTCCAGAAATCAGGCCATCGTGGAGAAAAGGCTTCTGCAACAA
ACAACGACGTTGTCGATGATGAAGATGACTCTGATAGTGATTTTGAAGATGAATTTGATG
AAAATGAAACATTTGTTGGACAGAATCGTTGCTTTTAAAAGACATTTGCCCCCAGGTAAGA
GACAAACAATTTCTAATTTTGGTTTACTAGCTCTTTTGTGAGAAATGCTTTTCACAA
AATCCGGAAACCTTGCCTTGGACTTTGACCACCCTGCTTTGTTACTCGGTGTGCCACTAT
CCTTATCTATACCTTGGCGAACAACAGCTAATCGAAATGGAAAAGACATTTGATTTACAAA
GTGATGCTAATAACATATTGGCCCAAGGTGAAAAGATGCTGCAGCAACAGCCAATTAA

>YNL131W, 152 aa (SEQ ID NO 330)

MVELTEIKDDVVQLDEPQFSRNQAIVEEKASATNNVDVDEDDSDSDFEDEFDENETLLD
RIVALKDIVPPGKRQTISNFFGFTSSFVRNAFTKSGNLAWTLTTALLLVPLSLSLAE
QQLIEMEKTFDLQSDANNILAQGEKDAAATAN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)

GAAAATACACACGGCGGAAGCCATCATCGAGGCCCAAAGCAAGGATAAAGCATGCTTTTT
CCTGGATAAACCAGAATATAATAAACCGATACCTGGGACCATAATCCACACACCTGCTGA
AGCCACACCGATCCATCCCATGTTGGCCAAGTCAAATTGTGTATTCAAATCTGTTGTCAA
CGAGTTACCACCCGTTCTTCGCCTGTAGGCGTACCTGTAAAATTGTAAGACATTGTTGA
TATTGTATTGTAATATATTAAGTATGATATATTACAAAATAAACTTCTTTCAAAGCTCT
GTGCAGACTTATTATTTAAGAAGGATATTTAATTTGAAAGGACGTGAAAGCACGAATGAT
TACTACCCCATGATGTTTGGTTAGCACATGTGTAATACTTATTGATAAGGCACAGGGTCTTC
AGTGGCTCGGAATGAACACCTCTGTACTGAATACTTATTGATAAGGCACAGGGTCTTC
ACGCCGCTTAGTATTTCGTCGATGCGTGAGCAATTGAAGCTTTTTACGAGGGAAATAGTCG
ATTTTACATTTCTTATCTTATCTGGCTTTGACTATTACCAGACACTCTTGATAAGCAGTA
ACAGCAGTAAGAAGAGACCGAAGGATTCTTCTTTGTTATCGGAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAGATGTCTTATCTTATCTTTCTTATCTTAAAGACCTACCATTGTTC
CTTTTCTATTTTGGCAGCCCGGGTATTCGCAAAGGGAAAAAAAAACCAAGACAGCATTCCT
TGTTTATTATGACTATTACAAAGCCAGGAATGATTTGATGGCCGACATGAATTACGTCG
TTTCCAAGAACAGAAGCTTAAACCGTCTGCTGAGCGGGGCGGTAATCGGTGA

>YNL143C, 130 aa (SEQ ID NO 334)

MREQKLKLTREIVDFTFLILSGFDYYQTLISSNSSKKRPKDSLLSEKKKKKKKKKKDV
LSYLSYKLDLPFVPFLFWQPGYSQREKNPRQHSFLFIMTITKPGMISMADMNYYVSKNRS
LRPAERGGNR

>YNL179C, 938 bp, CDS: 501-938 (SEQ ID NO 335)

ACAGCGGTTAATTTCAAATACCCTAATCGGAGGTCTTATCTTATTTTCAAGGGCAAGGC
TCTCCACATCGGTAAAGTGATGACCAGATAATGGAAAGTAGCAGAATTTTATTATGTGCC
ATACAAGCCCCGGAGAAACAGAGTAGCTAAAAAATTAAGGTGTGCAAAAAGTGGTTTGTTC
CCCGACGCCCCGGGCTTTCTCTCCCTGAATCTTTTCGTTCCGGCCCCCTCTCTCAATA
CCAGATCTGCATCTATACTAAAGCTGCAGTGAGAGTAAACCGGAAAATTTATCCTGCGTGT
TTGCTTCGGTCTTAGCTTTTACTTGGGTATGCGAGAACCCTCTAAGAGCTTAGACCGGTCT
TCCTCCCTAAAAAGAAAATTATAAAAGGTATTATCTGGACTAAAGCAAAAAAAAAACAA
CGTTTCGGCGTCCGCTCAAAATTTTCATTACGCTTCTTGGTCAAATCAGTTACGTAACGG
GTTATGACGAATACGATGAGATGAGTAATTGCAGAAGGCTCCTATGCAGACAGCTAAGCA
GTGCTTACTTGAATTACCTTCCCTTTTATTTCTTGATATATCGTCTTTTCTCTCTATC
TTAGTTCTTGCGAGTACTGGCAATCATGTTTCTCTTTTCTTTTCTTTTCTTTTATTTT
TTTTTTTTTTTTTACTTTTTCAGTTTCTCGTAGCTTTTCTTATTTTGTCTATTTAAAGTAA
GTTTAAATAGTACCTCACTAAACACGTACGGCCGATCCACCAACGAACAAAAGCACGAT
CCTTGACCCATCATTTGTATTCCAAAGCGTTGGAACATTCATTTTTTTTTTCCGGTCTAT
TGCACAAGACAATATCCAGAATATTCAGTTGGATAGGAAATACAAGACAGGTGGCACCCA
CAAAGCACACGCCGAAATATTTATTAAATACAATATAG

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>YNL179C, 145 aa (SEQ ID NO 336)

MSNCRRLLCRQLSSAYLNYLPFYFLIYRPFSLYLSSCEYWQSCFSFFFLFFLFFFFFTF
QFLVAPPILLFKVSLNSTLTKHVRPIHQRTKARSLTHHCIPKRWNHFFFFSGLLHKTIISR
IFSWIGNTRQVAPTKHTPKYLLNTI

>YOL150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)

TTCCCATTTCCACTGCTATTCTGTGCTATTGTCAGAACCATTGTTTACTTGAATGTTA
TTACTACCATTTTGTGAATCAAAAATATCTACTTCTTGTGGGGAGACGGGTAGAAGATTT
GTATTTTGGCAGACGTCTCTCAAATATATGGCCAAAACACCTTGATATTCTAGTTTATTTC
CATTCGTCCCTTCTTGAAGTCCCATTTTATACAGTGACGCATGTGGTGTGTGAAAAAGTAGT
TGCTTTTATTTTGGATCGTATCTCCCAATAACGTTGAAATTCAAAGCTTTTCTATAGAAT
TCTAACTGTGTGGCAGAGTTTCTGCTGCAGTTGCTGCTCCGGTCATTGTGCACAGCTTT
TCTTGTGATGTGTGCAAAGATAAATGCTTATCTGAACGTTTCTCTATTGTTTTTTCGTC
AATTTTCTTTTCTTTCTTTCGCTTTCGCGTTTTCGACATATTAAGCTGTATATAGAAGAGAAA
AATGCGCAGAGATGTACTAGATGATAAAAAATAATGTAAATAACGTTAATATATATAAAT
ATTATCTATTTTCATTTAAAGTTTATATTCTGCCCTCAAATTTTAAAAATTTGGGAGGCAG
TGTCGTCAATGGTCTCTTTCAAGTTCTGAACTTGAAACCTAACAAATTTCTTACTCTTTT
TATTATCAAGAGTAGCACCAGGGGTATTATGGGTAGCACCAGAACCTGGTTTCCCCACTG
GAATATTGCCCTTTTAGAACAGGGAAGTCTTCGTTAAGGATATCGAGAACATCCTGCATAG
TAAATCTGGCCTCCGATACGATTAGTCTTTGA

>YOL150C, 103 aa (SEQ ID NO 350)

MIKNNCANNVNIYKYLFSEFKVYILPSNFKIWEAVSSMVSKFLNLKPNNFLLFLLSRVAP
RVLWVAPEPGFPTGILPFRGTGKSSLRISRTSCIVNLASDTISL

>YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)

GCGTGAACATATGTCATATTTGCGATTTTAGGTACAATAAATATTATCATTATTATATTAT
GTTTGCATGTAGGTTCTACAAATACATTGTTGTACGCTATAGTTTCTTTCAAACCTAGA
AAGAATTTCGTAACAAAATAATCTCCAATATTTTATAGCACCTTATTAATATCAATGCTGC
AATACCTTCTCATTTCAACAATTGGCCCTCACCTCTTTTGTACAAAAAACGTCGCCATTG
ATAAAATAAGTAAGAAGCATATAAATTGGAATGTCCATTACGTAAAAGAAAAAAATCATG
TGTACATATTACGTAATAGAAATACGGAATTTTCTCGCGGAAGTAGATCTTCCGTGGAAAA
AAAGGAAAAAGTCCGATCAATATTGAAAAAGGGATCCTTAGTTTCCCACTATATAAGGA
GGAAAAGTCTATCTCTGTAGCGTTGATATAACGTGTACGATTTTCAAACAAACAGATAGC
AGTATCACACGCCCGTAAATATGTACGTTTTCGTTTTAGGTGCTAACGGGTTTCATTGCCC
AACACATTGTGCGATCTCTGTGTAAGGAAGACTATAAGGTCATCGGTTCTGCCAGAAGTC
AAGAAAAGGCCGAGAATTTAACGGAGGCCTTTGGTAACAACCCAAAATTTCTCCATGGAAG
TTGTCCCAGACATATCTAAGCTGGACGCATTTGACCATGTTTTCCAAAAGCACGGCAAGG
ATATCAAGATAGTTCTACATACGGCCTCTCCATTCTGCTTTGATATCACTGACAGTGAAC
GCGATTTATTAATTCCTGCTGTGAACGGTGTAAAGGGAATTCTCCACTCAATTAAAAAAT
ACGCCGCTGATTCTGTAGAACGTGTAGTTCTCACCTCTTCTTATGCAGCTGTGTTCGATA
TGGCAAAAAGAAAACGATAAGTCTTTAACATTTAACGAAGAATCCTGGAACCCAGCTACCT
GGGAGAGTTGCCAAAAGTGACCCAGTTAACGCCTACTGTGGTTCTAAGAAAGTTTGTGAAA
AAGCAGCTTGGGAATTTCTAGAGGAGAATAGAGACTCTGTAAAAATTCGAATTAAC TGCCG
TTAACCCAGTTTACGTTTTTGGTCCGCAAAATGTTTGACAAAGATGTGAAAAAACACTTGA
ACACATCTTGCGAACTCGTCAACAGCTTGATGCATTTATCACCAGAGGACAAGATACCGG
AACTATTTGGTGGATACATTGATGTTCTGTGATGTTGCAAAGGCTCATTTAGTTGCCCTTCC
AAAAGAGGGAAACAATTGGTCAAAGACTAATCGTATCGGAGGCCAGATTTACTATGCAGG
ATGTTCTCGATATCCTTAACGAAGACTTCCCTGTCTAAAAGGCAATATTCAGTGGGGA
AACCAGGTCTGGTGCTACCCATAACACCTTGGTGCTACTCTTGATAATAAAAAGAGTA
AGAAATTGTTAGGTTTCAAGTTCAGGAAGTTGAAAGAGACCATTGACGACACTGCCTCCC
AAATTTTAAAATTTGAGGGCAGAAATATA

>YOL151W, 342 aa (SEQ ID NO 352)

MSVFVSGANGFIAQHIVDLLLKEDYKVGISARSQEKAENLTEAFGNPKFSMEVVPDISK
LDAFDHVFQKHGKDIKIVLHTASPFCDITDSELDLIPAVNGVKILHSIKKYAADSVE

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RVVLTSSYAAVFDMAKENDKSLTFNEESWNPATWESCQSDPVNAYCGSKKFAEKAWEFL
EENRDSVKFELTAVNPVYVFGPQMFDDKDVKKHLNTSCELVNSLMHLSPEDKIPELFGGYI
DVRDVAKAHLVAFQKRETIGQRLIVSEARFTMQDVLIDILNEDFPVLKGNIPVGKPGSGAT
HNTLGATLDNKKSKLLGFKFRNLKETIDDTASQILKFEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)

TCCTGAACGGAAGCTGCAGTTTGCTCAGTACCTACACGCTCCTCTGACATAGAAGATGAT
CCATCTGTGGTTGTTGCAGCAGGTTTCAAGATCTTCTCCTGGGGCTCAGCAAATGGATTG
TTATCCAGATCATCATATGGATCATAAGGTACAGCCGAAGTCATTGTTTCAGAGGATAGAT
GGATTGACTAAGGGTACAGTACGGCAAAAAAATTAGATCAGCTTTTCAAAACAAACTA
TTTTGGCGTTTACCAAAACCAAAACAGTATATTCAACTAGTTCAATCACTCTTGAAAACG
TCCCTTTTCTACAAAATTAGGCTTTGAACCGGTGCTATGGAAAAAAGTGTAAAGAAAAACG
AAAAAACAGAAAAAGTCATATATATCTTATAACGAAATATCAGGGTGTTCGACTCAATCG
CCAGGTGCCGCTAACACAATCATTAGGATAGTCGGGCAATATATACGGTTCAATAGTCAC
TGAAAGTGATACACAGAATAATGACAAAGCTACAAGGACTACAGGGATTAAACACATCA
AAGCGGTGTATTGATATGGATGGCACATTATGCCTACCCAGCCTTGGATGTTTCCAG
CAATGAGAAACGCCATAGGATTGGAGGACAAATCGATTGATATCCTTCATTTTCATTGATA
CATTGCCACAGAAAAAGAAAAAAGAAAGCGCATGATAGAATAGAATTAGTTGAGGCAA
AAGCCATGAAGGAGATGCAACCGCAGCCTGGTCTGGTTGACATAATGAGGTATTTGACGA
AAAATGGTATTAGCAAGAACATATGTACTAGAAATGTCCGAGCCCCGGTAGAGACTTTTG
TAAAAAGATTTATTCATCCGAGCTTTTCGAGGTTTGAATATATTGTGACAAGGGAGTTTA
GGCCTACAAAACCGCAACCAGACCCATTATTACACATCGCCTCGAAGCTAAATATAAGGC
CCTTGGAATGATCATGGTAGGAGATTTCATTGACGACATGAAATCCGGTAGATCTGCTG
GATGTTTTCAGGTATTACTCAAGAATCATGTGAATGGACATTTACTGCTCGAACATAAAG
AACTAGTAGACGTTTTCAGTAGAGGATCTTTCCGAAATAATTGAATTGATTCAAAATATGA
ATAAAGAAAAGTTTCTAA

>YOR131C, 218 aa (SEQ ID NO 360)

MTKLQGLQGLKHIKAVVFDMDGTLCLPQPMFPAMRNAIGLEDKSIDILHFIDTLPTEKE
KKEAHDRIELVEAKAMKEMQPPGLVDIMRYLTNGISKNICTRNVGAPVETVFKRIPS
ELSRFDYIVTREFRPTKPQPDPLHLHIASKLNIRPLEMIMVGDSFDDMKSGRSAGCFTVLL
KNHVNGHLLLEHKELVDSVEDLSEIIELIQNMNKESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)

CATCTGAGTACTCGATTGTTTCATATTCCTGCCTTCATCAATGTGCCATATAGATCGCACC
CTGACGCATTTGCCCTTAGATCCTTTAGAAATTGAGAAACAGATTGGCATCCCAAAACCTG
ACAGTGCCAAGGAGCTAATATTTTATTGTGCTTCTGGCAAACGCGGGGAGAAAGCTCAA
AAGTCGCCCTCCTCACATGGATATTCAAACACCTCACTATATCCTGGCTCTATGAATGATT
GGGTTTCTCATGGGGGTGATAAACTTGACTTATAGCCTTGTATACTCTAGGTATGTACCC
TGCTGATTTTCGTAAGCTAGTAACGTATTATGCCATTTATGTCACACCGTTCATAATATT
TGCCATTATGCATTGGCTGTGATAGCGGCGGCGCAAAGAAATTAGGAAGTATAAAAAAAA
AATACAAAACCTTAATCTGAATGGAATAAGATAGCGATAACTCTCAACAAATGGAAGCGAG
ACAGAAGAAAAAGACCAACGATGTTCAAGCATAGTACAGGTATTTCTCTCGAGGACAGTTT
CTGCAAGATCGCCTACATTGGTCTGAGAACATTTACAACGAAGGCTCCAAAGATCTATA
CTTTTGACCAGGTCAGGAACCTAGTCGAACACCCCAATGATAAAAAACTATTGGTAGATG
TAAGGGAACCCAAGGAAGTAAAGGATTACAAGATGCCAACTACAATAAATATTCCGGTGA
ATAGTGCCCTGGCGCTCTTGGATTGCCCGAAAAGGAGTTTCACAAAGTTTCCAATTTG
CTAAACCACCTCACGATAAAGAATTGATTTTTCTTTGTGCGAAAGGAGTAAGAGCCAAAA
CTGCCGAAGAGTTGGCTCGATCTTATGGGTACGAAACACTGGTATCTATCCTGGTTCTA
TTACTGAGTGGTTAGCTAAAGGTGGTGCTGACGTTAAGCCCAAAAATAA

>YOR286W, 149 aa (SEQ ID NO 368)

MFKHSTGILSRTVSARSPTLVLRFTTTKAPKIYTFDQVRNLVEHPNDKLLVDVREPKEV
KDYKMPTTINIPVNSAPGALGLPEKEFHKVQFAKPPHDKELIFLCAKGVRAKTAELAR
SYGYENTGIYPGSITEWLAKGGADVKKPKK

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>YOR382W, 962 bp, CDS: 501-962 (SEQ ID NO 375)

AGTAAGCTCCTACAGTGAAATATCTGGGTGCTACTGACGCCAAGCCCTACAGCGATCGGA
ATGCGGGAACGGAAGTTAACGGGGCTTCCAGAACGGCGGAAGCGAATTGAACGAGGACGG
CAAACAAAACACCCAAAATTTCACTACTTAGAATGACCCCAAGAGCAGGGTGCATTTT
ATCAAGCGATCATTGAACTAACCTAAGTTCATATCCTGTATAGGATTTAAACAATGCACC
CTAAGTTCAAATGCACCCCCCTCGCCCCGAGCGGACCCTTGAACAGAGAAGCTGTTTCG
AGGTTACCCCAATTGGATCACTTGTATAATTTGTAATCGAGTTCGGATAAGATGTATACG
AATCTAACTGGGTGCAGTATAATTAGCATTTTTATATTACCTAGCAATATATGTATAAAAC
AGGAATGTGTGCGTGCCTTCAGGCAGAATTTTACGGTCCTTGTAAAAAGTCTATCATAAA
GCCATCACAAAACAATAATAATGAAATTCTCAACTATTTTCGGAGCTACTACAGTTATGA
CTGCCGTCTCGGCAGCAGCTGTGTGAGTGTAAATGACCACTAAGACTATTACTGCTACTA
ACGGTAATAACGTTTACACTAAGGTGCTTACCGACACCGCTGACCCTATCATTAGTTACA
GTACCCTAGAACTGTGCTTGTGAGTGTAGTGTACTTACACAAAGGTTGTCACCG
AAGGACCAGATACCACCTCTGAAAAGAGTACAACAAAGACACTTACTTTGACAAACGGTT
CAGGTTTCATCAACCAACCTTTACACCAAGACCGTCACTCAAGCCGTCGAATCATCTACAT
CCTCCTCATCCTCCTCATCCTCCTCCTCCTCCTCCTGCTCTTCTTCTGGTGTGCTCCTG
CTGCATTCCAAGGAGCAAGTGTGCGGTGCATTGGCCCTTGGTTTGATTTCTTACCTATTAT
AA

>YOR382W, 153 aa (SEQ ID NO 376)

MKFSTIFGATTVMATAVSAAVSSVMTTKTITATNGNNVYTKVVTDTADPIISYSTTRTVV
VSNSDATYTKVVTGEPDITSEKSTTKTLTLTNGSGSSTNLYTKVTQAVESSTSSSSSSS
SSSSSSSSGAAPAAFQASVGLALGLISYLL

>YPL078C, 1235 bp, CDS: 501-1235 (SEQ ID NO 379)

TAACTGTGTTGTGACGCAACTGCAACTCCCAGATGAAATACGGTCCGGTAAAGATAGGA
ATATTCTACTCTACAAGCATGAATATTTTAAACGCGGCGCAGTACTATACAGCATAACA
GGTCTTCCACGCATGAGAACTGTCCATGGCTAAATTAGTTCTCTCACACAGAATTAGAAA
TGTGCTGTGACAATGGCACATACGTAGATAAAAGATAAATATAATTCAGAATGGCTGTGG
CGACAACCTATTATCATAGAGGTGTCCCATCGAGCGAGCCTCATTGGCCGGGTAATCGACA
TCAATATTGAACCAATCACGACGCTTTTTCTCTTCACCGCTCATTCCGACCTTCACCACA
GGTTTGGGTAATTAAAATAGCAAGGGATTATAATTGCAGTTAGCAGTTTATGTTGACAAG
TTTATACTGTGCTAGGAAGGGTTATATTTTATTAAGACTGACGAGAATTCAGTACCTC
CTAAGTGCGAAGAGATAAAATGAGCATGAGTATGGGTGTCCGTGGCCTAGCGTTAAGGT
CCGTTTCTAAAACATTATTTAGCCAAGGTGTTTCGTTGTCTTCGATGGTGATTGGAGCCC
GTTATATGTCTTCCACTCCAGAAAAACAGACAGATCCAAAAGCAAAGGCTAACTCTATCA
TCAATGCCATTCCAGGTAATAATATTTTGACAAAGACGGGGGTTTTGGGGACTTCTGCTG
CCGCTGTCAATTTATGCCATTTCCAATGAATTGTACGTTATCAACGATGAAAGTATTTTAT
TGCTGACTTTTTTGGGTTTCACTGGTTTGTGCGCAAAGTATTTGGCGCCAGCATATAAAG
ATTTTGGCGATGCAAGAATGAAGAAAGTCTCCGACGTTTTAAATGCCTCGAGAAACAAGC
ATGTCGAAGCTGTTAAAGATAGAATCGACTCTGTCTCTCAACTACAAAATGTTGCTGAAA
CTACAAAGGTTTTGTTTGATGTTTCCAAGGAAACTGTTGAACCTGAAAGCGAAGCCTTTG
AATTGAAACAAAAGGTAGAATTAGCTCACGAAGCAAAGGCAGTCTTAGATTCGTGGGTTA
GATATGAAGCTTCTTGGCTCAATTGGAACAAAGGCAACTAGCAAAATCTGTCATCTCCA
GAGTTCAGTCAGAATTGGGTAATCCAAAATTTCCAAGAGAAAGTTTTGCAACAGTCTATAT
CTGAAATTGAACAATTGCTTTCTAAATTGAAGTAA

>YPL078C, 244 aa (SEQ ID NO 380)

MSMSGVRLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTDPKAKANSIINAIPGN
NILTKTGLVLTSAAAVIYAI SNELYVINDESILLTFLGFTGLVAKYLAPAYKDFADARM
KKVSDVLNASRNKHVEAVKDRIDSVSQLQNVAEETTKVLFVSKETVELESEAFELKQKVE
LAHEAKAVLDSWVRYEASLRQLEQRQLAKSVISRQSELGNPKFQEKVLQQSISEIEQLL
SKLK

>YPL085W, 7088 bp, CDS: 501-7088 (SEQ ID NO 383)

TTTTTCATGAGGAAGAGCCAGTGACAGTAAATAATAAAAGGTGAAATGATTAAACAATGA

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AAGCGGCAGAAAAATAAAATCAAACAGTGGCAGTATTGACTTTTGAAAATCAGAAGTTCA
TCCTAAGTTAAGACTTTCTCTTTTAAGTGCTTTCTCCTTCTCTCACTGTCTTATCGCTG
TATATCTCATTGTTGAATAATATAACACAACGTTATAAGTGATCATCACTTTCTGATCCA
TAATTTCAAACCTCAAGCGACCGTACATGTGGCATTTCCTACTATAAACTTACGAGCAAG
AGAAAGATATACGGAAAAGGTTAATTGGCAGGTTACACAAGATTTTGGTCATTGAATATT
TGCAGCCCTCCTGCTTGAGAACTGGACAACAACCTGTTATCAATATTCCTTTTCAAAAT
AGTGGTATTTAACTGGCCATAACCAAGGAAACCGTTGTACCTATTATTTTGTATAGTCTT
CATTTAATAACGTGTTAAGAATGACACCTGAAGCCAAGAAAAGGAAAAACCAAAAGAAGA
AGTTGAAGCAAAAGCAAAAAAAGCTGCTGAGAAAGCTGCTAGCCACAGTGAAGAACCAC
TTGAATTACCAGAAAGTACGATTAACAGCAGCTTCAACGACGACTCGGTGAACCGTACAG
AATCTGACATAGCTTCAAAATCTGATGTTCTCCTCCGGTCTCATCATCTACCAATATCTCTC
CGGCTAATGAAACACAACCTAGAAATACCTGATACTCAAGAATTGCATCATAAACTGCTCA
ACGACTCTGATCAACATGATATTACCGCGGACTCAAATGATTTGCCAGACAACCTCAATCG
TTGAACATGACTCTGTTATTACCCAAACAAAACCAGCCATGTCTCAAGAATACGAAGAGA
CTGCCGCTCACTTATCTTTCGAGAAATCCATCGCTCGATGTAGTCGCGGGAGAACTTCACA
ATAATAATGAACATACCCAGAAAATTGCCGTATCCGCTGTGGAAGAGGATTCTTTCAATG
AAGAAGAGGGTGAAAATCACGACAGCATAATAATTTTCATCATTAAACGATGCTACCCCTT
CTCAATATAATCATTTTCTCCCATCCGATGGCAATCTTCTTTCTCCAGAATTATCTCTG
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AGTATTGTAATGATAAGGAAATTAGTTTGAACGCAATAATGTGCTTCTGATGAACTTT
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AGGATATCGCTGATCAGGAACTGCAGAAAACCTTATTTACGCTCTAGTACAGAACCATCTG
AGAATAAAATAAGAAATTTCTGGTGATGATACCTCCATGTTGTTTCAAGATGACGAAAGTG
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ATACTCAAGAATCCGCACCGAACACAGATGATCGTGATAAGGGTTATGAAGGAAACGAAG
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CAGAAGATATCTTTACGGACACGACAAAACAGGTAGTTGAAGGCCAAAATGATTTCACTG
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TGTCTGCCGAAGCTGACATTATAGAACCCTGGTAAGGATATTCAAGATCAAGCCGAGGATT
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ACGCTGATGTAACGAGCAAAATCCCAAGAGAAACATGAAGATTTATTTGCTGCTTCTGGAA
ACGATGAGAAAACCTTCTTGGGAAGTTTCTGACGGTGAAGTATCATCGGGAAAGACGGAAA
ACAGCATGCAGACTAGTACTGAGAAAATAGCTGAGCAAAAGTTTTCGTTTGGGAAAACG
ACGACGACCTTTTGGACGACGACGACAGCTTTTGGCTTCTTCTGAGGAAGAAGACACAG
TACCTAATACCGATAATACAACGAATTTAACTCAAAACCAGTTGAAGAAAAAAGGCTT
CAAGATATAAACCTATTATCGAGGAGGAAGCAGGAATGCGTCAAGAGCAAGTTCAATTTA
CCAATACTACTGGCATTGTAACACCGCAGCAGTTCCACGGTTTGACTAAAACCTGGACTAG
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CTACTCAAAGGTTTGGCTCAGGGAATTTCTTTTAGTTCTTTGGACAAACCAATTCCACAGA
GCAGGAAAGGCTCTAATAACTCAAATAGGCCACCCGTGATCCCATTTGGGGACGACGAGC
CTCGATCTTCGAGAACTAACTCAGCGATCTCGCAATCTCCCGTTAATTATGCTTTCCCTA
ACCCATACAAAATTAACAACCTACAACAGGCTCCTATCCAATCAGGTATGCCTTTACCAA
ATACCAACATACCTCCCCAGCATTAAAAGTGGAACCAACCGTTTCTGCTCCTCCAATTC
GGGCAAGAGGGGTACGCAATGCCTCCGTGGGAAGTTACGCGTCTTTTGGTGCTAGACATG
CAACACAGTACGGCCTCAATAACGGGGTACCTCCGGTTTCGCCATATGGTCAAGCTACCA
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ATCCATCAGTTGTGCAAAACCTTGGCGCTTCGGCCGTAAATACCCCAATTTTGTAAAGA
CCCATAGAGGCCATACAAGCTCTATTAGTTCTGATACACCAAACAGAAATGAACACGCCT
CTAGATACGCACCCAACTATCAACAATCTTATCAGGTGCCATATACCTCACAACCTGTTG
GTCCTGTAGCTGGGAATTCAGCTATCAAAGCCAAACCCGAAGTTCTTATGCAGTTCCTA
TGATGCCCCAGGCTCAAACCTCAGCAAGTATTCAGCCTCACGCGAACATTCAACCGCTA
CTGGCATTTTACCTTTAGCCCCCTTACGACCTCTAGACCCCTTACAAGCCGCTACGAACT
TGCAACCCCGTGCAAGCAACATAACGGCTGCAAAATTCCTACCTCTTGCAAAATTTGCCAC
TTGCTGAAAACATACTGCCAGAAATATCACGCATCGAGCTACAAGTAGTGTGACCAC

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CACGACAGGAAAAATAATCCAATTAAAAATAGACAACGAGGCTTTATTACGCCGTCAATTTTC
CGATTTTTTCATTGGAGTGCTGCAACAAGGTCGTGTACGCAGTCCCCCTATCCCTGACC
AATCGCAGTACATGATTTTCATCAAGCATTTGTACAGGAAATAAAAGTGACACCAATTGACC
AGATAATTAAACCGAACGATATGCTCAAAAGCTTCCCAGGTCCTTTGGGTAGTGCCAAAT
TAAAAAAAAGGATTTAACCAAATGGATGGAAACCACTATTAAATCCATATCTGAAAATG
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CTGTTGTCTTGAATTTTGTATAGAGTTCCGTATATTTCTCACCAAAAGGGCTTGACAG
CCGCAGCTAGTACATTATTTATTATTGGTAACGTACCACCTTCTAATGAGCCAGTAATGG
CAGATTCAGACGTTATATTTGAAAGTATTGGAAACATGAATACTTTTGAAGCATTCTAT
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TTTTGCCCCAGAAGATATACCATGCATCTCTTTTACAAGAACAAAGGTTTGAACAGCCTGG
GGACAAAGTATACTGATTACCTCAGTTCCCTCAGTTTCGAAAACCTGCCTAAGAAAGATATTT
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ATAAATATATTTGGTGGCGATGATATTGATGCATTGAATAAAAAAATGATAAAAAGAAAG
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CATTCACACCTTTTCCAAGCTCAAGTTACTTCCGAAAGCTATGTGGATACTACAGCTCTTT
TGCAATAATGCCCATATGTACCAAGCCATAGTGTGCTGCATTCAAAGCCTTCCAATGTGT
CAAAGGGGTAGTTGAAGCAAACCTTACCGTATACGCATAGGATCGGTGATAGTTTGCAGG
GATCTCCTCAGCGCATTCATAATACACAGTTTCGCTGCTGCTGAGCCTCAAATGGCTTCTT
TGAGAAGAGTTAGAACAGACCAGCATACAAACGAAAAGGCTTTGAAGAGTCAGCAGATTT
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CGCAGGGATCGCTTATGTACTACCAAGTGTGGAAGCTTTGCCTATCGACCCTGTCTGCC
CGCAAGTTTCATGAGACGGGATACAATGATTTTGGTAAACAAACATTCTCAAAAAAGTATGC
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CATCGAAAATGGAATAATTCACCTCCCTCCATTGAAAATGAAAGAAGTAGCGAGGAGCAGC
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TCGAAAACAGACCGCTAACTCAGGATGAAAACAGTATCTCAGAGACAGTTCAATCCACAT
ACTTGCCAGCAGGAAGTATTTCAATGGAAGCTAAACCAATTTCTCAAGTGCAAGATGTTT
CAAGAAATGTTAATAATAAAGCATCCAACTTGTGGAGCAACATATGGCACCACCAAGC
CAAAAAGTACTGACGCAACCAAAATGAACTACTACCATACGTGCCTCAATCAACTGCCG
CTAGTGAGATGGCGATGAATCAACGATTCTGAAAACATCGCCTGCTATATATGCAAGAA
CTCACCAAGCACATGCATCCAATCCATCACAATACTTTCTTTGGTCAACCAAGCAAAATG
AAACTGCTTCATTTCGAATTATCTGAATCAACATCCCAGGCACAAAGTAATGGAAATGTTG
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AACCTACTATTAGGAAGGCTTCAACTAACCAATACAGGGCTTTTAAACCGTTGGAATCAG
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CAAGTAACAAGGACATAGATGACAAGTCTAATGGTTGGTTTGGTTGGTTGAAGAAAGATA
CTGGCGACAAAAAGTGTATAAGGCCAAGCTAGGTCATAAAAAACACACTATACTATGATG
AAAAATTGAAACGTTGGGTGAATAAGGACGCAACCGAAGAGGAAAAACAAAAAATTATTG
AAAGTTCCGGCACCACCACCTCCTCCAATCGTGAAACGTAAAGATGGCGGCCCAAGACAA

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AGCCACGTTTCAGGCCCATCAATAATTCCTACCTCCAGTACATGCCACATCAGTTATTC
CGAACAAATCCAATCACTGGTGAGCCTTTGCCGATCAAAACATCCCCTTCTCCTACAGGAC
CCAATCCAAACAATTCCTCATCACCATCCTCTCCCATATCAAGGATTTCTGGCGTAAACT
TGACTAGCAAAAAGGCAACGGTTTGGATGATTTATTGAGTTTGGCAGGAGGACCCAAAC
CAGCAAGTACGAGAAGGAAGAAGAAAACAGCGAGAGGCTATGTTAATGTAATGGATAACA
TACAATAA

>YPL085W, 2195 aa (SEQ ID NO 384)

MTPEAKKRKNQKKKLKQKQKKAEEKAASHSEERLELPSTINSSFNDDSVNRTESDIASK
SDVPPVSSSTNISSPANETQLEIPDTQELHHKLLNDSQHDITADSNDLPDINSIVEHDSVI
TQTKPAMSQEEYETAHLSSRNPSLDVAGELHNNNEHTQKIAVSAVEEDSFNEEEGENH
DSIISSSLNDATPSQYNHFLPSDGNLLSPELSSGDTPTHNVPLGTDNEINDDEYCNDE
ISLNANNVLPDELSKEEDERLKLETHVSTEEKQDIADQETAENLFTSSTEPSENKIRNS
GDDTSMFLQDDESDQKVPWEEDVKKDFHNENTNNTQESAPNTDDRDKGYEGNEALKKSES
CTAADERSYSEETSEDIFHGHDKQVVEGQNDFTGKNIENESQKLMGEGNHKLPLSAEADI
IEPGKDIQDQAE DLFTQSSGDLGEVLPWESTDKNADVTSSKQEKHEDLFAASGNDEKLPW
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TNLTSKPVEEKKASRYKPIIEEEAGMRQEQVHFTNTTGIVTPQQFHGLTKTGLGTPNQV
SVPNIVSPKPPVVDNRNFKINEEKKKSDAYDFPLEIISESSKKGHAKPVAVPTQRFGS
GNSFSSLDKPIQSRKGSNNRNPPVIPLGTQEPSSRTNSAISQSPVNYAFPNPYKIQQ
LQQAIPQSGMPLPNTNIPPAKLVETTVSAPPPIRARGVSNASVGSSASFGRHATQYGLN
NGVPPVSPYGQATINLPTANKYAPVSPTVQQKQYPSVVQNLGASAVNTPNFVKTHRGHTS
SISSTPNQNEHASRYAPNYQQSYQVPYTSQPVGPVAGNSSYQSQTRSSYAVPMPQAQT
SASIQPHANIQPPTGILPLAPLRPLDPLQAATNLQPRASNITAAANSLPLANLPLAENILP
EIIITHRATSSVAPPRQENNP IKIDNEALLRRQFPFIHWSAANKVVYAVPPIPDQSQYMIS
SSIVQEIKVTPIDQIIKPNDMLKSFPGLPSAKLKKKDLTKWMETTIKSIENESSTDMT
IWQLLEMKLNDKVNWNKISKLLYNSDELLMYLSQFPNGDMI PNAYRLDINCQMRVLAFL
QTGNHDEALRLALSKRDYALALVGLMGLKDRWSEVIQKYLEGFTAGPNDQKELAHFLL
LIFQVFGNSKMAIKSFYTNNETSQWASENWKSI VAAVLINIPENNEDPLLIPPVLEFL
IEFGIFLTKKGLTAAASTLFIIGNVPLSNPEVMADSDVIFESIGNMNTFESILWDEIY EY
IFSYPDKFKGFSSILPQKIYHASLLQEQGLNSLGTKYTDYLSSSVRKLPKKDILTINLTR
ELSEVASRLSESNTGWLAKPKLSSVWGQLDKSFNKYIGDDIDALNKKNDKKKVFDFGFTP
GSSANSSTVDLTQTFTPFQAQVTSQS SYVDTTALLHNAHNVP SHSVLH SKPSNVSKGLVEA
NLPHYTHRIGDSLQGSQRIHNTQFAAAEPQMASLRRVRTDQHTNEKALKSQQILEKKSTA
YTPQFGQNHVSVPMEKSNNSNPSLFADFPAPPKLGTVPSNYVSSPDLVRRESIIISTGSEFL
PPP KIGVPTKANSSQGS LMYSPSVEALPIDPVVPQVHETGYNDFGNKHSQKSMPEDESHT
SHDNSNADQNTLKD SADVTDETM DIEGPGFNDVKNLLPMEPNHQPTSTVNPIQTISSDIQ
PILQNTNVEVRGTDASKMENS LPSIENERSSEEQPENISK SASSAYLPSTGGLSLENRPLT
QIDNISYETVQSTYALPAGSISMEAKPISQVQDVPRNVNNAKSLVEQHMAPPKPKSTDAT
KMNSPYVPQSTAASADGDESTILKTPAIYARTHQAHASNPSQYFPLVNQANETASFEL
SESTSQASNGNVASENRFSP I KKA EVVEKDTFQPTIRKASTNQYRAFKPLESDADKYND
VIEDESDDDNMSTDEAKNRKEEKNVNMKKETKPSNKDIDDKSNGWFGWLK KDTGDKKVY
KAKLGHKNTLYYDEKLKRWNKDATEEEKQKIIESSAPPPPIV KRKDG GPKTKPRSGPI
NNSLPPVHATSVIPNNPITGEPLPIKTSPTSPTGPNPNNSPSPSSPISRI SGVNLT SKKAN
GLDDLLSLAGGPKPASTRRKKKTARGYVNVMDNIQ

>YPL190C, 2909 bp, CDS: 501-2909 (SEQ ID NO 387)

TAATCTTTCGCTACTTCAAGTTTCATAATCAATCGACTTCTGTATGGGTAAGCATCTGGT
GTGATGCAGTTTCATTATGACACCACAAATACAAAAGAGACTATTTAAATATGTATATAG
ATCACATTCCAAAAAAGAAAACCATTAATAATATCACTCTTTAATATTCCAAATTGAAAC
GAAAAAGCGCTATTCTTATTTCGCTTCCTAACTACCGCCCTAGTTCGTGCTTGCAATTTTT
TG TAGAACGATAAATTATGGTATCCCACGTGATTGAGTGTAACCTGAATTGTTGAAGAG
AAAATGAAGCGGAAGAAGCAAAGGACAAAAACAATTCAATTTGATTTTGCCACTTCTAAA
TGAAGGTCTAATAAAAGCTATCTTGAGCATCTTTATTAGATTCTGCACAGCAACAAGCGA
TTTTCTTTGGTCAAAATATAATAATTGACTTACGTTTTTCCCGGACTGTCCTTTCATAAT
ATAATAACCATCTGCAAGCCATGTCAGATGAAAACCATAACAGTGATGTTCAAGATATTC

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CTTCACCTGAACTATCCGTCGATAGTAACCTCTAACGAGAATGAATTGATGAATAACTCAA
GCCGAGACGATGGAATCGAATTTGACGCCCCAGAGGAAGAAAGAGAAGCCGAAAGGGAGG
AGGAAAAATGAAGAACAACACGAACCTGGAAGATGTGAACGATGAAGAGGAGGAAGATAAGG
AGGAAAAAGGAGAGGAAAAACGGGGAAGTAATAAACACAGAAGAAGAAGAAGAAGAAGAAC
ATCAACAAAAAGGCGGAAATGATGATGACGATGATGATAATGAAGAGGAAGAAGAGGAAG
AAGAGGATGATGACGATGATGATGATGACGACGATGATGATGAAGAAGAAGAAGAAGAAG
AAGAAGAAGAAGGCAACGACAACAGTTCCGGTAGGCTCAGATAGTGCCGCTGAAGACGGTG
AGGATGAGGAAGACAAAAAGGATAAAACCAAAGATAAAGAGGTCGAACCTCGCCGTGAAA
CATTTGAAAAAGAACAAAAAGGACGTAGATGAAGCTATAAAAAAAATAACTCGTGAAGAAA
ATGATAATACTCACTTTTCCAACATAATATGGAATGTTAATTACGATCTTTTACAAAAGC
AAGTCAAGTACATTATGGACAGTAACATGCTAAATTTGCCTCAGTTTCAACATTTACCTC
AAGAAGAAAAGATGCTGCGATTTTAGCAATGTTAAATTCAAATTTCTGACACAGCTCTTT
CCGTACCTCCTCATGATAGTACTATCTCAACAACAGCTAGCGCCTCAGCCACAAGCGGCG
CAAGAAGCAATGATCAAGAAAACCTCCATTGTCAGATGCCCAAAGACGTATGAGATTTTC
CTAGGGCGGATTTATCTAAGCCGATTACCGAAGAAGAACACGACCGTTATGCAGCCTATT
TGCACGGTGAAAAATAAAATCACCGAGATGCACAATATTCTCCGAAGTCAAGATTATTCA
TTGGTAATTTGCCGCTAAAGAACGTTTCTAAGGAGGATTTATTTAGGATTTTCTCTCCAT
ACGGTCATATCATGCAATCAATATCAAAAATGCCTTTGGATTCAATTCAGTTTGACAACC
CTCAAAGCGTTAGAGATGCAATTGAATGCGAGTCTCAAGAAATGAACCTTTGGCAAAAAGT
TGATCCTGGAAGTTTCTAGCTCGAATGCTCGTCTCAATTTGATCATGGTGATCACGGTA
CAAACAGTAGTTCTACTTTTATTTCTTCCGCAAAACGACCATTTCAAACTGAATCTGGTG
ACATGTACAATGACGACAATGGTGCTGGCTACAAGAAATCCAGAAGACACACCGTTTCTT
GCAACATTTTCGTTAAAGAACCAGATCGTACGTATGCCATTGAGGTTTCAACAGGT
TTAGGGACGGGACTGGTTTGGAAACTGATATGATTTTCTTGAAACCAAGAATGGAATGG
GAAAGCTTATCAATGATGCCGCATATAATGGGGTGTTGGGGCGTTGTTTATGTTAATAAAA
CACACAATGTAGATGTTTCAAACCTTTCTACAAAGGCTCACAAGGTGAAACGAAATTTGATG
AATATATTAGCATATCCGCTGATGACGCAGTTGCCATTTTTAATAACATCAAAAACAACA
GAAATAATTCTCGTCTTACTGATTACCGTGCTATGAGCCATCAGCAAAACATATATGGCG
CTCCTCCTCTTCTGTTTCCAAACGGCCAGCTGTGCGACCTCCTCCTCAAAACAACTATT
ACCAGGGTTACAGTATGCCTCCTCCACAACAACAGCAACAGCCATATGGTAATTATG
GGATGCCACCACCATCCCATGACCAAGGATATGGTTCTCAACCTCCAATTTCAATGAATC
AGAGCTACGGTTCGTACCAGACTTCTATTCCACCACCACCTCCACAACAACAAATTCCTC
AAGGGTATGGTTCGTATCAGGCTGGTCCGCCTCCTCAACCACCTTCTCAAACCTCAATGG
ACCAGCAACAACATATTATCTGCCATTCAAACCTTCCACCTAACGTTGTATCGAATTTGC
TTTCAATGGCCCAACAACAGCAACAACAACCTCATGCTCAGCAGCAATTGGTTGGTTTAA
TACAATCAATGCAAGGCCAGGCTCCTCAACAACAGCAACAACAGTTGGGTGGATATTCTT
CTATGAACTCATCTCTCCCCCTCCTATGAGTACCAATTACAATGGTCAAAATATATCTG
CAAAACCTCTGCCCCACCAATGTACACCAACCTCCGCCACCTCAACAACAACAACAAC
AACAACAACAGCAACAGCAACAGCAACAGCAACCTGCTGGCAATAATGTTCAAAGTCTAT
TAGATAGTTTAGCAAAACTACAAAAATAG

>YPL190C, 802 aa (SEQ ID NO 388)

MSDENHNSDVQDIPSELSVDSNSNENELMNNSSADDGIEFDAPEEEREAEEREENEQ
ELEDVNDEEEEDKEEKGEENGEVINTEEEEEEEHQKGGNDDDDDDNEEEEEEEEDDDDD
DDDDDDDEEEEEEEEEEGNDNSSVGSDSAAEDGEDEEDKKDKTKDKEVELRRETLEKEQ
DVDEAIKKITREENDNTHFPTNMENVNYDLLQKQVKYIMDSNMLNLPQFQHLPEEKM
ILAMLNSNSDTALSVPPHDSTISTTASASATSGARSNDQRKPPLSDAQRMRFP
PRADLSK PITEEHDRYAAYLHGENKITEMHNIPPKSRLFIGNLPLKNVSKEDLFRIFSPYGHIMQI
NIKNAFGFIQFDNPQSVRDAIECESQEMNFGKKLILEVSSSNARPQFDHGDHGTN
SSSTF ISSAKRPFQTESGDMYNDNGAGYKKSRRHTVSCNIFVKRTADRTYAIEVFN
RFRDGTGL ETDMIFLKPRMELGKLINDAAYNGVWGVVLVNKTHNVDVQTFYKGSQ
GETKFDYISISA DDAVAIFNNIKNNRNNRSRPTDYRAMSHQQNIYGAPPLPVPNGPA
VGPPPPQNTNYYQGYSMPPQQQQQPYGNYGMPPPSHDQGYGSQPPIPMNQSYGRYQTS
IPPPPPQQQIPQGYGRYQAGPPPPQPSQTPMDQQQLLSAIQNLPPNVVSNLLSMAQ
QQQQQPPHAQQQLVGLIQSMQQAPOQQQQQLGGYSSMNSSPPPMSTNYNGQNISAKPS
APPMSHQPPPPQQQQQQQQQQQQQQQQQQPAGNNVQSLDLSLAKLQK

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>YPL201C, 1886 bp, CDS: 501-1886 (SEQ ID NO 389)

ATTTTCATCACTTCATTAGTTATAAAAAAGGAGTTCCCATTCGAGGAGAAAATAATCATTGT
TTATTGTCGTAATTTTCTTTCCAATAACGATAACTGCAGTTTCCATTTCCAGGTGCGCCA
ATTGGTTGGACAACGTTGATGTTACCTTCCTTGTATGGAACCATCCATCATTTTCTAGT
TCTTCTTCTGCAATATTGCCTTTTGGGAAGAAGGATCGAAAGTAGCCATTTGCAGACACG
TTTTTACTATATTTACTGTATCTTCGATTGCGCGGCTAAAGTTGCCATATTATTATTATA
TTGCAGCTCAACCCCGCATTTCCGGAGTTTCTTTTTTTTTTATTGTTGGGTAATTTGGAGG
TCGGCGGCTATTGGTGGGCGGAAATGGTGACACACTTGTAATATATAAGGAGGAAATCC
TACATGTGTATAAGCGAAATCACAAGGATAAATGTATTGCTAAACACCCTCAAGAAAG
AAAAATAATCATAACGAAATCATGGGTATACCTATGCAAATATACCAGGATGGGAAGGGGG
TGCAATTTTACCACACGAGATATCAGAACGTAATTTGACGAACGGGCGAGCAAGTATGGCA
ACTACACGGTGAATAATGATTACCCACAGCTTCCAGATACGATAAAGGAACATATCGACC
AGCTTACCTTTAGCAATGTCGGAGAGGATGGTGGAGATGTTGGAAACTATTCTGAAGAAG
ACGATGATGGTGACGAAGAAAAGGAACCTGAAGATGTTTTTCGAAGTAACCGTGGGTGG
AATTTGTACGGATTAATAACTATTTTACTACCCACGATTTACAAAGTTTCAAAAGTTTTA
GAAATTTCAATAGCAAGTACTGGATTTTTTATTCTAATCAAGCAGAGGACAAAAAATTAC
TGCTGTATGACTTTAACGGCCAACATTTGATTTTTTATTAAGCAGCAATTTTACGGGCAGT
TGAATTTACTGCTATCGGACGCAATAATATGTATGGACTGCAATTTTGGTTATAATTCAA
ACACCATTCAAATTTTAGTTGGATTTTCAAGATGGAAGTTGTTAAAGCTAAACTGCGACT
TGAACGGAAACGTAAACAATCACTTGCTTTTGAAGGATCCTTCAACTTCCTCTCATCAAA
GCCACCTATCTATATAAATGTCTGGGCAGGTTTGTGTCACATTTTCGTTGTTCTTTTA
GTTTGAAAGATGGGCTGCTAATAACTTCTTTAGATCACCACAAAGCAATGGAAGTTTTC
AAAGTTTCCATACCAACATTTGATTTGCCGTGATGCTACGCACGACCACAAATGTCAAGT
CCGTTTTAAATTTCCCTCAGTTTACTTTTATACAAAGGAAATGATATGATTTTCCACTGCA
AGAATCTATTAGGATCGGATGCTTCCACGCTAAACAAGGAAATAAACTTTATGCTTAAAA
TAGACGAAGACGTTCAAAGATCGACTATCTTCTTAAAACGAATCACATTTTACTCGAAA
CCAACATGAGATATCTGTCCATTTCAACAAGAGACCCCATAGAGAATTCAAATTCCTCTC
CACCCGCTCAGACAGCGAGGTTTATCCAATATTTTACAAGACACAAGAACTTCATGTCC
ATGCTTCAGGAACAGGACGTCAGATAGCAAACAATGGGAAGTATATTTTATAACCGAGC
AACATCTCTACGGAACAGCGTTATCGGTATACAGTACTCTATATCTTCAAACGGTGGC
TGTTCTGTTGGCTACTCAGACATTAGGGCCAAATACGGTATAAGGAGTGTCAAAGATCTCT
TTGTTGGTAACTGTCCCTCTGTAAATAGCCAGTGTGACAATTCCTTACTGATGACAATA
ACATTCAAACAATTCCTTCTTAAATAA

>YPL201C, 461 aa (SEQ ID NO 390)

MGIPMQIYQDGKGVQFYHTRYQNVFDERASKYGNVTWNNDYPQLPDTIKEHIDQLTF SNV
GEDGGDVGNVSEEDDDGDEEKELEDVFRSNRGLEFVRINNYFTTHDLQSFKSFRNFNSKY
WIFYSNQAEKLLLYDFNGQHLIFIKQQFYGQLNLLSDAIICMDCNFGYNSNTIQILV
GFQNGKLLKLNCDLNGNVNHLKDPSTSSHQSHLSILNVWAGLLPHFVVSFSLKDGLL
ITSLDHQQSNGSFQSFHTNIDL PVDLRTTTNVKSVLNFPQFTLYKGNDMIFHCKNLLGSD
ASTLNKEINFMLKIDEDVQKIDYLLKTNHILLETNMRYLSIPTRDPIENSNSPPVSDSE
VYPIFYKTQELHVHASGTGRQIANNGKYIFITEQHLYGTALSVYKYSISFKRWLFVGYSD
IRAKYGIRSVKDLFVGNCPSVNSPVLITLDDNNIQTILLK

>YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2:
685-1176 (SEQ ID NO 393)

ACAAACCCCTGTCAATCTCCTGAAAAACAAAATTAAGTGCTTGAGAAGACCTTCAGAAGA
GTTGCATAGATAGGATGGGTGAGCGCAATTACTAGTTACGCAGTAAGTAGGTTATATGGC
TGCTGGAGGGGCGAGTACTGATTTAATCACAATCCGATTAAACTTCCTCCTGAAAAAAA
AAACTACATCAAGTCAAAGATTTTCATTCACTCTTTGGAAGGCTGTGTGGCATTTCTAA
CCTTTATTTTTTATCACCATTCTCGAATTTTCGTGGTTTCGCTTTCTTAGCGCCGTTATT
CTCTCTTCTTGTCACGTCAAAGGGAGTATGCGTAACCCCTTCAAGGTTGAACGAAAAA
AAAAAAATATGTCTTCAAATTTTTTTTTGATTTAAACTAAAAAACATTCCCTTGAAG
CTTGTTATTCGAAAGAAAGATCTAAATTTGCAATTGGTAGTGAAAACAAATAAACAAA
GACATAACCGCACTCCAATCATGTCCGAATATGCATCTAGTATTCACCTCAAATGAAAC
AATTCGATACCGTATGTAAGATGGTTTTATTGGTTCCATCGTCATCATGGTTCAAACAGC

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CAAATGACCCGACACACGTAACCGAAGCAGTTATACTAACAAGAAAGCTAATTTTCACCC
TCCTTGCTACATTTTCTTACAGAAGTACTCTGGTAATAGAATTTTACAGCAATTAGAA
AATAAACTAATTTGCCATAATCTTATTTAGTTGCTGGTTTAGGTTTCGCTTATCTCCTT
TTGATTTTTATTAAACGTCGGAGGTGTAGGTGAAATCTTTCCAATTTTGCTGGGTTTG
TTGCCAGCATATTTATCGTTGGTTGCTTTGAAGACACCAACGTCCACCGATGACACACAA
CTCTTGACCTACTGGATTGTCTTTTCATTTTTGAGTGTCAATTGAATCTGGTCCAAGGCA
ATTCTATATTTGATTCCATTCTACTGGTTTTTGAACCCGTTTCTTAATCTACATTGCC
TTGCCCTCAAACGGTGGCGCTAGAATGATCTATCAAAAGATCGTAGCCCCATTGACCGAC
AGATATATCCTAAGAGATGTTAGCAAGACAGAAAAGGATGAAATTAGAGCTTCCGTCAAT
GAGGCTTCTAAGGCTACAGGTGCTTCTGTTCAATTA

>YPR028W, 180 aa (SEQ ID NO 394)

MSEYASSIHSQMKQFDTKYSGNRILQOLENKTNLPKSYLVAGLGFAFYLILFINVGGVGE
ILSNFAGFVLPAYLSLVALKTPTSTDDTQLLTYWIVFSFLSVIEFWSKAILYLIPFYWFL
KTVFLIYIALPQTGGARMYQKIVAPLTDRIYLRDVSKEKDEIRASVNEASKATGASVH

YDR145W, 2120 bp, CDS: 501-2120 (SEQ ID NO 99)

AAGTGATTATCTGAATAATGAAAGATGGTAGGAAATAAGGTATTGAAACA
GGTTCAAACTTTAAAAGAAAACCTGCCAAATAAACTTTCTCGATGCGTAG
CTGAAATTTCAACTTCAAAAAAAAAAAAAACGCGTGAACCTTTCTACGTGC
AAAACGATGTGTATGAATCCCGTCTTAATTAGTAAATAGGGTCTAGTAAG
CGTAGCGAGGATGAATTAAATGCATTGTTGAATATGAAGAGCACCTTATG
GTATATAAATGTACAATCTTGATTTCATGACAGCTTTGCAAGTAAACGTAT
CAAATGAATATCACGATTTTGGCTGTATTACCCGGGCAGTATACGCGGCG
AATTTTGTTAAAAAATGTGTTAGACTTAAGTCGGAGCAAATGAATAATGG
GCATATATAGCGCATAGGTTTCGCTAGTGTAAAGACAGGAGACTGTCCAATA
GCATTGCAATCATAACCGAATCTTTGCCAGTGTGTGTATAAAATACGACA
ATGTCTTCCAATCCAGAAAATCTGGTGTAAATGCGAATAATAATACGGG
CACTGGTAACGCTGATGCGATCACAGGAGCTCAGCAAAATATGGTACTGC
AACCGAGACAGTTGCAAGAAATGGCCGCTAAGTTCAGGACATTACTGACT
GAAGCAAGAAATGTAGGTGAACTACTCCTAGGGGCAAGGAATTGATGTT
CCAAGCCGCAAAGATCAAACAGGTATATGATGCCCTTACACTGAATAGGA
GAAGACAACAGGCTGCGCAAGCCTACAATAATACTTCAAATTCAAATTCA
AGCAATCCAGCTTCTATTCTACTGAAAATGTCCCTAATTCATCACAGCA
ACAACAACAACAACAACAACAGACAAGAAAACAACAGTAACAAATTTAGCA
ATATGATAAAACAGGTTCCTACCCCGGAAGAGAACCAAGAATATGAAAAG
CTATGGCAGAATTTCCAAGTCCGTCATACGAGTATAAAGGAGAAAGAGAC
CTACTTGAAACAAAATATTGATAGGTTAGAACAAGAAATAAATAAACAGA
CGGACGAAGGGCCCAAGCAGCAGCTACAAGAAAAGAAAATTGAACTGCTT
AACGATTGGAAGGTGCTAAAAATTGAGTATACCAAGCTGTTCAATAATTA
TCAAAACAGTAAAAAAACATTCATGTAGAGTGTGCAAGACACAATCCGG
CTTTACATAAATTCCTTGCAAGAAAGCACTCAACAGCAACGAGTGCAGCAA
CAAAGGGTACAACAACAACAACAACAACAGCAGCAGCAGCAGCAACAGCA
GCAACAGCAACAGCAACAGCAACAGCAACGCCAGGGTCAAAACCAAAGAA
AGATTTCTAGTTCTAATTTCTACTGAAATACCCCTCTGTAACCGGCCCTGAT
GCACTGAAATCGCAGCAGCAGCAGCAGCAGAATACAATAACTGCCACCAATAA
TCCCAGGGGCAATGTTAACACTTCACAGACTGAACAATCGAAAGCTAAGG
TAACCAATGTAAATGCAACGGCATCTATGTTGAATAATATAAGTTTCGAGC
AAATCGGCAATATTCAAACAACAGAGCCTGCCATACCCATATCGGAAAA
TATATCTACCAAAAACACCAGCACCAGGTAGCTTATAGATCCAACAGACCTA
CAATAACTGGAGGTTCTGCTATGAATGCCAGTGCTTTGAATACACCAGCA
ACAATAAATTAACACCCCTATGAAATGGATACTCAGAGAGTTATGTCAAA
GCGTAAATTAAGAGAGTTAGTGAAGACTGTCCGAATTGATGAGGGTGACG
GTGAAACTGTCAATTGACGGTGATGTTGAGGAATTACTATTGGATCTTGCC
GACGATTTTGTTACTAATGTTACAGCTTTTCTTTGTAGATTGGCAAAACA
CAGAAAATCGGACAAATTTGGAGGCAAGAGACATTCAGTTACATTTGGAGA

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GAAATTGGAATATTAGGATTCCCTGGTTATTCCGCAGACGAAATAAGAAGT
ACAAGAAAAATGGAATCCCTCTCAAAATTATAACCAGAAATTGCAGAGTAT
CACATCAGATAAGGTAGCAGCTGCAAAAAACAATGGAAACAATGTTGCAA
GCTTGAATACAAAAAATAA

YDR145W, 539 aa (SEQ ID NO 100)

MSSNPENSGVNNANNNTGTGNADAITGAQQNMVLQPRQLQEMAAKFRTLLT
EARNVGETTPRGKELMFQAAKIKQVYDALTLNRRRQQAQAYNNNTSNSNS
SNPASIPTEVPNSSQQQQQQQTRNNSNKF SNMIKQVLTPEENQEYEK
LWQNFQVRHTSIKEKETYLKQNI DRLEQEINKQTDEGPKQQLQEKKIELL
NDWKVLKIEYTKLFNNYQNSKKTFFYVECARHNPALHKFLQESTQQQRVQQ
QRVQQ
ALKSQQQQQNTITATNNPRGNVNTSQTEQSKAKVTNVNATASMLNNISS
KSAIFKQTEPAIPISENISTKTPAPVAYRSNRPTITGGSAMNASALNTPA
TTKLPPPYEMDTQRMVSKRKLRELVTGIDEGDGETVIDGDVEELLLDLA
DDFVTNVTAFCRLAKHRKSDNLEARDIQLHLERNWNIRIPGYSAD EIRS
TRKWNPSQNYNQKLQSI TSDKVA AAKNNGNNVASLNTKK

YDR216W, 4472bp, CDS: 501-4472 (SEQ ID NO 109)

CAAAGAACAACGCCTTAAAAATAGGAAAACGTTTTTCGCTACAGGTGTTGT
TATTATTGTTGTTGTGCTGTTGTTTATTGTGCTATACTTGTGGTATTTAT
TCTGGACTTCCGATCGGAAATTTCTTCCCTTGAAGACCTTTTGAAGACA
ACAGTTATATATCATTTGATCTGAATTTCTCAGGCTATTTTCAAAATTCCA
TACCTCCTTATTCCAACATTTGCTCGACTACTATAGAAAAGCCTTATTCT
TTTATCTTTGAAAGAAAGGAGGTGTCATAGCAAAAGTTTATTGTTACT
CTGTTTTGTATATACTCCCTCTTATTTCGTTGGAAGTATAAGATTGATTGC
ATAAATTAACCAATCATTTTGCTACTTTCCCGGTTCTCCCTTTATTATAA
ACACTTCAGAAAAATATTCTGCTACTATTCCCTTACTTTACTATAAGAATT
TTGTTTTTCAAAAAAAAAAAAAATATAAAAAAATAATCATACTCTATTACT
ATGGCTAACGTAGAAAAACCAACGATTGTTTCAGGCTTTCCCGTTGTTGA
CTTGAATTCGTGCTTTTCTAACGGCTTCAATAATGAGAAACAAGAAATAG
AAATGGAAACGGATGATTACCGATTTTATTAATGTCATCATCAGCTTCC
AGAGAAAACCTCAAACACTTTCTCTGTGATACAGAGGACGCCAGATGGAAA
GATCATTACCACAAATAATAATATGAACCTCAAGATTAACAAGCAACTGG
ACAAGTTGCCCGAAAATTTAAGGCTTAATGGTAGAACCCCGAGTGGGAAA
CTAAGGTCATTTGTTTGCGAGGTTGTACGAGAGCGTTTCGCAAGACAAGA
GCACTTGAAAAGACATTACAGATCGCATACAAATGAAAAACCTTATCCCT
GTGGCCTCTGCAACAGATGCTTTACTAGGAGGGACTTACTGATCAGGCAT
GCTCAAAAATCCATAGTGGTAATTTAGGGGAAACGATTTCCCATACCAA
GAAAGTGTGAGAACTATACTAAAGCTCGGAAAAATTTCTGCATCCTCAG
TCAAGTTTCAAACTCCAACCTATGGTACTCCAGATAATGGTAATTTTGTG
AATCGCACTACTGCCAATACAAGAAAGAAAGCAAGCCCTGAAGCTAATGT
TAAACGTAAGTACTTGAAAAAACTGACGCGCAGGGCTTCATTTAGCGCAC
AATCAGCATCCAGCTATGCTTTGCCCCGACCAATCTTCGCTAGAACAACAT
CCAAAGGATCGTGTTAAATTTTCTACGCCTGAATTAGTTCCACTTGACTT
GAAGAATCCTGAACTTGACTCTTCGTTTGACCTGAATATGAATCTAGATT
TAAACCTAAATCTAGATTCCAATTTCAATATAGCATTAAACCGTTCTGAT
TCTTCTGGATCAACAATGAATTTGGATTATAAATGCCCCGAATCAGCAAA
TAACTACACATATTCTTCCGGCTCACCAACCCGCGCATATGTCGGCGCTA
ACACGAATTCTAAGAACGCTTCATTTAATGACGCACTTATTGTGCTCG
TCGTACTGGATAAAAGCCTATAATGATCATTTGTTTTCAGTATCTGAAAG
TGATGAAACTTCTCCAATGAACTCTGAATTAAACGACACTAAATTAATCG
TCCCAGATTTTAAATCGACTATACATCATTTGAAGGATTCAAGGTCCCTCC
TCTTGGACTGTTGCTATAGATAATAATAGCAATAACAATAAGGTATCAGA
CAACCAACCTGATTTTCGTGCTGATTTTCAAGAACTGCTGGATAATGATACTT
TAGGTAATGATTTGTTAGAGACCCTGCGGTTTTAAAGAATTTGAACCTT

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TTACATGATGATAGCGTAAGTGCTACCGCCACGTCAAATGAGATTGACCT
TTCCCATTTGAACCTATCAAACCTCTCCAATTTCTCCTCATAAGTTAATTT
ATAAGAATAAAGAGGGGACCAATGACGATATGTTGATTTCTTTGGGACTC
GATCATCCTTCCAATCGCGAAGATGATCTGGATAAGCTATGTAATATGAC
CAGAGATGTTCAAGCCATATTCAGTCAATATTTGAAAGGAGAAGAGTCTA
AACGATCCCTGGAAGACTTTTTATCAACGTCAAACAGGAAAGAAAAGCCA
GATAGCGGCAACTATACCTTTTTATGGGTTAGATTGTTTAACGTTATCGAA
AATATCAAGAGCTCTGCCGGCCTCCACTGTGAACAACAATCAGCCATCGC
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CATGGACTCTAATCCAAACTTGCTGTCCAAAGAATTGTTAATGCCAGCTG
TGAGTGAATTGAACGAATATTTAGATCTTTTCAAGAATAATTTCTTCCC
CATTTCCCTATTATTACCCAAGCTTGCTTGATTTGGATTGGATAGCTT
GCAACGATATACTAATGAGGATGGGTATGATGACGCTGAAAACGCGCAGT
TGTTTGATCGATTAAAGTCAAGGGACAGATAAAGAATATGATTACGAGCAC
TATCAAATCTTGTCATTTTCGAAAATCGTTTGTTTACCCTTATTTATGGC
CACATTTGGTTCTTTGCATAAGTTCGGTTACAAATCTCAAACAATAGAAT
TGTATGAGATGAGTAGAAGAATTCTACATTCTTTTTTGGAGACTAAAAGA
AGGTGTGCGAGTACAACAGTAAATGACAGTTATCAGAACATTTGGTTGAT
GCAATCCCTAATATTGAGCTTCATGTTTCGCTCTAGTTGCTGATTATTTGG
AGAAAATTGACTCCTCTTTGATGAAAAGGCAATTGTCCGCATTATGTTCA
ACGATCAGATCAAACCTGTTTACCGACAATTTCTGCAAATTTCTGAGAAGAG
TATCAATAATAACAATGAACCTTTAACATTTGGTTCTCCTCTTCAATACA
TCATTTTGGATCAAAAATTAGATGCACCTTAATGGCTTATGATTTTTGT
CAGTTCTTGAAATGTTTCTTCCATATTTAAATTCGATTGTCTATAAAGGA
AAAAGATGTTGAAACCATTATATATTTCCGACAATGAGTCAAAATGGGCCA
GTGAATCGATAATATGTAATGGGCATGTTGTGCAAAAAGCAAAATTTTTAT
GATTTTAGAAACTTTTATTACAGTTTCACGTATGGACACTTACACTCAAT
ACCAGAATTTTAGGGTCATCTATGATTTATTTATGAATACGATTTAAGAA
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GAGAGGAGTCTTGACACTTCTTCTATGGCAATGATAATATGGCAGCAAC
CAATAAAAATATTGCGATCTTAATTGATGACACCATAATTTTGAAAAATA
ATTTAATGTCAATGAGATTCATCAAACAGATTGATCGCTCGTTTACTGAG
AAGGTTAGAAAAGGACAAATAGCAAAGATATATGATTCCCTTTTTGAACTC
TGTGAGGTTGAATTTTTTGAAGAATTATTCAGTTGAAGTATGTGTGAAT
TTTTAGTAGCGTTGAACTTTTCAATCCGTAATATTTTCGTCPTTATACGTA
GAAGAAGAAAGTGATTGCTCCCAAAGAATGAATTTCTCCAGAGCTGCCAAG
GATCCACCTGAATAATCAAGCGCTTTCTGTCTTCAATTTACAAGGCTATT
ACTATTGCTTCATCCTAATTATCAAATTTTTATTGGATTTTGAAGCAACT
CCAAATTTAAGTTACTGAGAAATTTTTATTGAGTTGAGAAGCCTTGCGAA
TTCTATTTTACTTCCCACACTTTCAAGATTGTATCCGCAAGAGTTTCTG
GATTTCTGATGTGTATTTACGCAACAATTTATAAATAAAGATAATGGT
ATGCTTGTCCCTGGTPTATCCGCAAAATGAACACCATAATGGTGCAAGTGC
AGCTGTTAAGACTAAGTTAGCCAAAAAGATCAATGTTGAAGGGCTTGCAA
TGTTTATTAATGAAATCCTAGTTAACTCTTTTAACGATACCTCTTTTTTG
AATATGGAGGATCCTATTCGAAATGAATTTTCCCTTTGATAATGGGGACAG
GGCAGTGACAGACTTGCCTCGTTTACGACATTTCTTATCGGATACCGGCC
TAGAAGGTATTAACCTCAGCGGCTTAAATGATTTCGCATCAAACGTTTCT
ACTTTGAATCTTTTACGTTACGGGGAAAATCATTATCAAACATAAAAA
TGGTGGAAGGGGCAAGGATTTGCCGAAAAGTACCAATTATCTCTGAAAT
ATGTTACTATTGCCAAAGTTATTTTACCAATGTTAAAGAAAACCTACATT
CATGTGCATGTAGATAAGATGGCAAGTGATTTCACACTTTTGAAAA
TCATCTAAAGCGGAAACAGTTGA

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YDR216W, 1323 aa (SEQ ID NO 110)

MANVEKPNDCSGFPVVDLNSCFNNGFNNEKQEIEMETDDSPILLMSSSAS
RENSNTFSVIQRTPDGKIITNNNMNSKINKQLDKLPENLRNLNGRTPSGK
LRSFVCEVCTRAFAHQEHLKRHYRSHTNEKPYPCGLCNRCFTRRDLIRH
AQKIHSGNLGETISHTKKVSRTITKARKNSASSVKFQTPTYGTPDNGNFL
NRTTANTRRKASPEANVKRYLKKLTRRASFSQAQSASSYALPDQSSLEQH
PKDRVKFSTPELVPLDLKNPELDSSFDLNMNLDLNLNLDNLFNIALNRS
SSGSTMNLDYKLPESANNYTYSSGSPTRAYVGANTNSKNASFNADLLSS
SYWIKAYNDHLFSVSEDETSPMNSELNDTKLIVPDFKSTIHHLKDSRSS
SWTVAIDNNSNNNKVSDNQPDFVDFQELLNDTLGNDLLETTAVLKEFEL
LHDDSVSATATSNEIDLSHLNLNSPISPHKLIYKNKEGTNDMLISFGL
DHPSNREDDLDKLCNMTRDVQAIIFSQYLKGEESKRSLEDFLSTSNRKEKP
DSGNYTFYGLDCLTSLKISRALPASTVNNNQPSHSIESKLFNEPMRNMCI
KVLRYYEKFSHDSSESVMDSNPNNLSKELLMPAVSELNEYLDLDFKNNFLP
HFPIIHPSLLDLDLDSLQRYTNEGDYDDAENAQLFDRLSQGTDKEYDYEY
YQILSISKIVCLPLFMATFGSLHKFGYKSQTIELYEMSRRILHSFLETKR
RCRSTTVNDSYQNIWLMQSLILSFMFALVADYLEKIDSSLMKRQLSALCS
TIRSNCLPTISANSEKSINNNEPLTFGSPLQYIIFESKIRCTLMAYDFC
QFLKCFHHIKFDLSIKEKDVETIYIPDNESKWASESIICNGHVQKQNFY
DFRNFYYSFTYGHLSIPEFLGSSMIYYEYDLRKGTKSHVFLDRIDTKRL
ERSLDTSSYGNDNMAATNKNIAILIDDTIILKNNLMSMRFIKQIDRSFTE
KVRKGQIAKIYDSFLNSVRLNFLKNYSVEVLCEFLVALNFSIRNISSLYV
EEESDCSQRMNSPELPRHNNQALS VFNLQGYIYCFILIIKFLDFEAT
PNFKLLRIFIELRSLANSILLPTLSRLYPQEFSGFPDVVFTQQFINKDNG
MLVPGLSANEHHNGASAAVKTKLAKKINVEGLAMFINEILVNSFNDTSFL
NMEDPIRNEFSFDNGDRAVTDLPRSAHFLSDTGLEGINFSGLNDSHQTVS
TLNLLRYGENHSSKHKNGGKGQGAEKYQLSLKYVTIAKLFFTNVKENYI
HCHMLDKMASDFHTLENHLKGN

YBR112C, 3401 bp, CDS: 501-3401 (SEQ ID NO 51)

GGGTGCCGTATCGGCTCTAATTATTTTATCTCTCTATTTTCTTTCTTTTC
TCTGCGCTACTCCTTTCTCGATCGTTGCTACTCCCGTCGCTAGCCACTGG
TCTCCCGCGTACTGTACTCCATCTTTTTTTGGCGTTTTTCCCCTATCCAA
CTCGAACAAGGTTTGTTTAAATTTATTTTATTTTCTTTTCTTCGGTCGG
TCGTTCTTTTCCCTTCCGATTATCAAAGCAAAGCGCATTTTTTTCTTTG
TCTTTTTGTTTTTGTTCCTGTTCTCTGTTTTTTTACAAACCACGTCAG
GAGTTCAATTGAGAGAACTAGAATCAACAAAGCCAAATACGACAACGTCA
CTAGTCTTTGAACCAGAGGCGTATTTCCCGTTACCTCTTTTCCCATATTTT
TGTTTTTCTTTTTCTACTGTCTATAAGCCTTTAGACTAGTACTACAACATA
ACAGCAACAACAACAACAAAACACGACTGGAAAAAAAATTAGGAAAA
ATGAATCCGGGCGGTGAACAAACAATAATGGAACAACCCGCTCAACAGCA
ACAACAACAGCAACAACAACAGCAGCAACAGCAACAGCAGGCAGCAGTTC
CTCAGCAGCCACTCGACCCATTAAACACAATCAACTGCGGAAACTTGGCTC
TCCATTGCTTCTTTGGCAGAAACCTTGGTGATGGCGACAGGGCCGCAAT
GGCATATGACGCCACTTTACAGTTCAATCCCTCATCTGCAAAGGCTTTAA
CATCTTTGGCTCACTTGTACCGTTCCAGAGACATGTTCCAAAGAGCTGCA
GAATTATATGAAAGAGCACTTTTGGTAAATCCCGAACTATCAGATGTGTG
GGCTACTTTAGGTCAATTGTTATCTGATGCTGGATGATCTGCAAAGAGCTT
ACAATGCCTATCAACAGGCTCTCTACCACCTCAGTAATCCCAACGTACCG
AAATTATGGCATGGAATCGGCATTCTTTATGACAGATATGGTTCGCTCGA
CTATGCCGAAGAAGCTTTTGCCAAAGTTTGGAAATGGACCCCTATTTTG
AAAAGGCAAACGAAATTTACTTCAGACTAGGTATTATTTATAAACATCAG
GGTAAATGGTCTCAAGCTTTGGAATGCTTCAGATACATTCTCCCTCAACC
TCCTGCTCCCTTGCAGGAGTGGGACATATGGTTTCAGTTGGGTAGTGTTT
TGGAGAGTATGGGAGAGTGGCAAGGTGCGAAGGAAGCCTACGAGCATGTC
TTGGCTCAAAATCAACATCATGCCAAAGTATTACAACAATTAGGTGTGCT

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TACCGGTATGAGTAAACGTACAATTTTATGACCCCTCAAAGGCATTGGATT
 ATCTTCTAAAGTCGTTAGAAGCAGATCCCTCCGATGCCACTACATGGTAC
 CATCTCGGTAGAGTGCATATGATTAGAACAGATTATACTGCCGCATATGA
 TGC'TTTCCAACAAGCTGTTAATAGAGATTCAAGAAACCCATCTTTTGGT
 GCTCAATCGGTGTTTTATATTACCAAATTTCTCAATACAGAGACGCCTTA
 GACGCGTACACAAGAGCCATAAGATTAAATCC'TTATATTAGTGAAGTTTG
 GTACGATCTAGGTACTCTTTACGAAACTTGTAAACAACCAATTATCTGACG
 CCCTTGATGCGTATAAGCAAGCTGCAAGACTGGACGTAAATAATGTTCAAC
 ATAAGAGAAAGATTAGAAGCTTTAAACAAAGCAGTTAGAAAAACCCAGGCAA
 TATAAACAAATCGAACGGTGCGCCAACGAATGCC'TCTCCTGCCCCACCTC
 CTGTGATTTTACAACCTACCTTACAACCTAATGATCAAGGAAATCCTTTG
 AACACTAGAA'TTTCAGCCCAATCTGCCAATGCTACTGCTTCAATGGTACA
 ACAACAGCATCCTGCTCAACAAACGCCTATTAAC'TCTTCTGCAACAATGT
 ACAGTAATGGAGCTTCCCTCAATTACAAGTCAAGCTCAAGCTCAAGCTCAAGCT
 CAAGCACAAGCTCAAGCACAAGCACAAGCTCAAGCACAAGCACAAGCACA
 AGCGCAAGCACAAGCACAAGCACAAGCGCAAGCACAAGCACAAGCACAAGCACA
 CACAAGCACATGCACAAGCGCAAGCACAAGCACAAGCACAAGCACAAGCACA
 CAAGCACAAGGCGCAGGCACAACAACAACAACAACAACAAGCAACAACAACA
 ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA
 AGCAGCAGCAATTACAGCCCTTACCAAGACAACAGCTGCAGCAAAAGGGA
 GTTTC'TGTGCAATGTTAAATCCTCAACAAGGGCAACCATATATCACACA
 GCCAACAGTCAACAAGCTCACC'AAC'TGCAACCATTTTCTACACAAGCTA
 TGGAACATCCGCAAAGCTCTCAACTGCCACCTCAACAGCAACAAC'TACAA
 TCTGTTCAACATCCACAACAAC'TTCAAGGCCAGCCTCAAGCCCAAGCTCC
 CCAACCTTTAATCCAGCATAACGTGGAACAGAACGTTTTACCTCAAAAGA
 GATACATGGAAGGTGCAATCCACACTTTAGTAGATGCGCGCGTATCCAGT
 AGCACCCACACAGAGAATAACACAAGGTCTCCTCGTCAACCAACCCATGC
 CATTTCCAACGCAAGCTCCCGCAACAGGAATAACGAACGCTGAACCCACAGG
 TAAAGAAGCAAAAGTTGAAC'TCTCCAATTCAAACATCAACAAT'TAGTA
 AATACTGCTACTTCCATTGAAGAAAATGCAAAATCTGAGGTGAGCAACCA
 ATCGCCAGCAGTAGTGGAGTCTAATACCAATAATACTTCACAAGAAGAAA
 AACCTGTAAAAGCAAAC'TCAATACCTTCAGTAATTGGCGCACAGGAACCT
 CCACAGGAAGCTAGTCTGCTGAAGAAGCTACCAAAGCAGCTTCTGTTTTC
 TCCTTCTACAAAACCGCTTAATACGGAACCAGAGTCATCTAGTGTCCAAC
 CAACTGTATCATCAGAAAGTTCAACAACAAAAGCAAATGACCAAAGCACT
 GCTGAGACCATAGAAC'TTCTACTTGCTACTGTTCTCTGCAGAAGCAAGCCC
 TGTAGAAGACGAAGTAAGACAGCATTCTAAAGAGGAAAACGGCACAAC'TG
 AAGCATCTGCACCTTCTACTGAAGAGGCGGAGCCAGCAGCTTCCAGAGAT
 GCTGAAAAACAACAAGATGAAACCGTGCTACAACGATAACTGTAATCAA
 ACCTACTTTGGAACAATGGAAACAGTGAAAGAGGAGGCCAAAAATGCGTG
 AGGAAGAGCAAAACATCTCAAGAAAAATCCCAACAGGAGAACACACTTCCA
 AGAAAAATGTAGTAAGGCAAGTGGAAGAAGATGAAAAC'TACGACGACTA

YBR112C, 966 aa (SEQ ID NO 52)

[illegible]

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QAQAQAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQLPLPRQQLQQKG
VSVQMLNPQQGQPYITQPTVIQAHQLPFFSTQAMEHPQSSQLPPQQQQQLQ
SVQHPQQLQGQPQAQAPQPLIQHNVEQNVLQKRYMEGAIHTLVDAAVSS
STHTENNTKSPRQPTHAIPATGITNAEPQVKKQKLNSPNSNINKLV
NTATSIEENAKSEVSNQSPAVVESNTNNTSQEEKPVKANSIPSVIGAQEP
PQEASPAEEATKAASVSPSTKPLNTEPESSSVQPTVSSESSTTKANDQST
AETIELSTATVPAASPVDEVRQHSKEENGTEASAPSTEEAEPASRD
AEKQQDETAATTITVIKPTLETMETVKEEAKMREEEQTSQEKSPQENTLP
RENVVRQVEEDENYDD

YMR043W, 1361 bp, CDS: 501-1361 (SEQ ID NO 305)

AAGCTGTGCCAAACAAGGTCATCTCCAAATACTTACCAAAAAGCTAGGGC
GTACTGTACTGGAATCTCTGCTTTTTTCTTTACCTTACTTCAATTTGCCT
TGCTGTCTTTTTTACGTGTGTTTTGGCGTTTCTGCTTTTCTTTTTTATTA
CTCGTTGTGTAAATCATTTTCTAAGTATTATACATACTATATCATCGCA
TACCCAATCGGTTTCTTATTCTCACCACCTTTTTTCTGGAAAAATACATAG
CCTAACAAGCAATTTTATTTTACGTTTGTTAATTCATTATACTGATAATA
TTTTTGAATTTTTTTTTTTTTTGTATACATTTTTTTTAATCGCTGTTTTGT
CTGTTTTTTTTCGATTACGTTATAGGGAAAAAACGGGAAAGGAAAGAGAA
AAAAAAATTAGTGCAGAGCAATAAGAAGCGAAAATCAAAAAAAGTTTTG
GATCTGCAAGACTTGCTGTACGCAACAATATTATAGCCACCCAGCAAAA
ATGTCAGACATCGAAGAAGGTACGCCTACTAATAATGGGCAACAGAAGGA
GAGAAGAAAGATAGAAATTAAGTTCATCGAGAATAAAACAAGGCGCCATG
TGACATTTTCCAAAAGGAAGCACGGTATCATGAAAAAGGCGTTTGAGCTT
TCTGTTCTAACGGGGACCCAGGTCTGTGCTAGTCTGTTTCAGAAACAGG
TTTGGTATATACTTTTCAGCACGCCGAAGTTGAACCTATAGTCACGCAGC
AGGAAGGTAGAAACCTGATCCAGGCCTGTCTTAACGCCCTGATGATGAG
GAAGAAGACGAGGAGGAAGACGGTGATGATGATGATGATGATGATGATGA
TGGTAATGATATGCAACGCCAGCAACCACAACAACAGCAACCGCAACAAC
AGCAACAAGTATTGAATGCACACGCAAAATAGCTTAGGCCATCTAAATCAA
GATCAGGTACCGGCAGGCGCGCTGAAACAAGAGGTGAAGTCACAATTGCT
AGGCGGTGCCAATCCTAATCAAACTCAATGATTCAACAGCAGCAACATC
ACACGCAGAATTCACAACCACAACAGCAACAGCAACAACAACACAGCAG
CAAATGTCACAGCAACAATGTCACAGCATCTCGACCACAGCAAGGAAT
ACCACATCCGCAACAATCGCAGCCACAGCAACAGCAACAACAACAACAAC
AACTGCAACAGCAGCAACAGCAGCAACAACAACAACCCCTCACCGGCATT
CATCAGCCTCACCAACAGGCTTTTGCCAACGCTGCCTCCCCCTATCTGAA
TGCTGAACAGAATGCTGCCTACCAACAATACTTTCAAGAACCGCAACAAG
GCCAATACTAA

YMR043W, 286 aa (SEQ ID NO 306)

MSDIEEGTPTNNGQQKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFEL
SVLTGTQVLLLVVSETGLVYTFSTPKFEPIVTQQEGRNLIQACLNAPDDE
EEDEEEDGDDDDDDDDGNDMQRQQPQQQQPQQQQQVLNAHANSLGHLNQ
DQVPAGALKQEVKSQLLGGANPNQNSMIQQQQHHTQNSQPQQQQQQQPQQ
QMSQQQMSQHPRPQQGIPHPQQSQPQQQQQQQQQLQQQQQQQQQPLTGI
HQPHQQAFAANAASPYLNAEQNAAYQQYFQEPQQGQY

YPL089C, 2531 bp, CDS: 501-2531 (SEQ ID NO 385)

TTCCACGTTTCGCAAAAATACTTCCACGGTGACGAAGTCTGTCTCAGTCG
TATATTAAATGCAGAAATCGTCTTATCATTATTGGGCTCTCTTAACGGCG
CAGCATCACCGGGTGATGAATGCCAAGCCGAGAAAGAAAGAAAAAAT
TACTTCAGATTTCTGATAAAAAATAAACGGAAGAGATGAAAGCTAATAAT
AGAAACAGCTCGATCTTCTCTGAACAATAATAATTAAAGGACAGACAAA
AAGAAACGTAAGAAAGAAGCGAGCCTGTTCTAAAGTGTTCAACGACTGAT
TCAATTAGAACTGCCTACTCTGATAGCCAACCTCACTTTTGACTCGTTA

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AAGTAATTGAAAGCTGGCAAGCAGAATTATTCTTTTTCATCAAGGTT
TCTATCACGTTGTGAGGTTAATATCCCCCGAGCAAACAGGCTGAAGCGT
GAAAAAACTTAAATATTTAAAGTGTGCGAAAACTATACTATAGATACAAC
ATGGGTAGACGGAAGATTGAAATCCAGAGAAATTTCTGATGACAGAAATAG
GGCTGTCACGTTTATAAAACGTAAAGCTGGCCTTTAAAGAAGGCCCATG
AACTATCCGTTCTTTGTCAAGTAGACATAGCCGTCATTATACTGGGGTCC
AATAACACGTTCTATGAGTTTTCTCTGTGGATACGAATGATTTAATCTA
TCACTACCAAAATGACAAAACTTGCTTCACGAAGTGAAAGATCCCTCCG
ATTATGGAGACTTTCACAAAAGTGCATCCGTTAACATAAATCAAGACCTA
CTCAGGTGCTCTATGTCAAATAAGCCTTCGAAATCAAATGTTAAAGGAAT
GAACCAGTCAGAAAATGATGATGATGAGAACAATGATGAGGACGACGATG
ATCATGGCAATTTTGAGAGGAATTCAAATATGCATTCGAATAAAAAAGCC
TCTGATAAAAAATATACCGAGTGCACACATGAAGTTGTTATCCCCGACCGC
ACTCATTTCAAAGATGGATGGTAGTGAGCAAAATAAACGTCATCCTGAGA
ACGCGCTGCCGCCCTTTACAACATTTGAAAAGATTGAAACCGGATCCCTTG
CAAATAAGTAGAACTCCGCAACAGCAACAGCAGCAAAATATATCGAGACC
ATACCATAGTAGCATGTACAATCTTAACCAGCCTTCATCCAGTTCATCTT
CTCCTTCCACGATGGATTTTCCAAAATTACCAAGCTTTCAAACCTCTTCC
TTTAATGGTCGTCCTCCACCCATTTCCATTTACCCGAACAAGTTCAGTAA
GCCATTTACAAATGCATCCTCAAGGACCCCTAAACAGGAGCACAAAATTA
ACAATAGTGGCAGCAATAATAATGACAACAGCAACTACACTCAGTCACCA
TCTAATCTTTGGAAGACTCTATTTCAGCAGACTGTCAAAGCAAGAAGGAA
ATTGTCCGCCAGACCGGTACTTCGTGTGAGAATTCGGAACAACAATTTCA
CGAGTAATCCGCTATTCCAAGTGAACCTCCTCTGCCTCCTCCACATCG
GCCAACGGCAATAGTATGGGCTCTTCGCAGATAATGAAAGAAAAACAAAC
AAGTAGGTCTAGCAAAATTTCTCCACTATCCGCATCTGCCTCAGGCCCT
TAACTCTCCAAAAGGTAATAATGGCAGAATGGTAATAAAATTGCCAAAT
GCAAATGCGCCTAACGGTTCTAACAATGGTAATGGCAGTAACAATAACAA
TCACCCTTATCCTTTTCGGAAGTGGGTCTTCACCTCTTTTTTCTGCAACAC
AGCCATACATTGCCACTCCCTTGCAACCATCGAATATTCTTGGCGGACCT
TTCCAACAAAATACATCTTTTTCAGCTCAAAGACAAACCCAGCAATACCA
ACAAATGTCTTTCAAAAAACAGAGCCAAACAGTACCATTAACATAACAT
TAACCGGACGCCCCCTTCAACTTTTTCGGCCCTGAAACCAGCAATGGC
CCTCCAACCTGGTTCACTGCCATCGAAGTTCGTACATGATTTGATGAGTAA
TTCTCCAAATGTTTCTTCTATATCGATGTTTCAGACTGGTCAATGGGAC
CCAACAGTGCCAAGCCGGGAAACACAAACAATCCTGGTACTTTCCCTCCC
GTACAGACGGCCGTAAACAACGGCAACTCCAGCAATATCAGCAGCACTAA
CAACACTAACAACAACAACAATAACAACAACAACAGCAGCAACAACA
ACAGCAACAACGGCAACGACAATAACAGTAACAATAGCAATAACAGTTAC
TATAGTAATAATGAAGATGCACCCGTAAATGGAGCTGCTATTTCAGAACA
TACTACCGATGGTGACTCGAACAAATCAGTCCAACCTCAAGTACATATGATG
CTGCTGCCACCGCATATAATGGAAATACCGGGCTGACTCCATACATAAAAT
ACTGCTCAAAACACCACTAGGCACTAAATTCCTTAATTTTTCGACTGATAT
TTCAGGAGAAAAAATTCAGCAAAATATAA

YPL089C, 676 aa (SEQ ID NO 386)

MGRRKIEIQRISDDRNRAVTFIKRKAGLFKKAHEL SVLCQVDIAVILGS
NNTFYEFSSVDNTNDLIYHYQNDKNLLHEVKDPSDYGDFHKSASVNIQDL
LRSSMSNPKPSKNVKG MNQSENDDDENDEDDDDHGNFERN SNMHSNKKA
SDKNIPSAHMKLLSPTALISKMDGSEQNKRHPENALPPLQHLKRLKPDPL
QISRTFQQQQQQNISRPYHSSMYNLNQ PSSSSSSPSTMDFPKLPSFQNSS
FNGRPPPI SISPNKFSKPF TNASSRTPKQEHKINNSGNNNDNSNYTQSP
SNSLEDSIQQT VKARRKLSARPVLRVRI PNNFSSNSAIPSEPSASSTS
ANGNSMGSSQIMKENKTSRSSKISPLSASASGPLTLQKGNNGRMVILPN
ANAPNGSNNNGSNNNHPYPFGSGSSPLFSATQPYIATPLQPSNIPGGP
FQQNTSFLAQRQTQQYQQMSFKKQSQT VPLTTTLTGRPPSTFSGPETSNG

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PPTGSLPSKFVHDLMSNSPNVSSISMFPDWSMGFNSAKPGNTNNPGTFPP
VQTAVNNGNSSNISSTNNNTNNNNNNNNNNSSNNNSNNGNDNNSNNSNSY
YSNNEDAPVNGAAISEHTTDGDSNNQSNSSTYDAAATAYNGNTGLTPYIN
TAQTPLGTKFFNFSTDISGEKNSSKI

YOR372C, 2165 bp, CDS: 501-2165 (SEQ ID NO 371)
AAAATCGTGGTTACTTTTCATATTCCTTAAACACTTTTACCACTGTTACTGT
GCGCGTTTCGAGCGTAGCTTTCGTGGTGAATTTATTGTAAGATTCTCCAGC
TGGCTCGATAGTTCTGCCCTCCTGCGTATCCATATCCATTTCCGGTATGCTT
TTACTATTCAACCTAGTCGGCAATTTTTTTCACCTGAATATTGTTGAACAC
TTCTGGCATCCTAGATACTCATCTGTATTTATTCAATTATCTGTTGTGCAT
CGTTAATAGCATTCAGTAAACAAGTTTAGGTCACCTACCCGCATAAGCCT
TTTGGCGTTTGGCGTAACCTCCTCGCGAAAAGAAACGGGACGCAAAAAA
AAAAACAACAAAACAAGAACAACAACAACAACAATAAGGACAGAGCCTTAA
GGAGCTGCAAGGATCTTCTGAATATTTGGCATCGGCATTGTGGGTGGAAA
AAGTGTCCAAATTGGAATAAATTGGTCAGAATAGAGCATTGATTTCCAAC
ATGGACAGAGATATAAGCTACCAGCAAAATTATACCTCAACTGGGGCAAC
TGCAACTTCCTCAAGACAGCCCTCTACGGACAATAATGCAGATACAAATT
TTTTGAAGGTAATGTCAGAATTCAAATATAATTTTAACAGTCCGTTACCT
ACAACGACTCAATTCACCCACGCCCTATTCTTCTAATCAGTATCAACAGAC
TCAAGATCATTTTGCCAATACAGACGCTCACAACAGTTCGAGCAACGAAT
CGTCGTTGGTAGAGAACAGTATATTACCGCATCATCAGCAGATACAACAG
CAACAACAACAACAACAACAACAACAACAACAAGCTCTAGGTTT
ACTTGTAACCTCCTGCTGTGTCACAAGGACAGATACAAGTGAGACTTTGGACG
ATATCAACGTTCAACCTTCTTCTGTTTTGCAGTTCGGCAACTCTTTACCC
AGCGAATTTTTGGTTGCATCCCCAGAGCAATTCAAAGAATTTTTGTTGGA
CTCTCCGTCACCAATTTCAATTTCTTTTCAAAAACCTCCGGCAAAGACAC
CACTTCGATTGTGAACAGATTCTAACGGTGCTCAGCAAAGCACCACAGAG
AACCCAGGTCAACAACAGAATGTTTTTAGCAATGTCGATTGAACAATCT
TTTGAAGAGTAATGGAAAAACACCTCATCTTCATGCACCGGCGCATT
CACGCACTCCTCTGAGTAAGATTGACATGAATCTCATGTTCAATCAACCG
CTGCCGACATCTCCATCAAAAAGGTTCTCCTCCCTGTCGTTGACACCATA
TGGAAGAAAAATTTCTGAATGACGTCGGTACACCTTATGCAAAAGCATTGA
TATCGTCTAACAGCGCGTTAGTGGATTTTCAGAAGGCAAGAAAGGATATT
ACCACTAATGCAACATCCATAGGGCTGGAAAATGCCAACAACATCTTACA
GAGAACGCCGCTAAGATCTAACAATAAAAAATTATTTATTAACCCCCCC
AGGATACCATCAATAGCACTAGCACACTAAGGACAACGAAAATAAA
CAGGACATATCAGGCTCTTACCGACTACCATCCAATTAAATTCATCAAT
AACTAAATCTATCTCCAAATTGGATAACTCTAGAATTCCCTTGTTAGCTT
CGAGATCAGATAACATTCTGGATTCCAATGTGGATGACCAATTGTTTGAT
TTGGGGTTGACAAGATTACCTTTATCACCAACACCAAATTGTAATCTTT
GCATAGTACAACCACAGGTACATCTGCCCTTACAAATTCCTGAGCTACCCA
AGATGGGGTCTTTTAGAAGTGATACGGGAATCAATCCAATTTCAAGTTCA
AACACAGTTTCTTTTAAGAGCAAATCAGGCAATAATAATCAAAGGGTCG
AATCAAAAAAATGGGAAGAAACCTTCCAAATTTCAAATTATTGTGGCAA
ATATTGATCAATTTAACCAGGATACATCATCGTCATCTTTATCATCATCA
TTGAATGCAAGTTTCGAGTGCAGGGAATTCAAATTCAAACGTAACAAAGAA
AAGAGCAAGTAACTCAAAAGATCACAGTCTTTACTTTCTGATTCCGGAT
CGAAATCACAAGCAAGGAAAAGCTGTAATCTAAATCTAATGGAAATTTA
TTCAATTCACAGTAA

YOR372C, 554 aa (SEQ ID NO 372)
MDRDISYQQNYTSTGATATSSRQPSTDNNADTNFLKVMSEFKYNFNSPLP
TTTQFPTPYSSNQYQQTQDHFANTDAHNSSNESSLVENSILPHHQIQQ
QQQQQQQQQQQALGSLVPPAVTRTDTSETLDDINVQPSSVLQFGNSLP
SEFLVASPEQFKEFLDPSPTNFNFPHKTPAKTPLRFVTDNSGAQQSTTE

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NPGQQQNVFSNVDLNNLLKSNGKTPSSSCTGAFSRTPLSKIDMNLMFNQPLPTSPSKRFSSLSLTPYGRKILNDVGTPYAKALISSNSALVDFQKARKDI
TTNATSIGLENANNILQRTPLRSNNKKLFIKTPQDTINSTSTLTCKDNENK
QDIYSSPTTIQLNSSITKSISKLDNSRIPLLASRSDNILDSDNVDQLEFD
LGLTRLPLSPTPNCNSLHSTTTGTSAIQIPELPMGSPFRSDTGINPISSS
NTVSFKSKSGNNNSKGRIKNGKKPSKFQIIVANIDQFNQDTSSSSLSSS
LNASSSAGNSNSNVTKKRASKLRKSQSLSDSGSKSQARKSCNSKSNL
FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)

TTTCTTCAACAACGACGAGTTAACTATTGTGCTCTTTTGTGAGCCACCA
AATACACTCCATTCCAATAGCTTCGCACAGTGAGGCGAAAATTTTGAAC
AGCGCTAATGAATTATTTGTGAGCTCGGCGAGTTCAAATTTGAAGAAAAC
GCGGTGGGTTCGTTAACTATGGTTAGACGCTCAATGTCGCCCCGAAAGGA
AGGCTGTTCTCACTTTTTCGCGCGTTGCACCCCTTTCTCCGCGAAAAAAT
GAGAACGATGGATTTAAAATCAAGAGAATTGGCCCTTAGTAGTGGCAAATA
CTACCTTGGTTGGTTATCTTGTAAACGATTGGTAAGAAAGGGGCATCTCTG
TTTTCTTGATGTATATAAACAACATGATTTGATCATCTCAGATGGTCAGA
TTTATTAAAGACGTTTCTCTTTCCGCATTTTCGATTATTGTTATATTAA
TTTATCCTATATAGACAAGTCAAACCACAAATAAACCATACACACATACA
ATGTCCTGCTAAAGCCGAAAAGAAACCAGCCTCCAAAGCCCCAGCTGAAA
GAAACCAGCCGCTAAAAGACTTCCACTTCCACTGATGGTAAGAAGAGAA
GCAAGGCTAGAAAGGAAACATACTCTTCTTACATTTACAAAGTTTGAAG
CAAATCACCTGACACTGGTATTTCCAAAAGTCCATGCTATCTTTGAA
CTCTTTCTGTTAACGATATCTTTGAAAGAATCGCTACTGAAGCTTCTAAAT
TGGCTGCGTATAACAAGAAGTCTACTATCTCTGCTAGAGAAATTCAAACC
GCTGTTAGATTGATCTTACCAGGTGAATTGGCTAAGCATGCTGCTCTGA
AGGTACTAGAGCTGTTACCAAGTACTCTTCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)

MSAKAEKKPASKAPAEEKPAAKKTSTSTDGKKRSKARKETYSSYIYKVLK
QTHPDTGISQKSMILNSFVNDIFERATEASKLAAYNKKSTISAREIQT
AVRLILPGELAKHAVSEGTRAVTKYSSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)

ACCAACCAACTTCTTCCTTTGTCTCAATATCAAAGAAAAAAAAAAAAAC
CCACTGCTCAGATGTTATAAGGAAGGGGTGTTAACTTATATACAGGTTCA
TCTACCAGTCACCAGTCCATACAACTTGAACCGTCTGCGTACCAGTCCT
AATCAAAATGTTCCCTATCGCTTCCAGAAGAATACTGCTCAATGCTTCAG
TTCTGCCATTGAGACTGTGCAATAGAAATTTCACTACCACAAGAATATCC
TACAACGTCATACAAGATTTGTATTTGAGGGAATAAAAGACACCAAAC
GGCTCCAAGTACCTTGCAAGATGCTGAAGGTAATGTTAAGCCTTGGAACC
CACCACAAAAACCAATCTACCAGAATTGGAACCTCAAGGCCAGAGGCT
TTAAAGGCTTACACCGAGCAAAATGTAGAACTGCTCATGTTGCTAAAGA
GTCTGAAGAGGGTGAGTCAGAGCCAATTGAAGAGGATTGGCTAGTTTGG
ATGATGCTGAGGAAACCAAGAAAGTCATTGAACTTTTCATAGCATCCTC
CTTGTCGAAGAAAAACAAACAGAACCACAAGCTGAACAAGATCATTATT
TTTGGCTTTCTTCTCTCATCTTTTATATTGGAATCCAGTACAATAAAG
AAAAAGCAAAATACACTACGCACTCTTTGTAATCAGCCACACAAAATGCA
GAATTTATTTTTTAAACAAAAAATACAATTGTACATAGACACGTCTTTAT
CTTTCCTATTACTACTATTCTTTTATTTCATAAATACTATTACTTTCTAAGT
ATGACCTACGCTTCTTTGGTAAATAAATAA

YLR294C, 109aa (SEQ ID NO 282)

MMLRKPKKVIELFIASSLSKKKQTEPQAEQDHYFWLSSSHLFIFESSTIK
KKQNTLRTLNCNPHKMQLNFFKQKIQLYIDTSLSFLLLLFFYFNYYFLS

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MTYASLVNK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)

CTTTTCAGTTATTTACCTTCCTTTCTCTCAGTGTAATATTTGTGTGTC
ATACACACCGCTAAAAACCTTTGCATCAACTTATACCCCTACATTTCTATA
GACGCTATTTGGAAACAAGATGTAACCCCTTTTTCCTTTTAGTTTGTGAGA
TTTGTACTCGTAAAGAGTACGTTTATTTATTTATTCAAATTTTATCTTC
ATACCATGTAATATAAGCGCATATAATCACTACGATCTTAGTACAGCTA
GAATTGCTGACGCTTACAATTGCTTTTATTTGTTTGATTATATGCACGTATA
CATATAGTGTACGCAAAAAAAAAAAAAAGGCAGTACTTGATTGGCTACGCC
GCGCATCGTCCGAGAAATCCGGCCTGGTAGGGGCAGGTTTGAAGGCGG
ATAGAAATAAAGATGATATTATTTATTCATCCCATGAATAGTAGAACTC
GATATAAGATTCTAAACCAACAAGTACAGAAAGCAAAACAATAATAAATA
ATGGCTAATAAAGTTATTCAACTACAGAAATCTTCCAATCTTCCACTAA
ACCTCTATGGTGGAGACATCCAAGGTCAGCTTTATACCTGTATCCATTTT
ATGCTATTTTTCGGGTAGCCGTCGTTACACCACCTCTATACATTCCAAAT
GCTATTAGAGGTATCAAAGCCAAGAAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)

MANKVIQLQKIFQSSTKPLWRRHPRSAlylyPFYAIFAVAVVTPLLYIPN
AIRGIKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)

TTCTCATACGTATGTTTTTTTAGATTATGCACCTTCTTTGCCACAGTAAA
TGTGGCGGGGAAGATGTTGAGCTAGCGCCGTGCACAGTGAAGAGACGGA
GGCGATTGTGGGGTTTCATCGGATTGTGCGGGAAGAAGGCCTACACCGTG
TTGAGCCACCCCCCTCAGGAGTAAATTTACACAAACAGTGGTGGTGCC
TATGGTGGTATACGAGATAGTGATAGAAGCTGCTGGATTGGGGTAGAAAT
TTTGTAGGCGTTTATGGATATGGTATGGATATGGTATGGCTTGAGGTAGG
TAATCCAGACACCACTGGAAATATATATAAGGAGAGAGTTCTGGCAGGTA
GATTTGTACTCTCTCTACCACTTTCTTCTACTCCTTTTATTATGTAATG
TTTATTATAAGCACAGCAAAAACGTTAAATAAATCTAATAAGATTTTCATT
ATAACATAACATTAAAGCACACAAATTTCTAACACAAACACAATTCAAAC
ATGACCAGAACTAGCAAATGGACAGTCCACGAAGCAAAGTCTAACCCTAAA
GTATTTCAACCCATAACGGCAACTTTGGGGAGTCTCCAACCACGTCAAGA
GAGGAGGCTATGGGAAAGGCAATTGGGGCAAGCCTGGCGATGAGATTAAT
GACTTAATCGATTCTGGCGAAATTAAGACAGTCTTCAACAAGACCAGAAG
GGGCTCTAACTCCCAAAACAATGAAAGAAGGCTTTCTGATTTGCAACAAT
ACCACATCTAA

YLR327C, 86 aa (SEQ ID NO 288)

MTRTSKWTVHEAKSNPKYFTHNGNFGESPNHVKRGYgkgnwGKPGDEIN
DLIDSGEIKTVFNKTRRGSNSQNNERRLSDLQYHI

YHR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)

GTCATGCGCGCAATAGGAAAGCGCACGAAACAAATGAGTAATTCGTAGGA
AACAATGCAGCCCCCAGGGTCAGCAACTGACGTGACTCAGCCTGGCTTTT
GTAGAAAAAGATGACGCCCTGGCAGAGAGGTGGGGGAATTGAGGGGTCTT
CGCTACCCACCTTAAGTATGGAAGAATATGATGAAGAATATGATGATAAC
TCTTGGAAGCGAGCGGGCGGGTTCCATCACTTTTACGGATTGGTAACACA
GGGGCCTCAGTTCGATACTTGGTATTCAGGCTTCCAGCGTTGGTGAGTTT
AGTTAGCGGTATGGTATGCACATGGTGTGATGCTTGGTGGTAATCATTC
GTTAGGTGAATTGAGCAGTAGCGATATTAGATATATTTAGTATTTTATAG
CGTCTTTTTTGGTGGGGGAGGAAGGACAAAACCTGTCTCGTAAATATAAAG
GGACTGTTTCGATATCGCAGATACTAGAGTATAAATTTTCGATTGAGGCGAG
ATGACAACATATTTCAAGTTGGTAAAAGGTGCTACCAAGATCAAGTCAGC

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CCCCCCCCAAACAGAAGTATCTGGATCCGATACTGTTGGGGACCAGCAATG
AAGAGGATTTCTATGAGATCGTGAAGGGTTTGGATTCCCGAATTAATGAC
ACGGCGTGGACTATTGTGTATAAATCGCTGTTGGTGGTTCATTTGATGAT
AAGGGAGGGTTCCAAAGATGTTGCATTGCGGTACTACTCTAGGAACCTGG
AGTTTTTTGACATTGAAAACATACGTGGCTCCAATGGCAGTGGCTCTGGA
GACATGAGGGCACTTGATAGATACGATAATTATCTGAAGGTGAGATGCAG
GGAGTTTGGTAAAATCAAAAAGGACTATGTGAGAGACGGCTATCGAACAC
TGAAGCTGAACAGTGGCAATTACGGAAGCTCCAGAAACAAGCAACACTCT
ATCAATATAGCACTAGATCATGTGGAGTCCCTAGAGGTACAAATACAAGC
CCTGATTAAAAACAAGTATACACAATATGATTTGAGTAACGAATTGATCA
TATTTGGTTTCAAGCTGCTTTATTCAAGACCTGCTAGCGCTATATAATGCT
CTCAACGAAGGTATCATAACTCTGCTGGAGTCTTTTTTCGAACATATCTCA
TCATAATGCAGAGAGAACTCTAGACCTGTACAAGACGTTTGTGATTGGA
CCGAGCACGTTGTCAGGTACTTGAAGAGCGGAAGACTGCGGGCTTGAAA
ATACCCGTCATCAAGCATATCACTACCAAACGGTCAGATCGCTAGAAGA
ACATCTGATAGAGGATGATAAGACGCACAACACTTTTGTGCCCGTTGACA
GTTCTCAAGGAAGTGCTGGGGCCGTAGTAGCCAAATCTACTGCACAGGAA
AGGTTGGAGCAAAATCCGGGAACAAAAAAGGATAC TAGAGGCACAATTGAA
AAACGAACAAGTAGCGATTTCCCTGCTCTAACTACTGTACACGGCGGCTC
AATCTTACAACCCGTTTGGAACAGACTCTTCTATGCATAC TAACATTTCCA
ATGGCTGTGGCTAATCAAACGCAACAGATCGCAAATAACCCATTTGTATC
TCAAACCTCAGCCACAGGTGATGAATACACCAACCGCTCATACAGAGCCCG
CAAATTTAAACGTTCCCTGAATATGCAGCGGTCCAACACACAGTGAAC TTC
AACCCCTGTACAAGATGCTGGCGTAAGTGCCCAACAACGGGGTACTATTC
GATTAACAACCATTTAACACCCACATTTACAGGTGCAGGGTTTGGAGGAT
ACTCCGTTTACAGGATACAACCTGCCGCTTCTAATCAACAAGTCTCTCAT
TCACAAACTGGTTCTAACAACCCGTTTCGATTGCACAACGCCGCGACGAT
CGCAACAGGGAATCCTGCACACGAAAATGTCTTAAATAACCCATTTTCAC
GACCAAACCTTTGATGAACAAAATACCAATATGCCGCTACAACAACAGATA
ATAAGTAACCCCTTTTCAAAACCAAACGTACAATCAACAACAATTTCAACA
ACAAAAAATGCCCTTTGAGCTCGATCAATAGCGTTATGACAACCCCTACTA
GCATGCAGGGATCGATGAATATTCCTCAGCGTTTGTATAAAATGGAATTT
CAGGCTCACTACACTCAGAATCATCTCCAACAACAGCAACAACAGCAACA
GCAACAACAGCAACAGCAACAACAGCAACCACAACAGGGTTATTATGTGC
CTGCAACTGCAGGAGCCAACCCGTGTACAAATATAACTGGGACAGTTCAA
CCTCAAAATTTCCCTTTCTATCCACAACAGCAACCACAACCGGAACAGTC
TCAAACACAGCAACCAGTTTTAGGAAACCAATATGCTAACAACCTCAATT
TAATTGATATGTAA

YHR161C, 637 aa (SEQ ID NO 212)

MTTYFKLVKGATKIKSAPPKQKYLDPI LLGTSNEEDFYEIVKGLDSRIND
TAWTIVYKSLLVVHLMIREGSKDVALRYYSRNLEFFDIENIRGSNGSASG
DMRALDRYDNYLKVRCREFGKIKKDYVRDGYRTLKLN SGNYGSSRNKQHS
INIALDHVESLEVQIQALIKNKYTQYDLSNELIIFGFKLLIQDLLALYNA
LNEGIITLLESFFELSHHNAERTLDLYKTFVDLTEHVVRYLKSGKTAGLK
IPVIKHITTKLVRSL EEHLIEDDKTHNTFVPVDSSQGSAGAVVAKSTAQE
RLEQIREQKRILEAQLKNEQVAISPALTTVTAAQSYNPF GTDSSMHTNIP
MAVANQTQQIANNPFVSQTQPQVMNTPTAHTEPANLNVPEYAAVQHTVNF
NPVQDAGVSAQQTGYYSINNHLTPTFTGAGFGGYSVSQDTTAAASNQQVSH
SQTGSNNPFALHNAAT IATGNPAHENVLNNPFSRPNFDEQNTNMP LQQQI
ISNPFQNTYNQQQFQQQK MPLSSINSVMTTPTSMQGS MNIPQRFDKMEF
QAHYTNHLQQQQQQQQQQQQQQQQQQPQQGYVPATAGANPVTNITGTVQ
PQNF PFYPQQQPQPEQSQTQQPV LGNQYANNLNLIDM

YLR206W, 2342 bp, CDS: 501-2342 (SEQ ID NO 277)

TACACCCTGACTTTCCCCATCATACGACGATGCTCTAGTAAACTTGCACC

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CGCACCTGTTAGATAAACAAGTGCGCCCAAGATCACAATACCGAAGGGGC
GATATCACCACCTCAGTATTCTACAGTCGAGCATAGCGTAGTCTGGCAGTA
TCCCGCACGATCCATTGTATTGTTGTCCAAACCGCATTTTATGTGTAAC
GATTAATCGTATATACATGGCCCTACAAGAAATTACCCGCGGCGAAGGGT
GAAAAAAAAGTAGTGGAACCTAAAGAAAGAAGAGTTTAGTTACGGACCC
TTTCAAGGATTGACACACTCCCAATATTTTGCTACATTATGACCTTTGT
TGAAGGAGGCGTTTCGTTTATTTAATTATTTTGTCTGTTTTCCTACAAC
TGCGAATACGCTCACATTCTAGTTTGACCTTCACAAATTCCTATCATCTT
CTTTTGTATTATTTTGACACACCCCTATTAAAGTGTATTGTTTGTAAAGTA
ATGTCCTAAGCAGTTTGTTCGTTCTGCAAAGAACATGATGAAGGGCTACTC
ATCCACACAAGTGCTTGTGAGAGATGCCACGGCGAACGACTCGAGGACTC
CATCGATAGACACTCTCGACGATTGGGCACAGAGATCTTACGATTCCGGTG
GACTTCTTCGAGATTATGGATATGTTAGACAAGAGGCTGAACGATAAGGG
CAAATAC TGGAGACACGTTGCCAAATCGCTGACCGTTTGGACTATCTTG
TTCGTTTTCGGAGTGAGAACTGTGTGCTATGGTGCAGAGAGAAATTTTAC
GTAATTAAGACATTAAGGGAATTCAGACACGAAATGAGTCCGGATTGTA
CGAGGGACAAATTATCAGAGTAAAGGCTAAAGAACTCGTCTCTTTGTTGA
ATGATGAAGAAAGGCTACGCGAAGAGAGGCTTATGAATACAAGAAACAGA
AGGGCGAACAGAGCTGCTAGGCCAAGGCCAAGAAGACAAAGAACAGGAG
CAACCCACACGATTCTTCTCCCTCTTACCAGGACGATTGGAAGGGCCC
TAGAGGAGAGCAGAAATTACTGCTCAAGAAGATGAACAACGTAGAAGAGAA
CTGGCCCAGTACGACGATGAAGATCCTGACTTCCAAGCTGCCTTACAAC
AAGTAAAGAAGAAGAGGAGTTGAAGCAATTGCAGGAACCTACAGAGATTAC
AGAAGCAACAACAGCTCTGTCTCAATTTCAAGCTCCTTTACAACAACAA
CAACCACAACAACAACAGCGTACTACGACATTTTCGGTAATCCAATCTC
CCAAGATGAATACCTTACAGTATCAGTACCAACAGGACCAGGAACAAGCAA
TGGCTCAGCAAAGATGGCTGGACCAGCAGCAAGAACAACAGCAGCTTGCT
GAACAACAATATTTTACGACAGCAACAACAAGCTGCGGCCGCCGCTTCTGC
CTTGCAACAGCAACAACAACAGCCGCTAATATGCAACAACAACAACAGC
CCGCTGATTTTCAACAACCTTTGCCTACAGGTTCTAATAATCCGTTTTC
ATGGATAATCTTGAAAGACAAAAGCAGGAGCAACAGCATGCTCAATTGCA
AAGACAACAAGAAGAAGCTAGACAACAACAAGAACAATTGAAGCTACAAC
AATTGCAAAAGACAACAACAAGAGGAAGCTCAATTACACCAGAAGAGGCAA
GAAGAAGCCCAATTACAACAGCAGCAAGCCCAATTGCTACAACAGCAAGC
CCAGTTCCAGCAACAACAACCCCTTGAAGCAACAAGGACTGGGAACCAGT
CTATATCGGATAAATACAGCGACTTGAATACCTTGTAGCAACTGGTACA
GGGATAGATACTTTTGGTAACACTGGAGAGGCACGTATTCTGCAACA
TACAAAGACAGGCACATTTATAAATCTCAGGGTACAGGCTACAAACAGG
TTACTAATGAACCAAGAACAACCCCTTCTTAAGCAACCAATACACTGGT
TTACCAAGCACAATAATCGTGCCACGCAAAACAGGCTACGGGTTTGTTAA
CCAACCTCAAAGTCTCTCTACTAATCTCTCCTCAGCAAAATCCTACTGGTA
TAAGCTACTCTCAGCCACAACAGCAACAACAGCCACAGCAACAACCGCAA
TACATGCAAAATTTCCAACAACAGCAACCTCAATACGCCCAAAACTTCCA
ACAACAACCACAATACACTCAAAATTATCAACAACAACCACAATACATTC
AACCTCATCAACAACAACAGCAGCAGCAGCAGCAGCAACAGCAGCAACAG
GGATATACTCCTGACCAAGGTGTAAGCTTAATTGATCTTTGA

YLR206W, 613 aa (SEQ ID NO 278)

MSKQFVRS AKNM MKGYSSTQVLVRDATANDSRTPSIDTLDDL AQRSYDSV
DFFEIM DMLDKRLNDKGKYWRHVAKSLTVLDYLVRFGSENCVLWC RENFY
VIKTLREFR HENESGFDEGQIIRVKAKELVSLLNDEERLREERSM NTRNR
RANRAARPRRRQRTRSNPHDSSPSYQDDLEKALEESRITAEDEQRRRE
LAQYDDEDPDFQAALQLSKEEELKQLQELQRLQKQQQSLSQFQAPLQQQ
QPQQQPAYYDIFGNPISQDEYLQYQYQQDQEQAMAQQRWLDQQQEQQLA
EQQYFQQQQQAAAAASALQQQQTAA NMQQQQQQPADFQQPLPTGSNNPFS
MDNLERQKQEQQHAQLQRQQEEARQQEQLKLQQLQRQQQEEAQLHQKRQ

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EEAQLQQQQAQLLQQQAQFQQQPLKQTRTGNQSIDKYSIDLNTLLATGT
GIDTFGNTGEARIPAQHTKTGTFINSQGTGYKQVTNEPKNNPFLSNQYTG
LPSTNIVPTQTGYGFGNQPQSPPTNSPQQNPTGISYSQPQQQQPQQQPQ
YMQNFQQQPQYAQNFQQQPQYTQNYQQQPQYIQPHQQQQQQQQQQQQQ
GYTPDQGVSLIDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)

CACTTCTCAGAAATGCATGCAGTGGCAGCACGCTAATTCGAAAAAATTCT
CCAGAAAGGCAACGCAAAATTTTTTTTCCAGGGAATAAACTTTTTATGAC
CCACTACTTCTCGTAGGAACAATTTCCGGGCCCTGCGTGTTCTTCTGAGG
TTCATCTTTTACATTTGCTTCTGCTGGATAATTTTCAGAGGCAACAAGGA
AAAATTAGATGGCAAAAAGTCGTCTTTCAAGGAAAAATCCCCACCATCTT
TCGAGATCCCCGTGTAACCTTATTGGCAACTGAAAGAATGAAAAGGAGGAAA
ATACAAAATATACTAGAACTGAAAAAAGTATAAATAGAGACGATA
TATGCCAATACTTCACAATGTTTCAATCTATTCTTCATTTGCAGCTATTG
TAAAATAATAAAACATCAAGAACAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAACACAAAAACAAGTTTTTTAAATTTTAATCAAAAA
ATGTCACAAGACGCTGCTATTGCAGAGCAAACTCCTGTGGAGCATCTCTC
TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAAACAAGG
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTTCCAAAGAGACCAGCTTCTGCCTATGTCACTGTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTCGGTTGGGATACTG
GTACCATTTCTGGTTTCATCAATCAAAACCGATTTTCATCAGAAGATTTGGT
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAAGTGGTTT
GATTGTCTCCATTTTCAACATTTGGTTGTGCCATTTGGTGGTATTATTCTTT
CCAAATTTGGGTGATATGTACGGTGTGAAGGTGGGTTTGATTGTGTTGTT
GTCATCTACATCATCGGTATTATTATTCAAATTCATCTATCAACAAATG
GTACCAATATTTTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTA
TTGCCGTTTTATCTCCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA
AGGGGTACTTTAGTCTCTTGCTACCAATTGATGATTACTGCCGGTATTTT
CTTGGGTTACTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGC
AATGGAGAGTTCATTAGGTTTGTGTTTTGCTGGGCTTTGTTTTATGATT
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTGCTG
TTGATGATCCATCTGTTTTGGCTGAAGTCGAAGCTGTCTTGGCTGGTGTA
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG
CAAGACAAAGGTCCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTGAAACCTCTATTGTCTTGGG
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT
ATGGTTCGTCGTAATTGTTTGGTATGGGGTGCTGCATCCATGACTGCTTGT
ATGGTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA
AGACCAACCATCTTCCAAGGGTGCTGGTAACGTGATGATTGTCTTTGCCT
GTTTCTATATTTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTATGTC
GTTGTTTCTGAACTTTCCCATGAGAGTCAAGTCTAAGGCTATGTCTAT
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC
CATTTATTACTGGTGCTATTAACTTCTACTACGGTTACGTTTTTCATGGGC
TGTTTGGTCTTCATGTTCTTCTATGTTTGTAGTTGTTCCAGAACTAA
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC
CATGGAAGTCTGCCTCATGGGTTCACCATCCAGAAGAGGTGCCAACTAC
GACGCTGAAGAAATGACTCAGGATGACAAGCCATTGTACAAGAGAATGTT
CAGCACCAATAA

YDR342C, 570 aa (SEQ ID NO 120)

MSQDAALAEQTPVEHLSAVIDSASHSVLSTPSNKAERDEIKAYGEGEEHEP
VVEIPKRPAAYVTVSICIMIAFGGFVFGWDTGTISGFINQTD FIRRFG

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MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDMYGRKVGLIVVV
VIYIIIGIIIIQIASINKWYQYFIGRIISGLGVGGI AVLSPMLISEVSPKHL
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMI
GGMTFVPESPRYLAEVGKIEEAKRSIAVSNKVAVDDPSVLA EVEAVLAGV
EAEKLAGNASWGELFSSKTKVLQRLIMGAMIQSLQOLTGDNYFFYYGTTI
FKAVGLSDSFETSIVLGI VNFASFVGIYVVERYGRRTCLLWGAASMTAC
MVVYASVGVT RLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPYV
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFTPFITGAINFYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVLPWKSASWVPPSRRGANY
DAEEMTHDDKPLYKRMPSTK

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)

AAAAAATGTTTTTTAGGCAACGGAGATTGTTTTATCCACGTTTACCCC
ACAAAAAGTGCAGGTACATTGTGGGGCCCCGGCATCGAAAACCAGTTTTT
TTCCTTTAAACGCTGGAAAAAAGGAGAAATTATTGGAACTTTGAGAGA
ATAGTCCGTAGGCAAATTGAAAATGTTCTTAAAAAATTTCTGTTTCTTAC
TCATTGAGATTATTTCAGATGCCCTCCGTGCCCTTCATTGAAAAAATCCAA
GAGATGTCTCGGATCTGTATGCAGATTTTGGCTTGAGACAATGGAGAGC
AAATGGGTATACAATATAGAAAGCACAGAAACATATAAAAAGAGCTCGAG
AAAAGACATATGGTTTGTAACATCTTCTTCTTTTTTCCAATTTTTCTGT
TTTAATAATAAAAAACAAGAACAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAACACAAAAACAAGTTTTTTTAATTTAATCAAAAA
ATGTCACAAGACGCTGCTATTGCAGAGCAAACCTCTGTGGAGCATCTCTC
TGCTGTTGACTCAGCCTCCCACTCGGTPTTATCTACACCATCAAACAAGG
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCCTATGTCACTGTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTCGGTTGGGATACTG
GTACCATTTCTGGTTTCATCAATCAAACCGATTTTCATCAGAAGATTTGGT
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAAGTGGTTT
GATTGTCTCCATTTTCAACATTTGGTTGTGCCATTTGGTGGTATTATCTTT
CCAAATTGGGTGATATGTACGGTCGTAAGGTGGGTTTGATTGTCTGTGT
GTCATCTACATCATCGGTATTATTTATTCAAATTCATCTATCAACAAATG
GTACCAATATTTTCATCGGTAGAAATTTATTCGGTTTGGGTGTTGGTGGTA
TTGCCGTTTTATCTCTATGTGATTTCTGAAGTATCCCCAAAGCATTTA
AGGGGTACTTTAGTCTCTTGCTACCAATTGATGATTACTGCCGGTATTTT
CTTGGGTCTACTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGC
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCGTTGGCTTTGTTTATGATT
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTGCTG
TTGATGATCCATCTGTTTTGGCTGAAGTCGAAGCTGTCTTGGCTGGTGTA
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTGTAG
CAAGACAAAGGTCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT
ATGGTCGTCGTACTTGTGTGCTATGGGGTGCTGCATCCATGACTGCTTGT
ATGGTTGTCTATGCTTCCGTGGGTGTCAACAGATTATGGCCAAATGGTCA
AGACCAACCATCTTCCAAGGGTGCTGGTAACTGTATGATTGTCTTTGCCCT
GTTTCTATATTTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTATGTC
GTTGTTTCTGAACTTTCCCATTTGAGAGTCAAGTCTAAGGCTATGTCTAT
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTTCTTCACTC
CATTTATTACTGGTGCTATTAACTTCTACTACGGTTACGTTTTTCATGGGC
TGTTTTGGTCTTCATGTTCTTCTATGTTTTGTAGTTGTTCCAGAACTAA
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC
CATGGAAGTCTGCCTCATGGGTCCACCATCTAGAAGAGGTGCCAACTAC
GACGCTGAAGAAATGGCTCAGGATGATAAGCCATTGTACAAGAGAATGTT

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CAGCACCAAATAA

YDR343C, 570 aa (SEQ ID NO 122)

MSQDAIAIEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP
VVEIPKRPASAYVTVSIMCIMIAFGGFVFGWDTGTISGFINTDFIRRFG
MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDYGRKVGLIVVV
VIYIIIGIIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMI
GGMTFVPESPRYLAEVGKIEEAKRSIAVSNKVAVDDPSVLAEEVAVLAGV
EAEKLAGNASWGELFSSSKTKVLQRLIMGAMIQSLQQLTGDNYFFYYGTTI
FKAVGLSDSFETSIVLGIVNFASTFVGIYVVERYGRRTCLLWGAASMTAC
MVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPYV
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFTPFITGAINFYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVTMWEEGVLPWKSASWVPPSRRGANY
DAEEMAHDCKPLYKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)

ACAGTTTATTCTGGCATCCACTAAATATAATGGAGCCCGCTTTTAAAGC
TGGCATCCAGAAAAAAGAATCCCAGCACCAAAATATTGTTTTCTTCA
CCAACCATCAGTTCATAGGTCCATTCTCTTAGCGCAACTACAGAGAACAG
GGGCACAAACAGGCAAAAAACGGGCACAACCTCAATGGAGTGATGCAACC
TGCCTGGAGTAAATGATGACACAAGGCAATTGACCCACGCATGTATCTAT
CTCATTTTTCTTACACCTTCTATTACCTTCTGCTCTCTGATTGGAAAA
AGCTGAAAAAAGGTTGAAACCAGTTCCTGAAATTATCCCTACTTG
ACTAATAAGTATATAAAGACGGTAGGTATTGATTGTAATTCTGTAAATCT
ATTTCTTAAACTTCTTAAATTCTACTTTTATAGTTAGTCTTTTTTTTAGT
TTTAAACACCAAGAAGCTTAGTTTCGAATAAACACACATAAACAAACAAA
ATGGTTAGAGTTGCTATTAAACGGTTTCGGTAGAATCGGTAGATTGGTCAT
GAGAATTGCTTTGTCTAGACCAACGTCGAAGTTGTTGCTTTGAACGACC
CATTCATCACCAACGACTACGCTGCTTACATGTTCAAGTACGACTCCACT
CACGGTAGATACGCTGGTGAAGTTTCCCACGATGACAAGCACATCATTTGT
CGATGGTAAGAAGATTGCTACTTACCAAGAAAGAGACCCAGCTAACTTGC
CATGGGGTTCTTCCAACGTTGACATCGCCATTGACTCCACTGGTGTTTTTC
AAGGAATTAGACACTGCTCAAAAGCACATTGACGCTGGTGCCAAGAAGGT
TGTTATCACTGCTCCATCTTCCACCGCCCAATGTTGCTCATGGGTGTTA
ACGAAGAAAAATACACTTCTGACTTGAAGATTGTTTCCAACGCTTCTTGT
ACCACCAACTGTTTGGCTCCATTGGCCAAGGTTATCAACGATGCTTTTCGG
TATTGAAGAAGGTTTGATGACCACTGTCCACTCTTTGACTGCTACTCAA
AGACTGTTGACGGTCCATCCACAAGGACTGGAGAGGTGGTAGAACCGCT
TCCGGTAACATCATCCCATCCTCCACCGGTGCTGCTAAGGCTGTCGGTAA
GGTCTTGCCAGAATTGCAAGGTAAGTTGACCGGTATGGCTTTCAGAGTCC
CAACCGTCGATGTCTCCGTGTTGACTTGACTGTCAAGTTGAACAAGGAA
ACCACCTACGATGAAATCAAGAAGGTTGTTAAGGCTGCCGCTGAAGGTAA
GTTGAAGGGTGTTTTGGGTTACACCGAAGACGCTGTTGTCTCCTCTGACT
TCTTGGGTGACTCTCACTCTTCCATCTTCGATGCTTCCGCTGGTATCCAA
TTGTCTCCAAAGTTTCGTCAAGTTGGTCTCCTGGTACGACAACGAATACGG
TTACTCTACCAGAGTTGTGCGACTTGGTTGAACACGTTGCCAAGGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)

MVRVAINGFGRIGRLVMRIALSRPNVEVVALNDPFITNDYAAVMFKYDST
HGRYAGEVSHDDKHIIVDGKKIATYQERDPANLPWGSSNVDAIDSTGVF
KELDTAQKHIDAGAKKVIVITAPSSSTAPMFVMGVNEEKYTSCLKIVSNASC
TTNCLAPLAKVINDAFGIEEGLMTTVHSLTATQKTVDPGSHKDWRGGRTA
SGNIIIPSSGAAKAVGKVLPELQGLTGMAFRVPTVDVSVVDLTVKLNKE
TTYDEIKKVVKAAAEGLKGVLYTEDAVVSSDFLGDSSHSSIFDASAGIQ
LSPKFVKLVSWYDNEYGYSTRVVDLVEHVAKA

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YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)

CGACCCTCTGGTTAGATGACACTCCTGCCCCAACTGCCACGAATCTGTAA
CCCCATAACTATACCCGTACGCAGTACTAAAAATGTATGTAATTAGTAAA
TGTATGTAACAATTTACCGTTTTGTGTAACAATTCATTCAATTCATTCTT
TTGATCCTTTAGTACCGTCCGCACATGATGTCATTTCCCCCTCATTTTTG
TTTGCTGGTATGATTTCCCGCCCGGCGACGGTACGGCTGTTATCCAGCG
ATGCGGGGACTTCCGTCCACAGGTATCTTTTTCTCCAACCTCCAACAGAGAT
GGAAAATGAGGGGCGGGTGTAGGTAAGCAGAATGAGGAGAAAATTTGTAAT
GAAAATGGAAGTTTCGGCGGTATATATAAATGGGGGGGGTTTGTCTGGTGACA
ATTGACTTCACTCTCCTTTTCTCAAAAATTCCTTGGGTGTTAGGATTAGAA
GTATCTGGAAGAACCAACCAAGAAAACACAATAACAAAAATAAATAAAGC
ATGTTTCAGTAGATCTACGCTCTGCTTAAAGACGTCTGCATCTCCATTGG
GAGACTTCAATTGAGATATTTCTCACACCTTCCTATGACAGTGCCATCA
AGCTGCCCAATGGGTGGAATATGAGCAACCAACGGGGTTGTTTCATCAAC
AACAAGTTTGTTCCTTCTAAACAGAACAAAGACCTTCGAAGTCATTAACCC
TTCCACGGAAGAAGAAATATGTCATATTTATGAAGGTAGAGAGGACGATG
TGGAAGAGGCCGTGCAGGCCGCCGACCGTGCTTCTCTAATGGGTCTTGG
AACGGTATCGACCCTATTGACAGGGGTAAGGCTTTGTACAGGTTAGCCGA
ATTAATTTGAACAGGACAAGGATGTCAATTGCTTCCATCGAGACTTTGGATA
ACGGTAAAGCTATCTCTTCTCGAGAGGAGATGTTGATTTAGTCATCAAC
TATTTGAAATCTTCTGCTGGCTTTGCTGATAAAATTTGATGGTAGAATGAT
TGATACTGGTAGAACCCATTTTCTTACACTAAGAGACAGCCTTTGGGTG
TTTGTGGGCAGATTATTCCTTGGAAATTTCCCACTGTGTGATGTGGGCCTGG
AAGATTGCCCTGCTTTGGTCAACCGGTAACACCGTCGTGTTGAAGACTGC
CGAATCCACCCCATTTGTCCGCTTTGTATGTGTCTAAATACATCCACAGG
CGGGTATTTCCACCTGGTGTGATCAACATTTGTATCCGGGTTTGGTAAGATT
GTGGGTGAGGCCATTACAAACCATCCAAAAATCAAAAAGGTTGCCCTTCAC
AGGGTCCACGGCTACGGGTAGACACATTTACCAGTCCGCAGCCGCAGGCT
TGAAAAAAGTGACTTTGGAGCTGGGTGGTAAATCACCACAAATTTGTCTTC
GCCGACGCCGAGTTGAAAAAAGCCGTGCAAAACATTATCCTTGGTATCTA
CTACAATTCTGGTGAGGTCTGTTGTGCGGGTTCAAGGGTGTATGTTGAAG
AATCTATTTACGACAAATTCATTGAAGAGTTCAAAGCCGCTTCTGAATCC
ATCAAGGTGGGCGACCCATTTCGATGAATCTACTTTTCCAAGGTGCACAAAC
CTCTCAAATGCAACTAAACAAAATCTTGAAATACGTTGACATTGGTAAGA
ATGAAGGTGCTACTTTTGATTACCGGTGGTGAAAGATTAGGTAGCAAGGGT
TACTTTCATTAAAGCCAACTGTCTTTGGTGACGTTAAGGAAGACATGAGAAT
TGTCAAAGAGGAAATCTTTGGCCCTGTTGTCACTGTAACCAAATTCAAAT
CTGCCGACGAAGTCATTAAACATGGCGAACGATTCTGAATACGGGTGGCT
GCTGGTATTCACACCTCTAATATTAAATACCGCTTAAAAGTGGCTGATAG
AGTTAATGCGGGTACGGTCTGGATAAACACTTATAACGATTTCCACCACG
CAGTTCCCTTTTCGGTGGGTTCAATGCATCTGGTTTGGGCAGGGAAATGTCT
GTTGATGCTTTACAAAACCTACTTGCAAGTTAAAGCGGTCCGTGCCAAATT
GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)

MFSRSTLCLKTSASSIGRLQLRYFSLPMTVPIKLPNGLEYEQPTGLFIN
NKFVPSKQNKTFEVINPSTEEIEICHIEGREDDVEEAVQAADRAFNGSW
NGIDPIDRGKALYRLAELIEQDKDVIAIETLDNGKAISSSRGDVDLVIN
YLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAW
KIAPALVTGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKI
VGEAITNHPKIKKVAFTGSTATGRHIYQSAAAGLKKVTLELGGKSPNIVF
ADAELKKAVQNIILGIYNSGEVCCAGSRVYVEESIYDKFIEEFKAASES
IKVGDPPFDESTFQGAQTSQMLNKLKYVDIGKNEGATLITGGERLGSKG
YFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLA
AGIHTSNINTALKVADRVNAGTVWINTYNDFFHHA VPFGGFNASGLGREMS
VDALQNYLQVKAVRAKLDE

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YER177W, 1304 bp, CDS: 501-1304 (SEQ ID NO 151)

AGATAGATAGATATAGATAGATAATGGACGTAGTTATAGAACAGAAAATC
GGTAGATCGAAAACACAGGGGAAAAAGGGGGGGGGGGGGGGGAGACAGCG
CAGCCACGTGACGGGCTTCCTCTTTGGAAAGTGGAGCGAAGTTTTGCGGA
AGCTACTTTTATTCGGCCTGGAGTCAAAAGAGGAAGCTCGGTGGCAAATA
GCTTCCTCTTTGTGGCCGGGGCGCGGGGGGACGAGGCAAAAAGCAAAGAA
AAGCAAAAAAATAAAAAAACAACAAAAACAGGGGTATGAGAAAAAG
ACACGCTTTTCCACGCGCAGCAAAAAGGAAAAAGGAAAAAGGAAACTCTTT
ATTATTGGACCTTAAACCTGAAAACGAGACGAACCGTAACATAAAACCGT
GTAGTTTCTGCAAAAATAACTTAGTTTTTCTACTTTTCAAAATTGAGAG
CGCAAGCAAGTGAGAGAAAAAGCAAGTTAAAGATAAACTAAAGATAAAA
ATGTCAACCAAGTCGTGAAGATTCTGTGTACCTAGCCAAGTTGGCTGAACA
GGCCGAACGTTATGAAGAAATGGTCGAAAAATGAAGACTGTTGCCTCCT
CTGGCCAAGAGTTGTCTGGTCGAAGAGCGTAATTTGTTGTCTGTTGCTTAT
AAGAACGTTATTGGTGCTCGTCGTGCCTCTTGGAGAATTGTTTCTTCTAT
TGAGCAAAAGGAGGAGTCCAAGGAGAAGTCCGAACACCAGGTCGAGTTGA
TTTGTTCGTACCGTTTCAAGATTGAGACCGAACTAACTAAGATCTCCGAC
GATATTTTGTCCGTGCTAGACTCCCACTTAATTCCATCAGCCACCACTGG
CGAGTCCAAGGTTTTCTACTATAAGATGAAGGGTGACTACCACCGTTATT
TGGCTGAATTTTCTAGTGGCGATGCTAGAGAAAAGGCCACAAACGCCTCT
TTAGAAGCATACAAGACCGCTTCTGAAATTGCCACCACAGAGTTACCCCC
AACTCACCCAATCCGCTCTAGGTTTGGCTCTTAACTTCTCTGTCTTCTATT
ATGAAATTCAAACTCTCCAGACAAAGCCTGCCATTTGGCCAAGCAAGCT
TTTGACGACGCTATTGCTGAGTTGGACACTCTGTCTGAAGAATCATACAA
AGATAGCACACTTATCATGCAACTGCTAAGGGACAATTTAACCTTATGGA
CTTCAGACATGTCCGAGTCCGGTCAAGCTGAAGACCAACAACAACAA
CAACATCAGCAACAGCAGCCACCTGCTGCCGCCGAAGGTGAAGCACCAAA
GTAA

YER177W, 267 aa (SEQ ID NO 152)

MSTSREDSVYLAKLAEQAERYEEMVENMKTVASSGQELSVEERNLLSVAY
KNVIGARRASWRIVSSIEQKEESKEKSEHQVELICSYRSKIETELTKISD
DILSVLDLHSLIPSAITGESKVFYKMKGDYHRYLAEPSSGDAREKATNAS
LEAYKTASEIATTELPPTHPIRLGLALNFSVFYIEIQNSPKACHLAKQA
FDDAIAELDTLSEESYKDSLIMQLLRDNLTLWTSMDSESGQAEDQQQQQ
QHQQQQPPAAAEGEAPK

YOR267C, 2780 bp, CDS: 501-2780 (SEQ ID NO 363)

TAGTTCTATTTGGCTATATATTTTCAGAGTGACAAATCTTTAAGAGAGACA
AACTGAGAATTAGCATATAGAATCATTTCATACAACTGTTTACAAACAAGT
AAGCCCAAGACAGTTCCCAACCGCTTAAAGAAGTTTTTCTAGAGGGAGC
AAAGTTCGTTTACATTTACACACACAGTTTTTTTTTCTACTTTTTTGGGCC
TCTTCTTTTCCCGTTTTTTTTTCAAAAAGCTTAGAAATCTTCTTACCTCC
TATTTTCTAGAAATCGTGAAGAATTTCCAGATTTAACAGTTTTCCACTTT
TTCAATAAGGAAATAGTAGGAATAATAAAAAAGGATAGTAGTAACGATA
TACGTCGACTTTCCAGACTGGTCTCGAGCCGGAATTTAAATACAATAGCAG
CGTTTGACTACCACATTTGTAGCTCCGCTAGAATTGATCGAAAACAAAAAT
AATAACACTAATAATTATAATAATACGGTAGAACTATTTCTCGTATAAAG
ATGCCTAATCTATTGTGCGAGAAACCCATTCCATGGTCATCATAATGACCA
TCATCATGACCGTGAAAATTTCGTCTAATAACCCGCCACAGTTGATCAGAA
GTTCTAAATCTTTCTTAAACTTCATTGGTAGAAAACAAAGTAATGACTCA
CTAAGAAGCGAGAAATCTACAGATTCCATGAAATCTACCACAACCACTAC
AAATTATACTACAACAACCTTAATAACAACCCCATAGCCATTCTAATG
CAACCAAGTATCTCAACAACAACCTACAATAAATACTATGAAACAACCAAC
CACCATAATATTTCTCATGGGCTCCATGACTATACTTCTCCCGCTCTCC

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AAAACAAACCCACTCCATGGCAGAATTGAAAAGGTTTTCAGACCTTCTG
TAAATAAAAACTATCTATGTCCTCAACTTCGTTCCAAGAAACATAGCACC
CATTCCCCCCCCACCTTCAAAATCAACTTCTACAGTTAATTTAAATAATCA
CTATCGTGCCAGCATCCTCATGGCTTTACAGACCACTATGCTCATACCC
AGTCTGCTATACCGCCAAGTACCGATTCTATCCTATCTTTGTCCAATAAT
ATTAATATATATACCGATGATTGTATTCTGGCTCAAAAAATACGGGAAAT
GGGTAAGTTATTGGGTTCCGGTGCCGGTGGGTCCGTTAAAGTTCTTGTGA
GACCAACTGATGGTGCTACTTTTGCCGTCAAAGAATTACAGACCAAGGAAA
CCGAATGAGAGTGTGAAAGAATATGCCAAGAAGTGCAACCGCAGAATTTTG
TATTGGTTTCGACTTTACATCACCCAAATGTTATCGAAACTGTTGACGTTT
TCTCTGATTCTAAACAAAATAAATACTATGAAGTTATGGAGTACTGTCCG
ATTGATTTTTTTTGTCTGTTGTTATGACAGGCAAGATGTCTCGTGGCGAGAT
CAACTGTTGCTTGAAGCAATTGACTGAAGGTGTTAAATATTTACATTCTA
TGGGATTGGCACATAGAGATTTGAAATTGGATAATTGTGTCATGACTTCC
CAGGGTATTTTTGAAATTAATTGATTTTGGTAGTGCTGTTGTGTTTCAGATA
TCCTTTTGAAGATGGCGTAACGATGGCTCATGGAATCGTGGGTAGTGACC
CTTACTTAGCGCCGGAAGTGATTACCTCCACCAATCTTATGATCCTCAG
TGCGTCGATATATGGTCTATTGGGATCATATATTGTTGTATGGTGCTTAA
AAGGTTTCCATGGAAAGCCCCTAGAGATTCTGACGATAATTTTAGATTAT
ATTGTATGCCGGATGATATAGAACACGACTATGTTGAATCTGCCAGGCAT
CACGAAGAGTTACTGAAGGAAAGAAAAGAAAAGCGTCAAAGGTTTTTGAA
TCACAGTGAAGTTCCGCCATCAATCAGCAACAACCAGCTCATGAATCAA
ACTTGAAAACAGTTCAAAATCAAGTTCCAAATACTCCAGCATCTATACAG
GGTAAAAGCGATAACAAAACCAGACATTGTGGAAGAAGAAACCGAAGAAA
TAAAGAAGATGATAGCAATAATGATAAAAGAAAGCACGCCAGATAATGACA
AGGAAAGTACCATCGATATTAAATAAGCAAAAATGAGAATAAAAGCACG
GTAGTTTTCAGCTAACCCAAAGAAAGTAGATGCCGATGCCGACGCTGATTG
CGATGCTAATGGTGACTCTAACGGCAGAGTGGATTGCAAGGCTAACAGTG
ACTGCAATGACAAAACGGATTGTAATGCTAACAATGACTGCAGCAATGAA
TCGGATTGTAACGCTAAAGTTGATACTAACGTCAACACTGCTGCCAACGC
TAACCCTGATATGGTTCCCCAAAACAATCCACAACAACAACAACAAC
AACAACAACAACAACAACAACAACAACAACAACAACAACACCATCAT
CACCAGCATCAAAATCAAGACAAGGCCCATAGTATCGCTTCCGATAATAA
ATCGAGTCAACAGCACAGAGGACCTCACCATAAAAAAATTATTATGGCC
CATACCGTCTATTACGTCTACTACCACATGCTTCAAGACCTATCATGTCC
CGTATACTGCAAGTAGATCCAAAGAAAAGAGCAACCTTAGATGATATTTT
TAATGATGAATGGTTTGCCGCCATTGCTGCCTGTACCATGGATTCAAAAA
ATAAAGTTATTAGAGCGCCTGGCCATCACCATACATTGGTTAGGGAGGAA
AATGCTCACTTAGAGACCTACAAGGTTTAA

YOR267C, 759 aa (SEQ ID NO 364)

MPNLLSRNPFHGHNDHHDRENSNNPPQLIRSSKSFLNFIGRKQSNDS
LRSEKSTDSMKSTTTTTNYTTTNLNNTHSHSNATSISTNNNNNYETNH
HHNISHGLHDYTPASPKQTHSMAELKRFFRPSVNKKLSMSQLRSKKHST
HSPPPSKSTSTVNLNNHYRAQHPHGFTDHYAHTQSAIPPSTDSILSLSNN
INIYHDDCILAQKYGKLGKLLGSGAGGSVKLVLRPTDGATFAVKEFRPRK
PNESVKEYAKKCTAEFCIGSTLHHPNVIETVDVFSQKQNYEVMYCP
IDFFAVVMTGKMSRGEINCLKQLTEGVKYLHSMGLAHRDLKLDNCVMTS
QGILKLIDFGSAVVFRYPFEDGVTMAHGIVGSDPYLAPEVITSTKSYDPQ
CVDIWSIGIIYCCMVLKRFPWKAPRDSDDNFRLYCMPDDIEHDYVESARH
HEELKERKEKRQRFNLHSDCSAINQQQPAHESNLKTVQNQVPNTPASIQ
GKSDNKPDIVEEETEENKEDDSNNDKESTPDNDKESTIDIKISKNEKST
VVSANPKKVDADADADCDANGDSNGRVDCKANSDCNDKTDCNANNDCSNE
SDCNAKVDTNVNTAANANPDMVPQNNPQQQQQQQQQQQQQQQQQQHHH
HQHQNQDKAHSIASDNKSSQQHRGPHHKKIIHGPRYLLRLLPHASRPIMS
RILQVDPKKRATLDDIFNDEWFAAIAACTMDSKNKVIRAPGHHTLVREE

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NAHLETYKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)

TATTGGCGTCTGATTTCCGTTTTGGGAATCCTTTGCCGCGCGCCCTCTC
AAAAC TCCGCACAAGTCCAGAAAGCGGAAAGAAATAAAACGCCACCAA
AAAAAAAAAAATAAAAGCCAATCCTCGAAGCGTGGGTGGTAGGCCCTGGA
TTATCCCGTACAAGTATTTCTCAGGAGTAAAAAAACGTTTGT TTTGGAA
TTCCCCATTTTCGCGGCCACCTACGCCGCTATCTTTGCAACAATATCTGC
GATAACTCAGCAAATTTTGCATATTCGTGTTGCAGTATTGCGATAATGGG
AGTCTTACTTCCAACATAACGGCAGAAAGAAATGTGAGAAAATTTTGCAT
CCTTTGCCTCCGTTCAAGTATATAAAGTCGGCATGCTTGATAATCTTTCT
TTCCATCCTACATTGTTCTAATTATTCTTATTCTCTTTATTCTTTCTTA
ACATACCAAGAAATTAATCTTCTGTCATTTCGCTTAAACACTATATCAATA
ATGCAATTTTCTACTGTGCGTTCTATCGCCGCTGTGCGCGCTGTGCGCTTC
TGCCGCTGCTAACGTTACCACTGCTACTGTGTCAGCCAAGAATCTACCACTT
TGGTCACCATCACTTCTTGTGAAGACCACGTCTGTTCTGAAACTGTCTCC
CCAGCTTTGGTTTCCACCGCTACCGTCACCGTCGATGACGTTATCACTCA
ATACACCACCTGGTGGCCATTGACCACTGAAGCCCCAAAGAACGGTACTT
CTACTGCTGCTCCAGTTACCTCTACTGAAGCTCCAAAGAACACCACCTCT
GCTGCTCCAACCTCACTCTGTCACTCTTACACTGGTGCTGCTGCTAAGGC
TTTGCCAGCTGCTGGTGCTTTGTGGCTGGTGCCGCTGCTTTGTGTGTGT
AA

YLR110C, 133 aa (SEQ ID NO 276)

MQFSTVASIAVAASAAANVTATVSQESTTLVTITSCEDHVCSETVS
PALVSTATVTVDVITQYTTWCPLTTEAPKNGTSTAAPVTSTEAPKNITS
AAPTHSVTSYTGAAAKALPAAGALLAGAAALLL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)

TGTCTATTAGTAATCAAGAAAAGAACCCTAAATCATCGGCGTCCCCTGTG
GGGCTCTCGGAAAAACCGGTCCCTGACGTCAGTAAAAGATTTCGGCACAT
GGTCATGGGACCAGAGAAAAATTAATCCGACATGTGAATATTTCTTTCC
GTTAAGGTAGTGAGCGCGGATTTTTCTGATTTGTAATTATACGGGGAGC
TCTGGCCAAAAAGGTCAGTATTTGGTGATGAAGTTGAATATCATCTTTTG
ATTTTCTTCTGTATCATCTTTTCTTTTCCACACCCCTTCCGGACGGT
ATTACATATTTGTTGAGAGGTTAAATGAAAAATAAAGGGGTGGAAAAATTA
AGGACGAGATGTAAGGGAAAAAGCATAAACGAAACATTATATAAAGGAGCA
CAATTTCTCTCCCTTGCCAATTGTGCATATACCGTTTCTTTATAACGAA
ATTTCAACAAACAGAACACACAAGTACTACCAATAACCACAACAAAAC
ATGCTGACTTAGTTAACAAGAAATTTCCAGCTGGCGACTACAAATTCCA
ATACATTGCTATCAGCCAAAGTGATGCTGACAGTGAATCTTGTAAGATGC
CACAAACAGTTGAATGGTCCAAATTAATTTCTGAAAACAAGAAGGTTATC
ATTACCGGTGCTCCAGCTGCTTTCTCCCCAACCTGTACTGTCAGCCATAT
TCCAGGTTACATCAACTACTTGGATGAATTAGTTAAGGAAAAGGAAGTTG
ACCAAGTGATCGTTGTTACTGTTGACAACCCGTTGCTAACCAAGCGTGG
GCTAAGAGTTTAGGTGTTAAGGACACCACACACATCAAGTTTGCCCTCCGA
CCCAGGCTGTGCTTTACCAAAATCCATTGGTTTCGAATTAGCCGTCGGTG
ACGGTGTTTACTGGAGTGGTAGATGGGCCATGGTTGTTGAAAACGGTATC
GTTACTTACGCTGCCAAGGAAACCAACCCAGGTACCGATGTGACCGTTTC
CTCAGTCGAAAGTGCTTTGGCTCATTGTAG

YLR109W, 176 aa (SEQ ID NO 274)

MSDLVNKKFPAGDYKFQYIAISQSDADSESKMPQTVESKLIENKKVI
ITGAPAAFSPTCTVSHIPGYINYLDLVKEKEVDQIVVTVDNPFANQAW
AKSLGVKDTTHIKFASDPGCAFTKSIGFELAVGDGVYWSGRWAMVVENGI
VTYAAKETNPGETDVTVSSVESVLAHL

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YBL081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)
TTGTTGCAACAATTTTGGGATGCTTCTGCGTCGTACGACCTGTATTTAC
CTTCTCTAGCTCATCGCTTCCAGGGTCCACGTTAATTTTCAATTTT
CTTGCGTGTGGAAGATTTCAGGTCTCGAGAAATTTGTCAAAAATTTTTCAC
TAGATATTAAGAACTATATACATCGAATAAGATGCCAGCACAGAAGAGAT
AGGCAATCAGTTTAGATACTACAGACACTATCCAATAGTGCAAAGCAAAA
GCAGCATAGAAAAAGAGAATCCCGTTTCCAGCTTTTCTCTTTTCCCA
TTCGTTTTTCTGATCTTTTTTCTGTCATCGTGGCACCTAGAACAAGAGG
TACCTTCCATCCTTTCGCTTAATATTTGATACGACTTTTTTGATTTCAT
ATTATTTATTTGTTACTATTATTATTTATCATTTGGGTTTCGGTTTTTTGT
AATAATTTTCTTTTTTTTTTTTGGCTCTATTTCACTAAGACATCGTATAT
ATGCCAGGCCAGATAATCAGCATTCGGTTTTTGTGCGAGAACGAGGACAT
GGATAAATACTTGTGGAGTACCGCAGTTTGAAGCTCCTTCATCAGTCCA
GTAATTCCTTCCAGTCTCACAATGCGCCCTCCACCAGTCGAACTACCAC
CCCCATTACAATCACATGAAATACAACAACACTGGTAGCTATTACTATTA
CAACAACAACAATAACAGCAGTGTAACCCACATAACCAAGCTGGTCTAC
AATCCATTAAACAGATCTATTCCATCGGCCCGTACGGGGCTTACAACCAG
AACAGAGCTAATGACGTACCATATATGAATACCCAAAAGAAACACACAG
ATTTAGCGCTAACAAATAATTTGAACCAGCAAAAATACAAGCAATATCCCC
AGTATACGTCCAATCCAATGGTTACTGCACATCTGAAGCAAACGTACCCCT
CAACTGTACTACAATAGCAACGTCAATGCTCACAACAACAACAACAG
CAACAACAACAACAACAACAACAACAGCAACAACAACAACAATCTTT
ACAACCAGACGCAGTTCTCCACGAGGTACTTCAACTCGAACTCCTCTCCC
TCGTTGACTTCTTCCACTTCTAACTCATCCTCTCCATACAACCAAAGCAC
CTTCGAATACATTTTGGCGTCAACTTTCGGCAGCTTCCACAAATTTATCGT
CGTCATCATCAAAACACTCTATGCACACCAACCCAACCACTGCAACATCG
ACATCCGCCGATTTAATCAATGATTTACCCGTGGGCCCCACGTCCAGTTC
GCTTATCTCGGATCTACATTCTCCACCAACTGTATCTTTCCTACCAGCAA
GCCAAACCCCTGCTCATGTCTCCACCACATCTAGCTCTATTGGCACCAAC
ATAAACCACCGCAACATTACCATCCCCATCGCAAAGGGAGGATTTTTTC
GACGGCACCGAGTGAACATGTCTTCGTCCGCATCACTCTTGATGAATGATT
CTTCTTTAGGATGGGGGTCTAACCACATGAACGTATCTTCATCCTCTCAA
CCAGCATCATCAAGACCCTTTGGCATTGTGAATACTGACATGAGCGTTTG
GAGTTGA

YBL081W, 368 aa (SEQ ID NO 30)

MPGQIISIPFLSQNEDMDKYLLEYRSLKLLHQSSNSFQSHNAPSHQSNYH
PHYNHMKYNNNTGSYYYNNNNNNSSVNPHNQAGLQSIINRSIPSAFYGAYNQ
NRANDVPYMNQKKHHRFSANNNLNQKYKQYPQYTSNPMVTAHLKQTYP
QLYNSNVNAHNNNNNNNNNNNNNNNNNNNNLYNQTFSTRYFNSNSSP
SLTSSTSNSSSPYNQSTFEYILPSTSAASTNLSSSSSNNSMHTNPPTATS
TSADLINDLPVGPTSSSLISDLHSPPTVSFLPASQTLMSSTTSSSIGTN
INPPQHSPSPSQREDFSTAPVNMSSSASLLMNDSSLGWGSNHMNVSSSSQ
PASSRPFGIWNTDMSVWS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)

CTGTGATATTGGGTTACTTTGTAGTGCATTATTTCCATCAATATTAGCA
GTGTCTTCCAAGGTGAACCATTCGGTGGTAAACCATAGAGTAAAAAACA
AGTGGAATGGTATCGATTGTATAAAGTACGCAGATTTGCGAAAATACCA
GCAAGTTTGGCTTATGAATCAAATACAGCCCTTGTGAGAATACGATTAAT
GTAAATACCGACCAAAGATATGCTATCCATTGCATAAAATCCAACGGATG
ACCCGTGAACAATGCTAAATACCATAAGCACCACTGCATTTGTTTAGAA
TGGAAATACCTAAGACAATCTCAACTGCAAGGTATAGCGGCATAAACCCC
AAAAAGACTATGAAAAAATATGTTTGAGAACAGGTAGTAAATTTG
TGCTTTGCTTCGAATCCTTACAAGTTAAACAAAATTTATAGCGTTTGCCG
GAAACATACTTTTGAAGGGTTAGAAGAGATGATCTCATAACTAAGGTTA

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ATGGTTACAATTGGTAGTTCCCTCCCTGGTATTATTTCTTTTCTTCGTAGT
TTTTGTACAGATCACCTTATACAGCTTTACACAGATTTTCCCGCTTGTGT
GCACCTTTTTTTTCGAAGATTATTGAAGAGGGATGCGTTTGGTACAATAAA
AAACATAGGTTCCCAAACCTATATAAAATATATATATGTATATGTATATAT
ACTACATATATGCTTTTGAGAAAATATGTGAATGTTGAGATAAATTGTTGGGA
TTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAATATACTAGAA
GTTCTCCTCAAGGATTTAGGAATCCATAAAAGGGAATCTGCAATTCTACA
CAATTCTATAAATATTATTATCATCATTTTATATGTTTATATTTCATTGA

YDR366C, 132 aa (SEQ ID NO 126)

MVTIGSSSLVFLFFVVFVQITYTALHRFSRLLCFFSKIIEEGCVWYNK
KHRFPNLYKYIYVYVYILHICFEKYVNVEIIVGIPLLIKAILGIQNILE
VLLKDLGIHKRESAILHNSINIIIIILYVYIH

YDR154C, 851 bp, CDS: 501-851 (SEQ ID NO 101)

TAGACGGGCTTCCACGCGCTTCCACTCATTTCTGTCTCTGGTAATGGCCG
TGGCCCTTCTCACTTTGGTTGGGCTTACGCTGACAAGTGCTGTTCGATT
CCCTGTATAAATATAAACGTATTCTCTTGAGCCTTCTATCCTTTTGCCAC
TGTCGTCATCATTTGTTCCCTCCTTTTTCGCTAGATAGGTTATATTAAGAT
TTGTCTTGAATTTAATATCTCAACTCAATCCAACTCAACCGCTAATACT
ACCATGTCCCAAGTCTATTTTGATGTCTGAAGCTGATGGCCAACCAATTGG
CCGTGTCGTTTTCAAGTTGTACAACGACATAGTCCCAAAGACTGCAGAAA
ACTTCAGAGCTCTATGTACCGGTGAAAAGGGATTTCGGCTACGCTGGCTCT
CCATTCCACAGAGTTATTCCAGACTTCATGTTGCAAGGTGGTGACTTCAC
TGCTGGTAACGGTACCGGCGGTAAGTCTATCTACGGTGGCAAATTCCCAG
ATGAAAACCTCAAGAAGCACCACGACAGACCAGGTTTGTGTCCATGGCC
AACGCCGGTCCAAACACCAACGGTTCTCAATTCTTCATCACCACCGTTCC
ATGCCCATGGTTGGACGGTAAGCATGTTGTCTTTGGTGAAGTTGTTGACG
GTTACGACATCGTTAAGAAGGTTGAGTCCTTGGGTTCTCCTTCCGGTGCC
ACCAAGGCTAGAATTGTTGTTGCCAAGTCCGGTGAATTATAACCGCTCTG
CCTGGAACAATACAGCAAAAATTGAAACGAACTATTCTCTCTTAAATTAT
ATGTATATGTATAAGGTATGTGTATGTATGACAATCAATTCTTATAACTA
A

YDR154C, 116 aa (SEQ ID NO 102)

MKTSRSTTTDQVCCPWPTPVQTPTVLNSSSPFFHAHGWTVSMLSLVKLLT
VTTSLRRLSPVWLLPVPRLELLLPSPVNYNRSAWNNTAKIETNYSLLNY
MYMYKVCVCMTINSYN

YHR162W, 890 bp, CDS: 501-890 (SEQ ID NO 213)

CGCTCGCTTCCAAGAGTTATCATCATATTCTTCATCATATTCTTCCATAC
TTAAGGTGGGTAGCGAGGACCCCTCAATTCCCCACCTCTCTGCCAGGGC
GTCATCTTTTTCTACAAAAGCCAGGCTGAGTCACGTCAGTTGCTGACCCT
GGGGGCTGCATTGTTTCTACGAATTACTCATTTGTTTCGTGCGCTTTCC
TATTGCGCGCATGACTAGGATGGAAAAAAAAAAGAAGAAAAGAAAAGCGT
TGAGTATATAATAAGAAAAGAAGAAAAGTCCGAGAGAAAAGAAGCACAAA
GGTTTTTCTCGAGGAAAACAGTAAAGTTTGATACGCACATCGTTGACAT
CGCTGACTGCAATAGGAACTGAAATAGACGGCAAACCATTAGTTTCATTC
GAAAGAACGTATTGTGCGAGAATTATCACTCACTATATCAGAAAATTGACA
CACGAATTATATAAACGAAGTTATACAGAAAAAGATTAAAGAAAAGAAAA
ATGTCTACATCATCCGTACGTTTGCATTTAGGCGGTTCTGGCAAAGTGA
GACAGGCCCCAAGACGGTGCATTTCTGGGCTCCTACTTTGAAATGGGGTC
TGGTTTTCTCGCTGGATTTCAGCGATATGAAGAGACCGGTGGAAAAAATTTCT
GGTGCTCAAAATTTGTGCTGCTATCTACTGCGCTGATTTGGACTCGTTG
GTCCTTTGTTCATCAAGCCAAGAAACATCTTGTGCGCTTCTGTCAACTCGT
TTCTTTGTCTGACCGCTGGCTATCAATTGGGTAGAATTGCCAACTACAGG

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ATACGGAATGGCGACTCTATATCGCAATTGTGTAGCTATATTCTCAGCGG
CGCCGACGAAAGCAAAAAGGAAATTACTACGGGCAGATAA

YHR162W, 129 aa (SEQ ID NO 214)

MSTSSVRFAFRRFWQSETGPKTVHFWAPTLKWGLVFAGFSDMKRPVEKIS
GAQNLSLLSTALIWTRWSFVIKPRNILLASVNSFLCLTAGYQLGRIANYR
IRNGDSISQLCSYILSGADESKKEITTGR

YGR243W, 941 bp, CDS: 501-941 (SEQ ID NO 189)

CCTCCACCAAAGCAAAATGAAAACAAAGCCATACTGGGAAAAATCTGAAA
AAAAAATGGTAGGAGTAAAAGAAAAGAAAAATAAAGGTTACCCCTGCAG
TTTGGATAGTCGGGTAACATTTGGCCCTTTTCCTCCTTGATTGGATATTA
TTACCCCGATTACCCCTCATCTTGGGAGTGGCCCGCTTTTATTTCTCCCG
CCAATCGGCTATTAACGGCTTTACGTCATTCCGTGGGCGGGTCAAGCGAG
CCGCTCCCTGGTTTGGTCACGCAAAACCGAAAGGCTCAAACAAAACCTAAG
GCCATCATATATATATATGCGGCTGCGTGCGTGATTCTCCCGGATAATA
TGGTGCGTTGCAATTGGAGTATTGGAGAAAATTTCTTTTCCCTTTTCATT
ACGGCGGAAATACTTTCATATAAAAAAAGAATACAATCAGTCTTTAAGA
CTATACGCATAAGCATTCAAGACACATAGAAACACAAACCTATATTTTGA
ATGTCAGCATCAGCTTTTAATTTTGCCTTTAGAAGATTTTGAATAGTGA
AACAGGCCCCAAAACAGTACACTTCTGGGCCCCAACTTTGAAGTGGGGGC
TGGTCTTCGCAGGGCTAAATGATATTAAGAGGCCCTGTTGAGAAGGTATCA
GGAGCACAAAATTTATCTTTATTAGCGACGGCACTGATTTGGACGCGTTG
GTCGTTTGTTCATCAAGCCCAAGAACTATCTGTTAGCTTCCGTCAATTTT
TCCTGGGTTGCACCTGACGGCTACCATCTAACAAGAATTGCTAACCTTAGG
ATACGGAACGGTGATTCTTTTAAACAGGTTATTCACTACATAATAAAGG
GGAGACTCCGTGCAGCCGTGCGAGCAAAAGCAAACTGCATCCACATCGATGA
ACAAAGGTGTGATCGGTACTAATCCGCCAATAACGCACTGA

YGR243W, 146 aa (SEQ ID NO 190)

MSASAFNFAFRRFWNSETGPKTVHFWAPTLKWGLVFAGLNDIKRPVEKVS
GAQNLSLLATALIWTRWSFVIKPKNYLLASVNFLLGCTAGYHLTRIANFR
IRNGDSFKQVIHYIILKGETPAVAQAQTASTSMNKGVIQTNPPITH

YBR050C, 1517 bp, CDS: 501-1517 (SEQ ID NO 43)

AAGTACGATATGGTATAACTGTAACATTGAAGGACTGAAGGACTGAAGGA
CTGAAGGACTATAGTCAAGGGCCAATGGGGAAGGTCCCTTCCAGGCCATT
TGCCCGATAGTTTGTCTTCTCTTGCTTTTCCGACGGCCCGATTGCATGT
GGCGGGGCAGCACTGGATAAAAAACGTGGGGGGAGTGATTAAATTTATA
CGCTTATTGTGTCAACACGGAAACCTTATAGTTATCATTACTAACATCGC
AACAAGCTGCTTTTTTACTCGTTTTTAGCCACACCATAACCCCTTTAATT
AACTAATAATGCATAAAATAGTTATTGCTTCTTGAGTTGCAGCTTCTTCC
TGGACGTACTGTTATATATGGCATGTCTTCGCATGTCCGTCAAATTTAGC
GTTGTCTCGAAACTTAGGCTGTCTGCTTCTTGCTGTCTGTCTTCTGATAAAA
TAATATATTGGAATAAGAAAAAATAAGGAACAAGAAAGTGTGTGAGA
ATGACTTTGAGTAATTGCGACTCTTTGGATAACTTATTCCAGGACCCTCC
AGAGGAAGAAGAAAGTAGTAAATTCGTTGAGGCGGTCAGAACTTTGATGA
ATAGAAACGATATGGGATATCCTCCCGCCGCTGCAAATGGTACGTATTGC
TTAAAAAATCAAGTCTTTGAATGCCAAACAGTGGAAATAAACAAGAA
AAGAATGTGCATGTTGCCAGCAGTAAAGAAGAAAAATTTGCACTTTCACG
AGCAAAGAAGTTAATCTTGAATTTAAATTTATGGAAATTCATCAAGTTT
ATCAATTGTAGTAGTAAAAACAATTACAATAAAAAATAATAAGCATGTGAG
AAGCTCGAACAACACTGTAAAAAATGAAAAATGTTTTACCGTTACAAAAAC
ACAAGAAAGTGGACAATGATCAAAGATTGGAGAACCTTTTTTGGAGAAGC
TGGTTTAAGGCACGCAAAAGGAGAGATATAATGGGCAAGCCACGAGAGAG
GCATATCAAATTTAACGATAACGTTGAACAGTGTATTATAACTGATGAGC

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ATTTTCATACAAAGGCTTCCTTCTACACGGTTGAATTCGACTGATGAACAG
CGCCCTTGTTCAAAGTCTGAACTAGATCCCTGTATTGGCAACGCAGCAAG
TAAGCGAAGTTTCTATGATTATAACAGCGTTTACGTCGCGAGTGACGCAA
TTATTACGACTGCCGCTGCCACTGCCATTATCAGTAGTAATAGTGGAGAC
TATCAGCGTGGGCACGATGTTCCGCGATGTTCCAAGAAATGTTTTGTTACA
GGCAGGAGAAACAGATTTTCAGTAGTGTGCTTCGGGTTGACTCCGATCTCA
AGTTATCCAACATAAGTCATCATTTCCCCCGTAAAACCTTCGTCAACTTCA
AGTCATTGACCTTCATTTTCGAGTCGGAAACTGACACTGATACTGATAC
TGACGCTGAAACAGAAAATGACATTGACGCTTACATAGACACCAGTATAC
CCAACCTGCTCCTATAA

YBR050C, 338 aa (SEQ ID NO 44)

MTLSNCDSLDNLFDPPPEEESSKFVEAVRTLNRNDMGYPAAANGTYC
LKKIKSLNAKQWKINKKRMCLPAVKKKNFDFHEQRSLLNLNLWKFIFK
INCSSKNYNKNNKHVRSSNNIVKNNVLEPLQKHKKVDNDQRLNLFWRS
WFKARKRRDIMGKPRERHIKFNDNVEQCIITDEHFIQRLPSTRLNSTDEQ
RPCSKSELDPICIGNAASKRSFYDYNVYVASDAIITTAATAIISNSGD
YQRGHDVDRVPRNVLLQAGETDFSSVLRVDSDLKLSNISHHSPVKPSSTS
SHSTFIFESETDTDTDTAETENDIDAYIDTSIPNLLL

YEL071W, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)

TAGCTTGACCTGGTCAGATTAATCAGCTTCCAACGTTACTTCCCTTTTCGC
AAGAATCTACCCAAAATGTCTCGAGCATCTTGATAATTACAGTATCGTTC
GTCCCGACTTGGCATTGTGTTAAATTTCTAAGATGCTTCCATAGGAACA
TAATGTCAAGAAAGCACAACAAATTTGTCTGCAATGTCAACAGGAGTGGC
GCATTTTATGTTTTTTTCATTTTTTTTTTTTTTTGTGCGTGATCATTAAGCGG
GATATTGTCCACAGTCATCTAAAAGAATGACCATTTTCGACGACTTAGTTC
GGAAAATATTTCCAGCGGATGACACCACTTGCACAGTTGGTGACCGCCA
AATCTAAGTCACGCGCGGAAACTGAAAGGTTGTGAGTATATAAGTGATCA
CTCGCTTATATAACTGACGAGGCAGAACAGGGTGCCAAAATGCTCCTCAA
TATTTTATTCATTTGAGATTCAAGGCTTAAAGACAGCATATATAAGAATT
ATGACGGCGGCACATCCTGTTGCTCAGTTAACTGCCGAGGCATACCCATAA
AGTCAAGAGAAAACCCAAATTTCAAAGTTCTCGACTCGGAAGATTTGGCGT
ACTTTTCGTTTCGATTTTGTCAAATGATGAAATCTTAAACTCTCAAGCTCCA
GAAGAGCTTGCTTCGTTTAAACCAGGACTGGATGAAAAAATATAGAGGCCA
GTCCAATTTAATTTCTCTTGCCAAACTCCACTGATAAAGTGTTCAAGATTA
TGAAATACTGTAAACGATAAAAAGTTGGCAGTAGTACCACAAGGTGGTAAC
ACCGACTTGGTCGGAGCCTCTGTTCCGGTATTTGATGAGATTGTTCTTTC
TCTAAGAAATATGAACAAAGTCAGAGATTTTGATCCAGTTAGCGGGACTT
TCAAAGTGTGACGCGGGTGTCTGTTATGCGTGATGCGCATCAATTTTACAC
GACCATGACCATATCTTCCCATTTGGATCTGCCTTCTAGAAACAACTGTCA
AGTGGGCGGTGTAGTTTCAACAAATGCAGGTGGTTTGAACTTTTTAAGAT
ATGGGTCTCTACACGGTAATGTTTTGGGTTTGGGAAGTGGTGCTACCCAAC
GGTGAGATTATCAGCAATATCAATGCCCTAAGGAAGGACAATACTGGTTA
TGACTTGAAACAATTATTCATCGGTGCAGAGGGTACTATCGGTGTCGTTA
CTGGTGATCCATAGTTGCAGCAGCAAAGCCAAAAGCCTTGAATGCCGTA
TTTTTTGGTATTGAGAATTTTCGATACCGTTTCAGAAATTATTTGTCAAGGC
TAAAAGTGAAATTATCTGAGATTTTATCTGCTTTTGAATTCATGGACCGTG
GCTCCATTGAATGTACGATAGAATACTTGAAGGACTTGCCCTTCCCTCTG
GAGAACCAACACAACTTTTATGTTCTTATTGAAACGTCAGGGTCCAATAA
GAGACACGACGATGAGAAGCTGACTGCTTTCCCTCAAAGATACCACAGATT
CTAAATTAATTTCCGAGGGTATGATGGCTAAGGACAAAGCCGATTTTGAT
AGACTTTGGACCTGGAGAAAATCTGTTCCAACAGCTTGTAATCTTACGG
TGGTATGTACAAGTATGACATGTCACTTCAATTGAAAGATTTATATTCGG
TATCTGCGGCTGTGACGGAGAGATTAACGCAGCCGGTTTGATTTGGTGAT
GCACCAAAACCAGTTGTTAAATCATGTGGTTATGGTCATGTCCGTGACGG

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AAACATCCATTTAAATATCGCGGTAAGAGAATTTACAAAACAGATTGAGG
ACTTACTAGAACCATTTGTTTATGAATATATTGCATCAAAGAAAGGTTCC
ATCAGTGCTGAGCATGGGATCGGTTTCCATAAGAAAGGTAAGTTACACTA
CACCAGAAAGTGATATTGAAATTAGATTTATGAAGGATATCAAAAATCACT
ACGATCCAAATGGAATCTTAAACCCATACAAGTACATTTGA

YEL071W, 496 aa (SEQ ID NO 144)

MTAAHPVAQLTAEAYPKVKRPNPKVLDSEDLAYFRSILSNDEILNSQAP
EELASFNQDWMKKYRGQSNLILLPNSTDKVSIMKYCNDKKLAVVPQGN
TDLVGASVPVFDEIVLSLRNMNKVRDFDPVSGTFKCDAGVVMRDAHQFLH
DHDHIFPLDLPSRNNCQVGGVVSTNAGGLNFLRYGSLHGNVLGLEVVLPN
GEIISNINALRKDNTGYDLKQLFIGAEGTIGVVTGVSIVAAAKPKALNAV
FFGIENFDTVQKLFVKAKSELSEILSAFEFMDRGSIECTIEYLKDLPPPL
ENQHNPFVLIETSGSNKRHDDEKLTAFLKDTTDSKLISEGMMAKDKADF
RLWTWRKSVPTACNSYGGMYKYDMSLQKDLYSVSAAVTERLNAAGLIGD
APKPVVKSCGYGHVGDGNIHLNIAVREFTKQIEDLLEPFVVEYIASKKGS
ISAEHGIGFHKKGLHYTRSDIEIRFMKDIKNHYDPNGILNPYKYI

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)

GTGCAGAGGGTGAATCAACGGCCCCCTCACAGAAACCGCGCAGGAATTTT
TCTGGTGTTTGTATTTTTTTTTTCCCTGTACTTATCTCACTTTTCTTTT
CTAACTATTTTTTTTGCAATTTTTTGTGTACACTTTCCACAACATATAG
GATGGTTTAGTCATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTT
GTTCTTCATCGACTTCTCTCTGCTAGACTCTCTTTTTTAAAATTTTTTCA
TAGAATAAAAAACCAAGGATAACAAACATCTTCTTTTCGTTTCGCTTCAAAA
TAACTACAAATAAAAATGCAATTCTCTACCGTCGCTTCTATCGCTGCTA
TTGCCGCTGTTGCCCTCCGCCGCTTCTAACATTACCACTGCTACTGTCACA
GAAGAATCTACCACTTTGGTCACTATCACTTCTTGTGAGGACCACGTTTG
TTCGAAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAA
ATGACGTTATCACTTAATACACCACCTGGTGTCCATTGCCAACCCTGAA
GCACCAAGAATACCACTTCTCCAGCTCCAAGTAAAAGCCAACCGAAAA
GCCAAGTAAAAGCCAACCCAACAAGGTTCTAGCACTCAAAGTGTACCT
CCTACACTGGTGGCGCTGTTAAGGCTTTGCCAGCTGCCGGTGCTTTGTTG
GCTGGTGCTGCCGCTTTATTGTTGTAATTTACTCAACCTTTTCTTTAATA
TATTTTTTAGAAAAATGGTTAAGTACTTTTCCGTCAATACAGCTTCCACAA
AATCGTTTTATTTCATTAATAAGATATTCTGGTAA

YDR133C, 111 aa (SEQ ID NO 96)

MTLSLNTPPGVHCQPLKHQRIPLLQLQLKSQPKSQLKSQPNKVLALKLLP
PTLVPLRLCQLPVLCLWLVLPLYCCNLLNLFNIFLEKWLSTFPISQLPQ
NRFISINKIFW

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)

GGTAAAAGAAATGATCAGGGAGCGTTTCTTGCAACAGCAGCAACAGTACA
GGCAGCAACAGCAGAAGGATGGCAATTACGTAAAGCCCTCTCAGGACAAC
GTGGATAGCAAGGACTAACCAGACAGATTGAGGTCTTTCATGCATTACC
ACCAGTAATAATATTATACGGAATAATATAGTTTATATAATATCCATAAT
CATAATCATAATCATAATCATAATCATAATCGTGATATTGTACCAGCCCC
GCTTCTCCCCCTTTTGAAGTACCATTATTATCGGACCCTCTTTACCTTTGA
ATGGCTCAGTAAGGACCTTTGCGCAGCCGTAAGGGGGTCCGGAATACATT
TCCGGGGTTGATCCTCGAGGAAAAGTGCTATCTATATAAGGAGAAGCCCT
TCTAGATCCAAATATCAGGGGTAACCTTTCACAAGTGGCCAGGAACATAT
TCCAAGTTAAAAGAAAAAATAATTATTAGAAACCAATTACCAACACAAG
ATGCTAAGATCAAATTTATGCAGAGGATCTCGAATCCTTGCAAGACTGAC
CACTACACCAAGGACATACACATCTGCGGCGACAGCTGCGGCTGCGAATC
GGGGACATATCATCAAAACATACTTCAATAGAGATTCTACGACAATTACG

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TTCTCCATGGAGGAGTCCAGCAAGCCGGTTTCCGTTTGCTTTAACAACGT
TTTTCTTAGAGATGCCTCCCATAGTGCCAAGCTGGTGACCACGGGAGAAC
TGTATCATAACGAGAAATTGACCGCTCCTCAGGACATTCAAATTTCTGAG
GACGGAAAATCTCTAGTGGTGAAATGGAAAGATGGCGGTCATCACCAGTT
CCCTTTACAATTCTTTATCGACTATAAAGGTTCCAGTTTGTGTTTCGCCAG
CAACAAGAAAACAAGAATCCAGATATAGACCCAGTTATGGAATAAGCGC
ATCCTGAAAGATAACGTCAAGGACTTACTTTCTGTGAGCTACAACGAGTT
TATTGATCCTAAGGATGACTCCAAGCTTTTCCAAACGCTGGTCAACCTAC
AAAAGTTTGGTATCGCTTTCATTTCCGGTACTCCTTCATCCTCCTCTGAA
GGCCTTACCATACAAAAGATCTGTGAAAGGATCGGACCCATAAGATCGAC
TGTACATGGTGAAGGTACATTTGACGTGAATGCATCCCAAGCGACAAGTG
TTAATGCCATTATGCCAATAAAGACTTGCCGCTACATACGGATTTACCA
TTTTTAGAAAATGTGCCAGGTTTCCAGATTCTACAATCTCTACCTGCTAC
AGAAGGGGAAGATCCCAATACTAGACCCATGAATTACTTCGTGGACGCAT
TTTATGCTACCCGTAATGTAGAGAATCGGATTTTGAGGCTTATGAGGCT
TTACAAATGTTCCTGTAAATTATATATATGAAAACGGCGATAAGAGGTA
CTACCAATCCAAACCTTTAATCGAACATCAGGACATTAACGAGGACAATA
CTCTTCTGGGTAAATTATGAGGCCCTTGATTAAATGCATTAACCTACTCTCA
CCATACCAAGCACCTTTCACTTTCGGAATTTATGATAAGCCCTCAGATCT
AAATAATAATCTGGACTTGAATTTAATTACCACCCCAAGCAAACTAACAG
AGAGATTTTGTGTTAAGTCTTTCATTAGGGGGTTGAACCTGTTTCGAGAGT
CATATCAATGACTTCAACAATCAATTTAGATTGCAGTTGCCCGAAAACCTG
TTGTGTTATCTTTAACAACAGGAGAAATTTGCATGCTAACTCTTTAACAA
GCTCAAACCAGCAATGGTTAAAGGTTGCTATTTGATTTCTGATACTTTC
AAGAGTAAATTAAAGTTCTTGAAGAGAAGTTTCTCATGACAAATAA

YHL021C, 465 aa (SEQ ID NO 194)

MLRSNLCRGSRLARLTTPRTYTSATAAANRGHIIKTYFNRDSTTIT
FSMEESSKPVSVCFNNVFLRDASHSAKLVTGELYHNEKLTAPODIQISE
DGKSLVVKWKGHHQFPLQFFIDYKGSSFVSPATRKQESRYRPLWNKR
ILKDNVKDLLSVSYNEFIDPKDDSKLFQTLVNLQKFGIAFISGTPSSSSE
GLTIQKICERIGPIRSTVHGEFTFDVNASQATSVNAHYANKDLPLHTDLP
FLENVPGFQILQSLPATEGEDPNTRPMNYFVDAFYATRNVRSDFEAYEA
LQIVPVNYIYENGDKRYYSKPLIEHHDINEDNTLLGNYEALIKCINYS
PYQAPFTFGIYDKPSDLNNLDLNLITPAKLTERFLPKSFIRGLNLFES
HINDFNNQFRLQLPENCCVIFNNRRIILHANSLTSSNQWLKGCYFDSDTF
KSKLKFLEEKFPDHDK

YKL054C, 2717 bp, CDS: 501-2717 (SEQ ID NO 237)

CCTGCTCTAGACGAAGCTAGGGAGGAGGCGCCGTTTGAAAATGGCGGCAA
ACTAAAAGAAGTTGACAAATGAAGTATATATTTTAGCACAGAATGTGCAT
TATTCAACATGTAAATACTAATACTGCAATATCGACTTATAATAATGTAT
AGTGATCCGTATATTAATAGATCTGTTTCAATTCCTTACCTTTTATGGAT
ATCCGTCACCCGTGATTCCGTCGGAGGTGAGCACTCGCCCAATAAATAA
CGGGAAATGGTGGCAAAAAGTAGTGGCGGGAAAAGGAAAATTTTCGTTTC
TCTCCCATATAAACGTTTCATTCCTTTTCTTAAGTCTTTTACAGTAATTT
CAGAAACATTCGTATTTTATATTTGATCTTTTGAAGCTACAAGAAAACT
CTTACCAATTACCCCAAAAAAATCACCATCATAAAGTACTTACATATTTA
TTTTTGTGTTGGTGGTTTTCTCAATATAATCTACATCATATATATATA
ATGTCTACACAATTTAGGAAGTCTAATCATAATAGTCATAGTAGTAAAAA
ACTAAATCCTGCGCTAAAGTCCAAAATAGATACGCTTACAGAATTGTTCC
CTGACTGGACGAGTGATGATTTAATTGATATAGTTCAAGAATATGATGAT
TTGGAAACTATAATTGATAAAATTACTTCCGGCGCAGTGACAAGATGGGA
TGAAGTAAAGAAACCTGCTAAGAAGGAAAAATATGAAAAAAGGAGCAAC
AACACTCATATGTCCCTCAACAACATTTGCCAAATCCAGAAGATGATATT
ACATATAAGAGTTCTAATAATAGCAATTCTTTTACTTCTACAAAGCATAA

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CAGTAGTAACAATTATAC TCAAGCCAGAAATAAGAAGAAGGTACAAACAC
CACGAGCTCATACAACCGGGAACATGTTAATCTCGACAAGGGGAAGCAC
GTACCATCCAAGCCTGTTTCAAACACTACATCGTGGGCAGCAGCTGTTTC
TGTAAGATACTAAACATGACGTTCTCTCAAGATTCAAATGATAACAATAATG
AAGAATTAGAAGCACAAGGGCAACAAGCGCAGGAGAAAAATCAAGAAAAA
GAGCAAGAAGAGCAACAACAGCAGGAAGGGCATAATAACAAAGAAGAACA
CAAACAAATAGAGCAACCTTCTTTATCTTCAAAGAAAACAACCTTCTAGGA
CATCTGCTTCAACAACCAAGAAAATGTCGTGGGCTGCAATTGCTACACCA
AAGCCAAAGGCTGTTAAAAAGACCGAGTCTCTCTTGAAAAAGCTTGCTGA
ATTGAAGAAAGAAATAAGCGATATTAAGAAGGATGACCAAAAGTCTGAAG
CTAGTGAAGAAAAAGTTAATGAACAAGAAACATCTGCACAAGAACAAGAG
GAGGAGACTGCTGAACCTTCTGAAGAAAATGAAGACAGAGTCCCTGAAGT
GGACGGAGAAGAAGTCCAAGAAGAAGCTGAAAAAAGGAACAAGTAAAAG
AAGAGGAACAGACAGCGGAAGAGCTGGAACAAGAACAAGATAATGTTGCT
GCTCCAGAAGAAGAAGTTACAGTTGTTGAAGAAAAGGTTGAAATTAGTGC
TGTTATTTTCAGAGCCTCCAGAAGATCAAGCTAATACTGTACCTCAACCAC
AACAACAATCCCAACAACCACAGCAACCACAGCAACCACAGCAACCACAG
CAACCACAGCAACCACAGCAACAACAACAACCACAGCAACCACAACAACC
ACAACAACAACCTACAACAGCAACAGCAACAGCAACAACAACCAGTACAAG
CTCAAGCTCAAGCCCAAGAAGAACAATTATCTCAAACTACTATACTCAA
CAACAGCAGCAACAATACGCTCAACAACAGCATCAGTTACAGCAACAGTA
TTTGTCCCAACAACAACAATATGCTCAGCAACAGCAACAGCATCCACAAC
CTCAATCACAACAACCTCAATCACAGCAAAGTCCACAAAGTCAAAAACAA
GGGAACAACGTGGCTGCCCAACAGTACTACATGTATCAAAACCAATTTCC
TGGATATTCTTATCCAGGTATGTTTGATTCAACAAGGATACGCTTACGGTC
AACAATATCAGCAACTTGCTCAAAAACAACGCTCAAACTAGTGGTAATGCT
AACCAATATAATTTCCAACAAGGTTATGGTCAAGCAGGCGGAACACTGC
TGCTGCTAATTTGACTAGTGCTGCCGCTGCTGCTGCCGCTTCTCCAGCTA
CAGCTCAGCCCCAACCTCAACAACAACAGCCATACGGTGGCTCATTCATG
CCATACTACGCCCCTTTTACCAACAGTCATTCATATGGTCAACCTCA
ATACGGTGTAGCTGGTCAATATCCATACAGTTACCAAGAACAATTACA
ACTATTACCAAACTCAAAACGGTCAGGAACAGCAAAGTCCAAATCAAGGT
GTTGCCCAGCATTTCTGAAGACTCTCAACAGAAGCAATCACAACAGCAACA
GCAACAGCAACCTCAAGGTCAACCCCAACCTGAAGTTCAAATGCAAAATG
GCCAACCTGTTAACCACAACAACAATGCAGTTCCAACAATACTATCAA
TTCCAACAACAACAGCAACAAGCTGCTGCCGCTGCCGCTGCTGCTGCCCA
ACAAGGTGTACCATATGGCTACAACGGTTATGATTACAATTCTAAAAATT
CAAGAGGTTTCTACTAA

YKL054C, 738 aa (SEQ ID NO 238)

MSTQFRKSNHNSHSSKKNLPALKSKIDTLTELPDWTSDDLIDIVQYDD
LETIIDKITSGAVTRWDEVKKPAKKEKYEKKEQQHSYVPQQHLPNPEDDI
TYKSSNNSNSFTSTKHNSNNYTQARNKKKVQTPRAHTTGKHVNLDKGKH
VPSKPVSNNTSWAAAVSVDTKHDVPQDSNDNNNEELEAQGQQAQEKNOEK
EQEEQQQQEGHNNKEEHKQIEQPSLSKKTTSTRTSASQPKMSWAAIATP
KPKAVKKTESPLENVAELKKEISDIKKDDQKSEASEEKVNEQETSAQEQE
EETAEPSEENEDRVPEVDGEEVQEEAEKKEQVKEEQTAEELEQEQDNVA
APEEEVTVVEEKVEISAVISEPPEDQANTVPQPQQQSQQPQQPQQPQQ
QPQQPQQQQPQQPQQPQQQLQQQQQQQQQPVQAQAQAQEEQLSQNYVTQ
QQQQQYAQQQHQLQQQYLSQQQQYAQQQQQHPQPQSQQPQSQQSPQSQKQ
GNNVAAQQYMYQNQFPGYSYPGMFDSQGYAYGQQYQQLAQNNNAQTSGNA
NQYNFQQGYGQAGANTAAANLTSAAAAAASPATAHAQPQQQQPYGGSFM
PYAHFYQQSFYQGQPYGVAGQYPYQLPKNNYNYQTQNGQEQQSPNQG
VAQHSEDSQQKQSQQQQQQQPQGPQPEVQMONGQPVNPQQQMFFQQYYQ
FQQQQQAAAAAAQAQGVYGYNGYDYNKNSRFGY

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YLR311C, 848 bp, CDS: 501-848 (SEQ ID NO 283)

ACAAAACAGACTTAGTTATTTTATGGTATACAACAAAAGCTCGAATGAAA
GACGGTTGGCACAAGAGAATTAACAAAATAAACGGAGGAAGAATAAAGTT
ACACCTATTTCTCAAGAATCTTTTAAATCCGCTCAAGAAAGTTTAAGGG
TATTGCATAAAGAACAGAAACGCCGCTGGAAAAGGCTCTTTGTGCTACTT
CATAATAAATACAGGCAATTTTCTCCACATATTAAGAGGTATTTTCGATCA
TTCTTGCCAAAAAGCAAAACAATGTTGGTCGGGATCCAGATTGCAGTTGC
GCAAGCTTCGTTTCAAGTCAATGAAACCATTCCGAGTTTTTTCAGTTTAAG
GTTTCGCAAAGATACCAACTGGTTTGTAAAGCAGCTGAAACGGTTCGGATT
GAAATTACAGCATTTCGAGGATGTATAAAGCGATGTCAGAATGCAGGAAAA
AAAATTATTTTAAGTGCAAACTAGATCATCCAAAACCCAGCATGAAGA
ATGAAATTAACAAAAGAAAAAAGAAACGACTGCTTAGTAGGAGTGTCTATA
TATCCCTCCTTTAAATTTTTTACACTTACTTTTCTTTTTTTTATTGAGAA
TAGAAAAGGTGCATCTCTCTCTCTCTCTCTCTCTATCTCTATCTCTAAGG
TTTTATTACTTTCATAACGTATGCTATCCATCTCTTTTCTTTTTTTTTTG
TTTTGTATTCCCTTTTTTACTCAGTTAGATTCACTACTATATTTAC
ATATTCTTCGAAGCTTTTATGAGTTAAATATTTTGTGCTTTATGGGGCA
GAAAATAGTCGACGTCAGTCACCTCCAGGTTATTATGTAATTCGCTAA

YLR311C, 115 aa (SEQ ID NO 284)

MKLTKKKNDCLVGVSYIPPLNFFTLTFLFLRLRIKVHLSLSLSLSLSLR
FYFHNVCYPSLFLFFCFVIPFFYSVRFILLYLHLRSFYELNILLLYGA
ENSRRQSPPGYVIR

YMR107W, 848 bp, CDS: 501-848 (SEQ ID NO 309)

AGAGCAGAAATGATGAAGGGTGTAGCGCCGTCCACTGATGTGCCTGGTA
GTCAATGATTTACGTATAACTAACACATCATGAGGACGGCGCGTCACCCC
AACGCAAAAGAGTGACTTCCCTGCGCTTTGCCAAAACCCCATACATCGCC
ATCTGGCTCCTGGCAGGGCGGTGATGGACATCAGCCGCTCCCTTAATT
GCTAAAGCCTCCACAAGGCACAATTAAGCAATATTTCCGGAAAGTACACC
AGTCAGTTTGGCTTTTATGACTGGGTTCTAAGGTACTAGATGTGAAGTA
GTGGTGACAGAATCAGGGAGATAAGAGGGAGCAGGGTGGGGTAATGATGT
GCGATAACAATCTTGCTTGGCTAATCACCCCATATCTTGTAAGTGAATAT
ATAAATAGGAGCCTCCCTTCCATTTGCAACTCCATAAAATTTTTTTTGT
AGCCACTTCTGTAACAAGATAAATAAAACCAACTAATCGAGATATCAAT
ATGGGTAGTTTTTGGGACGCATTCGCAGTATACGACAAGAAAAAGCACGC
AGATCCAAGTGATATGAGGAAACCATAACAACACAGGAGACAGTAAAA
CGCAGGTTATGTTTTCGAAAGAGTACCGTCAACCTAGGACACATCAGCAA
GAGAACTTGCAGAGCATGAGAAGATCTTCATAGGATCACAGGACAGTTC
CGATGTTGAGGACGTTAAGGAAGGGAGATTACCCGAGAAGTAGAAATAC
CAAAGAATGTTGACATCTCTAACATGTCGCAAGGTGAGTTTTTTAAGACTT
TACGAAAGTTGAGGAGGGGGAACCCGACAATAAAGTAAATAGATAA

YMR107W, 115 aa (SEQ ID NO 310)

MGSFWDFAVYDKKKHADPSVYGGNHNNTGDSKTQVMFSKEYRQPRTHQQ
ENLQSMRRSSIGSQDSSDVEDVKEGRLPAEVEIPKNVDISNMSQGEFLRL
YESLRRGEPDNKVN

YKL066W, 944 bp, CDS: 501-944 (SEQ ID NO 243)

GAAAAACATCTCATAAATCATCCCTGGAAAAATGTCTAGTCAAACAGAAA
GAACTTTTATTGCGGTAAAACCAGATGGTGTCCAGAGGGGCTTAGTATCT
CAAATTCTATCTCGTTTTTGAAGAAAAAGGTTACAACTAGTTGCTATTAA
ATTAGTTAAAGCGGATGATAAATTAAGAGCAACATTACGCAGAGCATG
TTGGTAAACCATTTTTCCCAAAGATGGTATCCTTTATGAAGTCTGGTCCC
ATTTTGGCCACGGTCTGGGAGGGAAAAAGATGTGGTTAGACAAGGAAGAAC
TATCTTGGTGCTACTAATCCTTTGGGCAGTGCACCAGGTACCATTAGAG

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GTGATTTTCGGTATTGACCTAGGCAGAAACGTCTGTCACGGCAGTGATTCT
GTTGATAGCGCTGAACGTGAAATCAATTTGTGGTTTAAGAAGGAAGAGTT
AGTTGATTGGGAATCTAATCAAGCTAAGTGGATTATGAATGAATAACTT
ATGGCATGGGAGGGTACATATGAGCGCCTTTTTTTCTCGCTTTGGGCAG
CTCATATCATGTTCCCTCACTAGCTAATAATATAATGAATTTTTTAGAAG
GAGCACGATTATATAAAAAAATACCACTTATGTGCTACCCTTATATAC
GAATTTATAATACTTAATGACGCTTCAATGACGCCGTATGTCAAATGCTT
TTGGCTCCCACTGAAATTGCCACACTTCCCTCTCTTTCCGAACTTTATA
GTATCATCGAAAAATACAAGTTGGCAAAGGTCTATTACAATCGCGGAACG
TACGATGTTTCATACGGTTTTCAGCGAATAGTCTTGTAATATCCGGAAGCAT
GCCTACCGGCATTATTATAGGTAGTTCATCGCCCTTGGACTATGTAGGGG
TACAAGTAANTAGGCAACTTGAAATGGATCTCCCTATTGAATGA

YKL066W, 147 aa (SEQ ID NO 244)

MAWEGTYERLFFLALGSSYHVP SLANNIMNFLEGARLYKKNTTYVATLIY
EFIILNDASMTDPVKCFWLPVKLP HFLLLSELYSIIIEKYKLAKVYYNRGT
YDVHTVSANSLVISGSMTGIIIGSSSPLDYVGVQVNRQLEMDLPIE

YML053C, 1139 bp, CDS: 501-1139 (SEQ ID NO 295)

GAGGCGACACCTGCTAATGTTTACAATTTTCCCGATTGGGGTGCTAGAGG
CATAAGTGGGCTACATGGCACAGCACGGCAGTGCAGAGTGAGAAAATAT
GACTTCACGCTCGAGGCGAGGCCACGCTTTCGAAGCTTCGAATGCCACTA
CCTAGACCATTTGCTGTTTTGTACCTTCACGGTCCCATTAGAGACATTTTA
CTTAATGCAAGATTGCCATATCCGTTGTCATGGTACCAAACAGGGTAATA
ATTTCTAGAAATCATGATACACGTATGACATCTGGGTAACCTAATCCATC
TGGGTAACCGATTTTTCTCTCCCTTTGCTTTCTCTTTACCACCTCAGCTGA
CTTTATTATTTTTTTTATATTTTTCATTTTGACAAAATTATATAGTTAGG
AAGAATACAATAGGACTGCGACAGAAACAGATAAGGGCTCTTTTTTCTTG
GGGTTGGCTGCTTTTATTCAATTAATTTAAGACTCAAGTGTGCTGCGTGAA
ATGCTCTCATACTATGAACACAATACTGCGTTCCAAACAAACAATTGCAA
TTCCGGTAGCAATGCCGCCACTACATACAACAGCGACGCCAATAATGATA
CGATCATGAATAAAAGAAAAAATGACCATTTTCGAGTTTGATACACACACT
TTCTACCAAAGATCGAAGAGAACAAAACGAGATTCTGTAAGTACAAAGTT
TTCGGTTCGGTTCCGGGTGTGCTAATCTTAATAACAACAACAACAATCA
TCATCAACAACAACAACAACAATAATAATAATAATAACCATAATCAT
AATAACAGCAATAATACTGCAACCTACAATAATATTCAATTATAAAAAAAA
TATCGAAATATGTCCCCTGAAACCGGTTAGTATGCACCACACTATGAACA
GCCGCTTACTGAACGAATCTGAATTTTATTCTGAAACAGAAGAGTACATG
ATTCATGCTTATTTTCGGTAACACTAATCGCGACATAACAGGCACGAGTCC
TACTGGAAGTGTAGTATTATACAACACCAGTATCATCTTCTACCATCCC
AAAGTATAATTGCATCACAAGCACCCGGTACTGCCATGGCCGCGTTGACT
AACAACAATATCGCTAACGATTACATGGATATAGATTAA

YML053C, 212 aa (SEQ ID NO 296)

MLSYEHNATFQTNNCNSGSNAATTYN SDANNDTIMNKRKNDHFEFDHT
FYQRSKRTRDSVSTKFSVSGCANLNNNNNNNIIINNNNNNNNNNNNNH
NNSNNTATYNNIHYKKNIEICPLKPVSMHHTMNSRLINESEFYSETEEYM
IHGYFGNTNRDITGTSPTGSASIIQH QYHLLPSQSIIASQAPGTAMAALT
NNNIANDYMDID

YOR121C, 806 bp, CDS: 501-806 (SEQ ID NO 355)

GGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAACGA
AATTGGTGAAATTGTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCA
ATGGTTTGATATTCAAGGCCAAAAGTTCATGTTGTTGAGAGCTGACGAT
AGAAGTATCTACGGTAGACATGATGCTGAGGGTGTGTTTGTGTAAGAAC
TAAGCAAACCGTTATTATTGCTCATTATCCACCAACCGTACAAGCCGGTG

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AGGCCACCAAGATTGTCGAGCAATTGGCTGACTACTTGATTGGTGTTCAA
TACTAATTTATGCAGGTAAAGTTTTCTTGCCCTTATACACCACCTATTCTG
GCATCTGCGGGATTTCGCTTCCCTATTTTACAAATATTTTATTGATTGACG
CTAATTATCACTGTAAAAGGCGCACTTTTTATATGTAGTCACATCCGGTA
TTTAACATATTTACGAAACAGTCTTAAGAATATCGACATTTGATATACTT
ATGTTTAATTTATCTACATATTACAATCATACGAGAAACACGCAAAAACA
ATTACTTGAATACTTCGAAAGGAGACCAATTTGGATGTACAACCCTTTTT
TCGCCCTTTTCTTCGATATGTTATTGATAGCTTCAAAGTCCTCAGTAGA
CAAAGTAAATATTTTCTGTTGTTTTGATTTCGATCGGGATTACAGATT
TTGGCAAGACAACATAACCTCTTTGGACGTGCCAGCTAATAACAACGTGT
CCGGGTTGAACGTTATTTTTCTTCGCAATTTCAAGGATAACCGGTTCTTT
CAATAG

YOR121C, 101 aa (SEQ ID NO 356)

MFNLSTYYNHTRNTQKQLLEYFERRPIWMYNPFFALFLRYVIDSFKVLRS
QSKYFPVRFDSIGIHRFWQDNITSLDVPANNNVSGLNVIFLRNFKDNRFL
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)

ATATGGTTTCATCATTTTGTCTCAATTGTTCTCCATTTGGGTTACCTTTTT
TGCCAGTTGGTCGTACTTGAGGTTTTTCCAGAACTTGCACCCTTGAATT
GTCCCTCTTTGCCAACAATAATTCTCAAGGTGGTCAGGAAATATTGGTC
GGCGATGCATCTGATACTTTTCAATTGATTTACTTCTTTCTGATCTAAT
TAAGCCGATTTTGAGGCCGATTTTCAATTTTCAATTTATAATGTAGTTGTTG
TAAAATTTAAAGTCATTAAACCTTTTTCATGATATTGATATAGATATTGGG
AACACCATCGCAGAAAGTAGAGGCCCAAAAAAATTATGACTGTAGAAGA
AAGACGAAGACAGTTAGCTTTTACAAGTTTTGGAAGAGCGTATGGTAAACC
CTTGATATATGGATCTATATAACTTGAAATATGCTCTATTATATCGTGAT
TTAATGACGGCTGTTGGCATTTCGGTCTTTACCAAGGTAGTAGGATTTGT
ATGCTGAATGTGCGCCAGTACTATCGAACCATAGAAACCCATATATTCCC
CAATATTAATAATTCTACTGAGAAATGGGTGAATTTTGAAATAATTGTTG
GGATTCCATCGTTGATAAAGGCTATAATATTAGGTATACAGAATGTACTA
GAAGTTCTCCTCGATGATATAGGAATCCCATAATGGAATCTATATTTCT
ATGTACCAATATTACGATTATTCCTCATTCCATTTTCATATGTTTCATTAT
CCTATTACATTATCGATCCTTGCATTTTCAGCTTCTCTAACTTCGGTGAC
AGCTTCTATAATAACTTATGTCACTATCTAACACCGTATATGATAATATA
TTGA

YOL106W, 117 aa (SEQ ID NO 342)

MLNVRQYYRTIETHIFPNINNSTEKWVNFEEIVGIPSLIKAILGIQNVL
EVLDDDIGIPIMESIFLCTNITIIPHSISYVLSYIIDPCISASSNFGD
SFYNNLCHYLTPYMIY

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2:
947-1487 (SEQ ID NO 17)

CCGATGGAACGTTCTGAAAAAGAAGAATAATTTAATTACTTTCTCAACTAAAAATCTGGA
GAAAAACGCAATGACAGCTTCTAAACGTTCCGTGTGCTTTCTTTCTAGAATGTTCTGG
AAAGTTTACAACAATCCACAAGAACGAAATGCCGTTGACAATGATGAAACCATCATCCA
CACACCGCGCACACGTGCTTTATTTCTTTTTCTGAATTTTTTTTTTCCGCCATTTTCAAC
CAAGGAAATTTTTTTTCTTAGGGCTCAGAACCTGCAGGTGAAGAAGCGCTTTAGAAATCA
AAGCACAACGTAACAATTTGTCGACAACCGAGCCTTTGAAGAAAAAATTTTTCACATTGT
CGCCTCTAAATAAATAGTTTAAGGTTATCTACCCACTATATTTAGTTGGTCTTTTTTTT
TTCCTTCTACTCTTTTATCTTTTACCTCATGCTTTCTACCTTTCAGCACTGAAGAGTCCA
ACCGAATATATACACATAATGGCATCCACCGATTTCTCCAAGATTGAAACTTTGAAAC
AATTAAACGCTTCTTTGGCTGACAAGTCATACATTGAAGGGTATGTTCCGATTTAGTTTA

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CTTTATAGATCGTTGTTTTCTTTCTTTTTTTTTTTCCTATGGTTACATGTAAAGGGAA
GTTAACTAATAATGATTACTTTTTTCGCTTATGTGAATGATGAATTTAAATTCCTTTGGTC
CGTGTATTATGATGGGAAGTAAGACCCCGATATGAGTGACAAAAGAGATGTGGTTGACTA
TCACAGTATCTGACGATAGCACAGAGCAGAGTATCATTATTAGTTATCTGTTATTTTTTT
TTCCTTTTTTTGTTCAAAAAAGAAAGACAGAGTCTAAAGATTGCATTACAAGAAAAAGT
TCTCATTACTAACAAGCAAAATGTTTTGTTTCTCCTTTTAAAATAGTACTGCTGTTTCTC
AAGCTGACGTCACGTCTTCAAGGCTTTCCAATCTGCTTACCCAGAATTCTCCAGATGGT
TCAACCACATCGCTTCCAAGGCCGATGAATTGACTCTTTCCCAGCTGCCCTCTGCTGCCG
CTGCCGAAGAAGAAGAAGATGACGATGTGATTATTTCGGTTCCGACGATGAAGAAGCTG
ACGCTGAAGCTGAAAAGTTGAAGGCTGAAAGAATTGCCGCATACAACGCTAAGAAGGCTG
CTAAGCCAGCTAAGCCAGCTGCTAAGTCCATTGTCACTCTAGATGTCAAGCCATGGGATG
ATGAAACCAATTTGGAAGAAATGGTTGCTAACGTCAAGGCCATCGAAATGGAAGTTTGA
CCTGGGGTGCTACCAATTTATCCCAATTGGTTTCGGTATCAAGAAGTTGCAATTAAC
GTGTTGTGCAAGATGACAAGGTTTCCTTGGATGACTTGCAACAAAGCATTGAAGAAGACG
AAGACCACGTCCAATCTACCGATATTGCTGCTATGCAAAAATTATAA

>YAL003W, 206 aa (SEQ ID NO 18)

MASTDFSKIETLKLQNLASLADKSYIEGTAVSQADVTVFKAFQSAYPEFSRWFNHIASKAD
EFDSFPAASAAAAEEEEDDVDLFGSDDEEADAEAEKLKAERIAAYNAKKAAPAKPAK
SIVTLDVKPWDDETNL EEMVANVKA IEMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVS
LDDLQQSIEDEDHVQSTDIAMQKL

>YAL060W, 1649 bp, CDS: 501-1649 (SEQ ID NO 19)

AAAGACTACGAGAATCAATAACGAGGCTAAACTGCGTCACACATGATTGTGATTGAGTA
CTCACGTTCTCGTGTAAATCCCGCGGCTTCTTGTTTACTAACTTTTCTTTCTCTCATA
GCATTCTCTTGACAGTGTTPATATACATCATATGTACATTTATCGAGCCAATCGAGGGC
AGCAGTTTAAACATCAAGCCGGATTGCTCACGCTACTTTGACCCCTTTTCGTTTCGACGG
AGAGAAGAAACCGGTGTTTCTATCCTTGCCATTCTTTCTCCTTACGGGGTCTTAGC
CTGTTTCTCTTGATATGATAATAGGTGGAAACGTAGAAAAAAAATCGACATATAAAAGT
GGGGCAGATACTTCGTGTGACAATGGCCAATTCAAGCCCTTTGGGCAGATGTTGCCCTTC
TTCTTTCTTAAAAAGTCTTAGTACGATTGACCAAGTCAGAAAAAAAAGGAACT
AAAAAAAGTTTAAATTAATTATGAGAGCTTTGGCATATTTCAAGAAGGGTGATATTCCT
TCACTAATGATATCCCTAGGCCAGAAATCCAAACCGACGATGAGGTTATTATCGACGCTC
CTTGGTGTGGGATTGTGGCTCGGATCTTCACGAGTACTTGGATGGTCCAATCTTCATGC
CTAAAGATGGAGAGTGCCATAAATTATCCAACGCTGCTTTACCTCTGGCAATGGGCCATG
AGATGTCAGGAATTGTTTCCAAGGTGGTCCATAAGTGACAAAGGTGAAGGTTGGCGACC
ACGTGGTCTGTGATGCTGCCAGCAGTTGTGCGGACCTGCATTGCTGGCCACACTCCAAAT
TTTACAATTCCAAACCATGTGATGCTTGTGAGGGGAGTGAAGGTTGAGTACCCACG
CCGGTTTGTAGGACTAGGTGTGATCAGTGGTGGCTTTGCTGAACAAGTCGTAGTCTCTC
AACATCACATTATCCCGGTTCCAAAGGAAATTCCTCTAGATGTGGCTGCTTTAGTTGAGC
CTCTTTCTGTCACCTGGCATGCTGTTAAGATTCTGGTTTCAAAAAAGGCAGTTCAGCCT
TGGTTCTTGGTGCAGGTCCCATTTGGGTTGTGTACCATTTTGGTACTTAAAGGGAATGGGGG
CTAGTAAAAATTGTAGTGTCTGAAATTGCAGAGAGAAGAATAGAAATGGCCAAGAACTGG
GCGTTGAGGTGTTCAATCCCTCCAAGCACGGTCATAAATCTATAGAGATACTACGTGGTT
TGACCAAGAGCCATGATGGGTTTGATTACAGTTATGATTGTTCTGGTATTCAAGTTACTT
TCGAAACCTCTTTGAAGGCATTAAACATTCAAGGGGACAGCCACCAACATTGCAGTTTGGG
GTCCAAACCTGTCCCATTTCAACCAATGGATGTGACTCTCAAGAGAAAGTTATGACTG
GTTGATCGGCTATGTTGTGCAAGCCTTCAAGAAAGTTGTTGCTGCCATCCACAACGGAG
ACATCGCCATGGAAGATTGTAAGCAACTAATCACTGGTAAGCAAAGGATTGAGGACGGTT
GGGAAAAGGGATTCCAAGAGTTGATGGATCACAAGGAATCCAACGTTAAGATTCTATTGA
CGCCTAACATCACGGTGAATGAAGTAA

>YAL060W, 382 aa (SEQ ID NO 20)

MRALAYFKKGDHFTNDIPRPEIQTDDEVIIDVSWCGICGSDLHEYLDGPIFMPKDGEC
KLSNAALPLAMGHEMSGIVSKVGPVKTKVKVGDHVVDAASSCADLHCWPHSKFYNSKPC
DACQRGSENLC THAGFVGLGVISGGFAEQVVVSQHIIIPVPKEIPLDVAALVEPLSVTWH

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AVKISGFKKGSSALVLGAGPIGLCTILVLKGMGASKIVVSEIAERRIEMAKKLGVEVFNP
SKHGHKSIEILRGLTKSHDGFDSYDCSGIQVTFETSLKALTFKGTATNIAVWGPKPVPF
QPMDEVTLQEKVMTGSIGYVVEAFEEVVRAIHNGDIAMEDCKQLITGKQRIEDGWEKGFQE
LMDHKESNVKILLTPNNHGENK

>YBL058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)

TTATTTACATAGTGCCATTGAACACTTTTCAAGCAAACCTACGCCAGCCGGACGCAGACAA
TAACACACACACAAAAGAGTCTTGCAGGTTCTCTTTTAGCGGCAACGGGCATGACACTAG
GTATATTTGGTATGGGCATCACAGGGACATGTTGGAGCTGGGATGTTTCATCATTTTCAGG
AACTAAAGCAACGTCTGGAAAGCGTGCCAACAACGAATTTGTAGTGACAAACATGCCTC
TGGATAAAAGAAGCCAGCAAGTAGTGACAGCTTAGTTAAGACACACAATTCATCTCTTT
GTAAATAGTGTTATACCATAGTAGTAGTTTCAATAATATATATCCACTACTTATATGTGTT
ACCCGCATTAGAACTCTTATTTGGTGGCGAAAATCGATGGCAATAAAGAACGGAAAGGGGTT
TAATAGTTGTATGCTTAAACATATTTTCGATTTAAATATATAAGAAACGTCGGTAGCACAAC
AATTAACCTCATTATTTAGGTATGGCGGAAATACCTGATGAAACCATCCAGCAGTTTCATGG
CATTGACCAATGTGTCTGCATAACATAGCCGTTCAATATCTCTCTGAATTTGGAGATTTAA
ATGAAGCACTAAATTCCTATTATGCTTCTCAAACGGATGACCAAAAGGATAGAAGAGAGG
AAGCACATTGGAACAGACAGCAGGAGAAGGCCCTCAAGCAAGAAGCCTTCTCCACCAACT
CTTCGAATAAAGCCATAAATACGGAGCACGTTGGTGGGTATGTCCAAAACCAGGATCCT
CACAAGGTAGCAACGAGTACTTGAAGGAAAGGTTCTACCTCTCCTGAACCAACCAAGG
GTAGTAGCCGCTCTGGAAGTGGTAACAACCTCAGGTTTATGAGCTTTTCGGATATGGTAA
GAGGTCAAGCTGATGATGACGATGAAGATCAACCGAGAAATACTTTTGCTGGTGGTGAAA
CATCCGGCTTAGAGGTTACAGATCCTTCAGATCCTAATTCATTACTGAAGGATTTGCTGG
AAAAAGCGAGAAGGGGTGGTCAATGGGCGCTGAAAACGGATTCCGTGATGACGAAGACC
ATGAAATGGGTGCCAATAGGTTTACTGGAAGAGGTTTATGATTAGGGTCAACCATCGACG
CAGCAGATGAAGTCGTAGAAGACAACACTTCACAATCACAACGTAGACCAGAAAAAGTCA
CAAGAGAAATTACATTTTGGAAAGGAAGGTTTTCAAGTGGCCGATGGTCCGCTTTTATCGCT
ATGATGATCCTGCGAACAGTTTCTATTTGAGCGAGTTAAATCAAGGGAGGGCTCCATTAA
AGCTCTTAGATGTGCAATTTGGACAAGAAGTTGAAGTTAATGTATATAAAAAATTAGATG
AGTCTTATAAAGCTCCGACGAGAAAACTGGGCGGTTTTTCAGGCCAGGGCCAAAGACTAG
GATCTCCTATCCCGGGTGAATCGTCACCTGCGGAGGTTCCAAAGAATGAGACACCCGCTG
CTCAGGAACAACCCATGCCGGAACATGAGCCAAAACAAGGCGACACCTCCATCCAAATTA
GATACGCAATGGCAAAAGAGAAGTTTTGCACTGCAATTCACAGATACAGTAAAGTTTTT
TGTATGAGCATGTGACATCAAATGCGAACACTGACCCATCGAGGAATTTACCTTGAATT
ATGCCTTTCTATCAAACCAATAAGCAACGATGAGACAACATTGAAGGACGCTGATCTGC
TGAATCCGTTGTCGTGCAAAGATGGGCATGA

>YBL058W, 423 aa (SEQ ID NO 24)

MAEIPDETIQQFMALTNVSHNIAVQYLSEFGDLNEALNSYYASQTDQKDRREEAHWNRQ
QEKALKQEAFTSNSSNKAINTEHVGGLCPKPGSSQGSNEYLRKKGSTSPPTKGSRRSGS
GNNSRFMSFSMDMVRGQADDDDEDQPRNTFAGGETSGLEVTDPSDPNSLLKDLLEKARRGG
QMGAEANGFRDDEDHEMGANRFTGRGFRLGSTIDADEVVEDNTSQSQRPEKVTREITFW
KEGFQVADGPLYRYDDPANSFYLSELNQGRAPLKLDDVQFGQEVEVNVYKKLDESYKAPT
RKLGGFSGQGRLGSPIPGESSPAEVPKNETPAAQEQPMPDNEPKQGDTSIQIRYANGKR
EVLHCNSTDTVKFLYEHVTSNANTDPSRNFTLNYAFPIKPISNDETTLKDADLLNSVVVQ
RWA

>YBR039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)

TTGAGATTTTCCAAGTAGTAACCTCATCTTTCTGAGTGTGCTATCAAATACATACTAAGGA
GAATAAAGCTTTGTTATTACGTATTCTTCATCCTTATGGGTAGAGAGCGCACTGTTTTAG
TACATTTTCTAGACGTGCAACGTAGAGCAATTGTCGATAAAACAAAAAAGTAAGAA
GATATATGAATAGGACGTGTCGCTAGAACTAGTAAGTATATGATGGAGATATAATAAGTG
AATTATTCGATATTTAATGAACGTTCTCATTTATTTGGAAGAAATGTTTATCACGTGATG
GAGAACCAATGAGCGGCGAGTAACCTACGCGAGGAACCCGACCGCAATAACGATTAAAGA
AGGCCCGGAAGGGAGATGCTTAAATGATTATCACTCAGTTAAAAAAGACAAATAAGAAAC
TATTGAGACTGAACCGTTTTGGTTAATTTTCAGGTGGAAACAATTGAAGACGAGCAGTAAA

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CATTATTTTATTTAGTAGTCATGTTGTCAAGAATTGTATCAAACAATGCAACAAGCTCCG
TAATGTGCCACCAAGCGCAAGTGGGTATTCTTTATAAGACTAACCCAGTGAGAACTTATG
CTACTTTTGAAAGAAGTGGAAATGCGTTTGAAATCTATCAAAAATATTGAGAAGATCACAA
AAACTATGAAGATTGTTGCATCTACAAGATTGAGTAAAGCTGAAAAGGCTAAAATTTCCG
CAAAGAAGATGGATGAAGCAGAGCAGTTGTTTTACAAGAACGCCGAAACCAAAAATTTGG
ATGTTGAGGCTACTGAAACAGGTGCTCCTAAAGAGTTGATTGTTGCTATCACCTCTGATA
AGGGGTTGTGTGGTTCTATCCACTCTCAATTGGCTAAAGCTGTGAGAAGACATTTGAATG
ATCAACCAAACGCCGATATAGTCACTATTGGTGATAAAATTAAAATGCAGCTATTGAGAA
CCCATCCTAACAACATTAAATTGTCTATTAATGGAATTGGTAAAGATGCCCCAACTTTCC
AAGAATCTGCTTTGATTGCCGATAAGTTATTGAGTGTGATGAAGGCCGGCACTTACCCAA
AGATTTCCATTTTCTACAATGACCCAGTGTCTTCCCTATCTTTTGAACCATCTGAAAAAC
CGATCTTTAACGCCAAGACCATTGAACAATCCCCATCATTTCGGCAAATTTGAGATCGACA
CGGACGCAAACGTTCCAAGAGATTTGTTTGAATATACTTTGGCTAACCAAATGTTGACAG
CAATGGCTCAAGGTTATGCTGCTGAAATTTCCGCCAGAAGAAACGCTATGGATAACGCTT
CCAAGAATGCCGGTGATATGATCAATCGTTACTCTATCTTGTACAACAGAACAAGACAAG
CTGTCAATTACTAATGAACGTTGATATTATTACTGGTGCTTCCTCTTTGGGATGA

>YBR039W, 311 aa (SEQ ID NO 42)

MLSRIVSNNATRSVMCHQAQVGILYKTNPVRTYATLKEVEMRLKSIKNIKITKTMKIVA
STRLSKAEEKAKISAKKMDAEQLFYKNAETKNLDVEATETGAPKELIVAITSDKGLCGSI
HSQLAKAVRRHLNDQPNADIVTIGDKIKMQLLRTHPNNIKLSINGIGKDAPTFQESALIA
DKLLSVMKAGTYPKISIFYNDPVSSLSFEPSEKPIFNAKTIEQSPSFGEIDTDANVPR
DLFEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNEL
VDIITGASSLG

>YBR062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)

CCATTTTGGTGACCAACTCTCCTACCCGAATTACTGTGATGATATATACTCTTCGTTTTTC
TAGTAATGGCTTCTATTTGCTTAAGTTGGTCAAAATTTGTTGTGGGCGGC'TTTGTTTGCA
CCGAGGAGCGCTCAGTTCTGTTATAATACCAGTTTTGCCACTCCTAAACTACTAAAGAAAT
AATAGAAAGATATATTCATCAAACATAATCACAATCAAAAAATGTCTACATATGAAGGT
ATGTAATGATATATTATGAAGTAAGTTCCCCAAAGCCAATTAACTAACCGAATTTTAATC
TGCACCTCATCATTAGATTAGAGGAACATGGAATACAACAAAACCAAGGGATTACCAAGA
AGTAGGAGGAAC'TTACAGGAGGAGCAGAGAAGACAGGTCAAGATCCCAACTGCAAGGTC
TATTT'CAAAAC'TTTGGTAACACCAGTGGTGAGGGTGATGCACATTAGATTCAACACTAC
TTTTACGATTATTATCGCAAATGCTTCCAGAATCATTACAGGAAGAATGGTTGCAAGAAA
TGGATAAAGGCAAGAGTGC'GGGCTGTCTTGATACTTTTGCAGCCTCTTTACCACGAATCA
ATAAAAAAAGCTCAAAGCAACTGACAAC'TGCTCCATTTGTTACACTAATTATTTAGAAG
ATGAGTACCCCTTAGTAGTTGAATTACCTCATTGCCATCATAAGTTTCGACTTAGAGTGT
TGTCTGTCTGGCTATCTCGAAGTACAACATGTCCATTATGCAGAGATAATGTTATGGGCC
ACCGAATCATTATGAGATTGATACAAC'TGAAGCAGAACTGGAAGAAGATTGGGGTATGT
ACGGTTAA

>YBR062C, 115 aa (SEQ ID NO 46)

MLPESLQEEWLQEMDKGSAGCPDTFAASLPRINKKKLKATDNCISICYTNYLEDEYPLVV
ELPHCHHKFDLECLSVWLSRSTTCPLCRDNVMGHRIINEIDTTEAELEEDWGMYG

>YBR101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)

AATGATGAAATGTTATCCCCAGGGTCCATTAAAGTCATCCAGAAAACAGATAGATGGATTG
AAGGCCGTAGGTTTGGATTTTGTCTACAAATTGGACGAGTTTATCAAAAAGAACAGTGAT
AAAATTCGCTAAACAAGATCACAGAAAATAAACCTCACTTCAATATATATGATGTGTAGG
TAGGGTATATACTTATAACCACTGCTGTGACAGTGTACTAACCTATTTCTATTTTGTAG
GTAAGCTTTTCAGCTACTGGTTGGTCAAGTTGGGCCCTATTAAGGTTGTAATCAGCTTAT
TCGTTTGAAATGATATACCTCTTGGACTGGAATCTTCTGGAAGTTTTTTGGAGGTTAGAA
AAGAGGAAGGCATCTCGCGCTGACAGAAATTTGCTTATAAACCAGCGATTGGCTATATCT
AAAAGAGCACTCATCGTCAGTCAGAAAGCCATTACCTTTCAACGAAAGAGTAAAAATAGAA
AAAAAACACATACATAACTATGGAAGGCTATTACAGTGGTCTATTGCGAATTCCTCAAG

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GGGACAAAGAAGCTATGGCTAGGGCCGGCCAACCTGATCCTAAATTGCTACAGCAGTTAT
TCGGTGGTGGTGGTCCTGACGATCCAACCTTAATGAAAGAAATCCATGGCTGTTATTATGA
ATCCGGAGGTTGACTTAGAAAACAAAACCTCGTTGCATTTGACAACTTTGAAATGTTGATTG
AGAACTTAGATAATGCTAATAATATCGAAAATTTAAACTGTGGGAGCCATTGTTGGATG
TTCTTGTTCAGACGAAGGATGAAGAACTACGTGCTGCTGCTTTATCCATTATTGGAACGG
CTGTGCAAAACAACTTGGATTTCGAAAATAATTTTCATGAAATACGACAATGGTCTGCGAA
GCCTTATCGAAATAGCTAGTGACAAGACAAAGCCACTCGACGTGAGAACAAAAGCTTTTT
ACGCACTATCTAATCTAATAAGAAACCACAAAGATATCTCAGAAAAGTTTTTCAAATTAA
ATGGGCTCGACTGCATAGCACCTGTATTAAGTGATAACACCGCCAAACCAAACTGAAAA
TGAGAGCCATTGCCTTATTGACCGCATATTTGTTCATCTGTTAAGATTGATGAAAATATAA
TCAGTGTGCTGAGAAAAGGATGGAGTAATTGAAAGTACGATTGAGTGCTTGTCTGACGAGA
GTAACCTTGAACATCATAGATAGAGTTCTGTCTTTTCTCTCTCACCTGATATCTTCCGGAA
TAAAATTTAATGAACAGGAATTGCACAAATTGAACGAAGGTTACAAACATATCGAGCCTC
TAAAGGACAGACTTAATGAAGACGATTATTTAGCCGTAAAGTATGTATTATGA

>YBR101C, 290 aa (SEQ ID NO 50)

MEKLLQWSIANSGDKEAMARAGQPDPKLLQQLFGGGGPDDPTLMKESMAVIMNPEVDLE
TKLVAFDNFEMLIENLDNANNIENLKLWEPLLDVLVQTKDEELRAAALSIIGTAVQNNLD
SQNNFMKYDNGRLSLIEIASDKTKPLDVRTKAFYALSNLIRNHKDI SEKF FKLNLGLDCIA
PVLSDNTAKPKLKMRAIALLTAYLSSVKIDENIISVLRKDGVIESTIECLSDENLNIID
RVLSFSLSHLISSGIKFNEQELHKLNEGYKHIEPLKDRLNEDDYLA VKYVL

>YBR139W, 2027 bp, CDS: 501-2027 (SEQ ID NO 55)

GGAGGAGTCAAGGGCCTGGAAAGTACGGATCCTGTAGAAATATCACTGGCAATTATACTG
AGTTTATTGTTGGTGTGTGCTATTCATATTTGAGCTGGTATTGGACGAAAGCAAGGATAAT
GAGTTTGTGTCTACTGACTCCAACACCCTAGGCTGGATTGATCTTTCTCCATCCTTTAA
TTTTAACCTTTTAATTAGTGGTTGGATCAAGTTTTCGAGACTATTCCAATCTGTGACTGT
TTGGATAAAATAGTTTTTGACTCGTTTAGTATAATCCTTTTTCTAAAAAGTGCTTAGAGTT
CTCTAAGATGTTCTTGTTFACAATGTGAGCGATTTAGGAAATTTCTTAAAAATGGCCGAG
GCGGCGCTAGCATTTCTACGAAAGGTGAGATAACGCTTCGTTATCGAAAAATGTCAGGGGA
CAGGGGTATATAAGAACGAAAATGTGCATCCTGCATTTTTCTTTAAAAACAGCTATACA
AAAAGTGATACCGACATACAATGAAGTATCTAAACTTAGTTTTCTGTGCTTCAGCTTCTTA
TTAGCATCAAATACGCCTCATTCGGCCGAGCCTTTTCTCTTTTGAAGATGATACCACCT
TTGCCAATTTGGATAAACAGCTAAAGCTTCACAGAATACACAGCAAACCTTTAAATTGG
ACCGTTTGAATCACGATGATCCGCTGTTTACAACTTTTATTTCTTCTGTGGACACAGATT
ACAGTTTGAGACTTAGAACAGTAGATCCTTCTAAACTAGGAATTGACACCGTAAACAAT
GGTCGGGTACATGGACTATAAGGATTTCCAAACACTTTTTTTACTGGTTTTTTTGAAAGTA
GGAACGATCCTGCTAACGACCCAAATTATTCCTTTGGTTAAATGGTGGACCTGGTTGTTCCT
CGTTTACTGGGTGCTATTTGAACTAGGCCCTCATCAATTGGCGCCGATATGAAACCAA
TCCACAATCCCTATTCCTTGAATAATAACGCTTCAATGATCTTCTTAGAACAGCCACTCG
GAGTCGGCTTTTCTATGGTGATGAAAAAGTCTCTCTACAAAAATTAGCAGGCAAAGATG
CGTACATTTTCTTGGAATTGTTTTTTGAAGCTTTTCTCATTTACGCTCCAACGATTTCC
ACATTGCAGGCGAATCCATATGCAGGACATTATATCCCTCAAATTGCACATGAGATCGTTG
TCAAGAACCCCTGAAAGAACGTTCAATTTAACTTCAGTTATGATTGGTAATGGTATCACAG
ACCCTTTGATTCAAGCAGATTATTTATGAACCAATGGCATGCGGGAAAGGGGGCTATCACC
CTGTCTCTCATCAGAAGAATGTGAGAAAATGAGTAAAGCTGCAGGTCTGTGCTAGGT
TGAACAAGTTATGTTATGCTTCTAAATCAAGTTTACCATGCATAGTCGCCACTGCTTACT
GTGACTCTGCACTTTTTGAACCGTACATTAACACAGGACTCAACGTCTATGACATTAGAG
GGCCCTGTGAAGATAATAGTACTGATGGTATGTGTTATACAGGTCTCCGCTATGTCGACC
AGTATATGAATTTTCTTGAAGTTCAAGAAACGCTAGGGTCCGACGTGCATAATTATTCCTG
GCTGTGATAATGACGTGTTACCCGATTTTTGTTTACGGGCGATGGAAGTAAACCATTTC
AACAATATATTGCTGAATTATTAATCACAACATTCCGGTATTAATATATGCGGGTGATA
AGGATTATATTTGTAATTGGCTGGGAAACCATGCTTGGTCCAATGAGTTGGAATGGATCA
ATAAACGTAGGTATCAGAGAAGGATGTTAAGACCATGGGTCAAGTAAAGAAACAGGTGAAG
AGTTGGGACAAGTCAAGAACTATGGCCCTTTACCTTTTTGAGAATATACGATGCCGGTC
ATATGGTGCCCTATGATCAACCGGAGGCAAGTTTGGAAATGGTCAACAGTTGGATTTCCG

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GTAATCGTGCTTTTTTCGGATCTTTCCACCTTGGAATGCTAGTTAG

>YBR139W, 508 aa (SEQ ID NO 56)

MKYLNLFVFLQLLISIKYASFGRAFSLFEDDTTFANLDKQLKLQNTQOTLKLDRNLNHHDD
PLFTTFISSVDTDYSLRLRTVDPSKLGIDTVKQWSGYMDYKDSKHFFYWFFESRNDPAND
PIILWLNGGPGCSSFTGLLFELGPSSIGADMKPIHNPYSWNNNASMIFLEQPLGVGFSGY
DEKVSSTKLAKGDAYIFLELFFFAFPHLRSNDFHIAGESYAGHYIPQIAHEIVVKNPERT
FNLTSVMIGNGITDPLIQADYYEPMACGKGGYHPVLSSECEKMSKAAGRCRRLNKL CYA
SKSSSLPCIVATAYCDSALLEPYINTGLNVYDIRGPCEDNSTDGMCYTGLRYVDQYMNFP
VQETLGSVDHNYSGCDNDVFTGFLFTGDGSKPFQYIAELLNHNIPVLIYAGDKDYICNW
LGNHAWSNELEWINKRRYQRRMLRPWVSKETGEELGQVKNYGPFTFLRIYDAGHMVPYDQ
PEASLEMVNSWISGNRAFSDLSTLENAS

>YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)

TGCACATGTTGAGTATGCGTATTGGGCATTTCCTATTCTGAGAAGGAGTATGAAATAAT
TGCCGAGGGTTCAGAATGCTCTTTTAGAAATAAAATGAATGTAAATAGTTGGAATGTAT
CTTTAAGTAGACAAATGCAGGTAAGTTTATGAGTGGCCTTTGCGGATTAACAGTATGCTCTT
AGTGCAAAACACGAAAAGAGCTCCCAATCTTTGAACACAATCGACCACGGAGGAACAATA
CACGTAGAAGGGGATAACTAAACCTTTGTCGTGCAAGAGTATTGGAGGACACACTAACAG
CAGAACCTTTGCCCTTCTTAACCTCTTGTATTATGATTGCTTGAAGTATTACACATGTAATAAA
AGATGATTATTTTTTTTTTCTTAAAAAAGTTCTTTCTTTGAAGATCCCCCTGATAAAA
AAGATCAATAATGGAAACGCTAATCATAATCAAATCGGGAGGAGAAATAAACGCAAGAAG
TGTGCGTTTCTAGCTGAGTAATGGTGACAAGACATAGAGTGACTGTACTCTACAATGCC
CTGAGGATATCGGTAATCATATGCGCCAAAATGACACTCATTTGACTGTTCTGTTGGAGGTT
CTGGTGTGGTTTACAAACAAAGGTGGCTATTAGAGAGGACTGGAAGCTTGGATAAATCCT
TTACGAGAATCACTTTGGAGGCCAGAGCGGACTTGGCTAGAAGTTTAAGCGTTATAGAAA
ATGAAC TGAGTGTGGCTTTTTCAGTTTACTCAAATCTTTCGGATGTGCCGGAAGGTTTA
TTACTAACCCAGTCTACAATTCATTTACAGTGAGAAGTTTGACATAGAGCAGTACTTGC
CTCCCGAAGTAGATTGAATCTGTCTATGGAATCCAGAAGATTTTACATATGATATATCAG
TGGAGCCACACAAATCCAAATTGTTGAATATCGTCTGTTGAAACAGGGTGAAGAATTTA
CAATTGCAAGAGTGAAAGATGAGAAACTCGAAGTAGGTGTATTCTTTGTGGATGCAAGTG
ATGAAAGTGATGTCGATATTGGTGGAATACGTTGTAATTGGAGGATGGACGATGGTAAAA
TGGAAAGATGTCAGAAAACATCCTTATTGTATAAACAGGGCCATATCGCATACAATCACT
CGACGACTACGACATCACTATATCTGAATGAACCTATCGGTTTGCATCCAAAAATCATGA
TTGATCTCACAGATTTTGAAGAAGCCCTAAATGCATGTATCTAATGCACCTGCAATTGC
CGTTAGAATTATTTATCGATAAATCCAATCCTCTCCCTTACTACTTTTGGAGAAGACG
ACTTAGAATTACCAGAATACTCTCTTCGAGATAAGGCATGGGGTTCTGAAAGTATCTTTG
AATTGAAAGCCGGCACAATGAATGAAGTGACATTGCATAGATATATTGAGCCTTCTA
ATAATAAAGGGGATAAATTAGAAGTTTCATTTGATCCAGAAGTTATATTAGCCTGCGACA
CAGGTGACAATAAAGTTTCCCGTAATCCATTTTATAAAAAAGGTCTAGGATATGAATCTC
TCTTTACAGACGATACTACATTCGCCCATTTGAACTCGACAACCTTTCTAGTACCAATTC
CAAGGCC TGACACAAAGGATTATTCCAAGATCAAAAATGGTACGTTACTATGCTTACTCA
TCTCCATCATATACATTTTCTCCAAGGTATTTGGTAACAACAAGAAGAAAAGATCAGTAA
AACGGGAATAA

>YCL052C, 416 aa (SEQ ID NO 68)

MVTRHRVTVLYNAPEDIGNHMRQNDTHLTVRGGSGVVLQQRWLLERTGSLDKSFTRITWR
PRADLARSLSVIENELSGFSVYSNSSDVPERFITNPVYNSFHSEKFDIEQYLPPEVDLN
LSWNPEDFTYDISVEPTQIQIVEYRLKQGEFTIARVKDEKLEVGVFFVDASDESVDI
GGIRCNRMRDDGKMERCQKTSLLYKQGHIAYNHSTTTTSLYLNPIGLHPKIMIDLDFE
ERPCKMYLMLHLQLPLELFDKFQSSPLLLFGEDDLELPEYSLRDKAWGSESIFELKAGTM
NEVTLHTRYIEPSNNKGDKLEVSDPEVILACDTGDNKVS RNP FYKGLGYESLFTDDTT
FRHLNSTLLVPIPRPDTKDYSKIKNGTLLCLLISIIYIFSKVFGNNKKRSVKRE

>YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)

GTACAAAAATGATTACGAAAATATAGATGATGTAAGCAAGGTACGGTTATAAACAGTTAA

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CATATAAGTTTACTTCACTTTTTTGCTGACTCCTTTACTTGTCTTCCCTGCACTTTGATT
TTACTTCAGAAAAATAAGATATATGTTTCTGATAAACTTTTAGGTTAGCGGAGAAGAT
GTTGCCACGAATATCATGTAATTGAAAGGCAACGAAAGGTCTATCGTTTGCCATTCATAA
TGTGATTCGACTTGTCTTTTTTCATTGTAACAGACATGAAACGTTTCCTTTACGTCCCTAT
GAATTTTTGTTGGCTGAACTGGGCGCTGCAGGGGCTGGACGATCCAAATGCGCGGATTTT
GAACAATTATGAGAATCCGAATTTAAAGAAAGGGAAAAACAAATTTAATAACAGGCAGACG
TGAGAGAAGAAAAGGAAACGCTGTGATATAGAAAACATACAAATCCTATTATAAGAAGC
CAGAAGAAAGCTGATACAAAGATGAGTTGGGAAGGTTTAAAGAAAGCTATCAACAGAGCTG
GTCACAGTGTGATAATTAAAGAAAGTGCACAAGACCATGATAAAGAGTATGACATGGAAG
AAGTCGTTATAAAAGTTCTTCAAAGAGCAGGTGAGGCATTACAAAAGGAAGCCAAAGGTT
TCTTGGACTCATGTGAGAGCTGTGACAGCATCACAGACTACCATTGCCGAGGTCATCTCTA
ACCTCTATGACGATTCAAATATGTTGCTGGTGGTGGTTACAACGTTGGTAACATATTATT
TGCAATGTGTTCAAGATTTTGATAGCGAACTGTTAAGCAATTAGACGGGCCCTTAAGAG
AAACCGTACTAGATCCAATAACAAAGTTTTTCGACGTATTTCAAAGAAATTGAGGAGGCCA
TAAAAAGAGAGACCATAAGAAACAAGACTTCGATGCTGCGAAGGCAAAAGTTTCGTAGAT
TAGTGGACAAACCTGCTAAAGATGCCCTCTAAACTGCCAAGGGCTGAAAAAGAAATTGAGCT
TAGCTAAAGATATTTTCGAAAATCTTAATAACCAATTGAAAACCTGAACCTACCACAGTTAG
TTTCATTAAGAGTACCTTACTTTGACCCAAGTTTTGAAGCTTTAATCAAGATTCAGCTAA
GGTTCGTACTGATGGTTACACTCGTTTAGCGCAGATTCACCAATATTTGGACCAACAAT
CAAGAGACGACTATGCCAATGGGTTATTAGACACTAAAATCGAAGAACTATTAGGACAAA
TGACAAGCCTAGATATTTGTGCGCTCGGGATAAAATAA

>YCR009C, 265 aa (SEQ ID NO 74)

MSWEGFKKAINRAGHSVIIKNVDKIDKEYDMEERRYKVLQRAGEALQKEAKGFLDSLRA
VTASQTTIAEVISNLYDDSKYVAGGGYNVGNYYLQCVQDFDSETVKQLDGPLRETVDPI
TKFSTYTFKEIEEAIIKKRDHKQDFDAKAKVRRLLVDKPAKDASKLPRAEKELSLAKDIFE
NLNNQLKTELPQLVSLRPYFDPFSFEALIKIQLRFCTDGYTRLAQIQYLDQQSRDDYAN
GLLDTKIEELLGQMTSLDICALGIK

>YCR010C, 1352 bp, CDS: 501-1352 (SEQ ID NO 75)

GAGCTCCGTGGAATAGGCGAGCGGCTGAGTGGTTCTCCAAGCTACGGTTTTTACGTGTAG
CCCCATGTGAGCAAGCCAAACAAGGGCCCTTAAAGGCGTGACTACAAAAGGGGCGGGTT
GGAAGGTCATCTGCAGCGAGATACGAAAAGATTTTTTGCCAGATTTGCGGTTGGGCGGCT
ATTTTCGGTATTGTTGGGGTAACAAACGTTGGGGAAGACTGCATTTTCTTACAGCTTTTTT
TCGTTATCGCGGGTTGGGCGGCTATGGCGCCTTCTCCTCTGTACTCCAACCTGTCAGAGA
CACCAAGCTGTATATAAAGCACCTTGGTTGGATCGTATTTCCCTGAGATCTTGCTATAGG
TTCATTTTATATATCGTCCAATAGCAATAACAATACAACAGAACTACTAGCATCTGTTT
ATAAGAAAAAGGCAATAGTCGACAGCTAACACAGATATAACTAAACAACCACAAAACAA
CTCATATACAAACAAATAATATGTCTGACAAGGAACAAACGAGCGGAAACACAGATTTGG
AGAATGCACCAGCAGGATACTATAGTTCCCATGATAACGACGTTAATGGCGTTGCAGAAG
ATGAACGTCATCTCATGATTCGTTGGGCAAGATTTACACTGGAGGTGATAACAATGAAT
ATATCTATATTGGGCGTCAAAAGTTTTTGAAGAGCGACTTATACCAAGCCTTTGGTGGTA
CCTTGAATCCAGGGTTAGCTCCTGCTCCAGTGACAAATTTGCTAATCCTGCGCCCTTAG
GTCTTTTACGCCTTCGCGTTGACGACATTTGTGCTGTCCATGTTCAATGCGAGAGCGCAAG
GGATCACTGTTTCTAATGTTGTCGTCGGTTGTGCTATGTTTTATGGTGGTTTGGTGCAAT
TGATTGCTGGTATTTGGGAGATAGCTTTGGAAAATACTTTTGGTGGTACCGCATPATGTT
CTTACGGTGGGTTTTGGTTGAGTTTCGCTGCAATTTACATTCCCTTGGTTTGGTATCTTGG
AAGCTTACGAAGACAATGAATCTGATTTGAATAATGCTTTAGGATTTTATTTGTTGGGGT
GGCCATCTTTACGTTTGGTTTAAACGTTTGTACCATGAAATCCACTGTTATGTTCTTTT
TGTTGTTCTTCTTACTAGCATTAACCTTCTTACTGTTGTCTATTGGTCACTTTGCTAATA
GACTTGGTGTCAAGAGCTGGTGGTGTCTGGGAGTTGTTGTTGCTTTTCATTGCTTGGT
ACAACGCATATGCAGGTGTTGCTACAAAGCAGAAATTCATATGTACTGGCTCGTCCATTC
CATTACCATCTACTGAAAGGGTAATCTTTTAA

>YCR010C, 283 aa (SEQ ID NO 76)

MSDKEQTSNGNTDLENAPAGYSSHDNDVNGVAEDERPSHSLGKIYTGDNNEYIYIGRQ

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KFLKSDLYQAFGGTLNPG LAPAPVHKFANPAPLGLSAFALTTFVL SMFNARAQGITVPNV
VVG CAMFYGGVLVQLIAGIWEIALENTFGGTALCSYGGFWLSFAAIYIPWFGILEAYEDNE
SDLNNALGFYLLGWAIETFGLTVC TMKSTVMFLLFLLALTFLLLSIGHFANRLGVTRA
GGVLGVVVAFI AWYNAYAGVATKQNSYVLARPFPLPSTERVIF

>YCR021C, 1499 bp, CDS: 501-1499 (SEQ ID NO 79)

ATCGAAAGCGTGCTTTGTGAAGAATATTTGGTATGGCTAAAGTAAGCAAAGCCATATCCCG
ATCCCGATCCCGACTCTTATTCGGATCCCTTCCGCCACATCCTGCATGTTTATTCGAATA
CCAAATTAGCTCATCTTCGTTATTTTCATCATCCCTTTCTGCTATGGCAAGGACAAAGTTT
TTTCTAGCATCTCATCGAAAACCTTCTCTCCCTAATTGGCCAAAGTTTTCATATTCATC
ATCAGTTAGAAAGTATAATATCAATCCCTTACCTCATTAACAAGTTGTATCACACTAAAAA
AATCATATATAAGTCTGTGAGAGTCTTCAATTATTTAGCGTAACACCTATTCACCTTTCTA
ATCTTGTTTCTTGTTTTTACATTCTGCAATACAACACAACAACAAATATTAACCTCAATTA
TTATTATTTTATAATTACAAAAACAAAACAACAAGTTTGAGACTTTAATATCTTTTGATTA
CTAAAAACAACAAATTTCAAATGAACGATACGCTATCAAGCTTTTTAAATCGTAACGAGG
CTTTAGGGCTTAATCCACCACATGGCCTGGATATGCACATTACCAAGAGAGGTTCCGGATT
GGTTATGGGCAGTGTTTGCAGTCTTTGGCTTTATATTGCTATGCTATGTTGTGATGTTCT
TCATTGCGGAGAACAAGGGCTCCAGATTGACTAGATATGCCCTTAGCTCCTGCATTTTTGA
TCACTTTCTTTGAATTTTTTGCTTTCTTCACTTATGCTTCTGATTTAGGTTGGACTGGTG
TTCAAGCTGAATTTAACCACGTCAAGGTTAGCAAGTCTATCACAGGTGAAGTTCCCGGTA
TTAGACAAATCTTTTACTCGAAATATATTGCCTGGTCTTGTCTGGCCATGCCTTTTAT
TTTTAATCGAGTTAGCCGCTAGTACTACTGGTGAGAATGACGACATTTCCGCCTTGGATA
TGGTACATTCCGTGTTAATTCAAATCGTGGGTACCTTATTCTGGGTTGTTTCGCTATTAG
TTGGTTCATTGATCAAGTCCACCTACAAGTGGGGTTATTACACCATGGTGTGCTGCTGCTA
TGTTGGTTACCAAGGTGTGATATGCCAACGTCAATTCTTCAATTTGAAAAC TAGAGGGT
TCAATGCACCTTATGCTGTGTACCTGCATGGTAATCGTTTGGTTGTACTTTATCTGTTGGG
GTCTAAGTGATGGTGGTAACCGTATTCAACCAGACGGTGAGGCTATCTTTTATGGTGT
TGGATTTATGTGATTTTGCCATTTATCCATGTTACTTGCTAATTGCAGTCAGCCGTGATG
GCAAATTGCCAAGGCTATCTTTGACAGGAGGATTCTCTCATCACCATGCTACGGACGATG
TGGAAGATGCGGCTCTTGAAACAAAAGAAGCTGTTCCAGAGAGCCCAAGAGCATCTGGAG
AGACTGCAATCCACGAACCCGAACCTGAAGCAGAGCAAGCTGTGGAAGATACTGCTTAG

>YCR021C, 332 aa (SEQ ID NO 80)

MNDTLSSFLNRNEALGLNPPHGLDMHITKRGS DWLWAVFAVFGFILLCYVVMFFIAENKG
SRLTRYALAPAF LITFEFFAFFTYASDLGWTGVQAEFNHVKVSKSITGEVPGIRQIFYS
KYIAWFLSWPCLLFLIELAASTTGENDDISALDMVHSLLIQIVGTLFWVVSLLVGS LIKS
TYKWGYTIGAVAMLVTQGVICQRQFFNLKTRGFNALMLCTCMVIVWLYFICWGLSDGGN
RIQPDGEAIFYGVLDLCVFAIYPCYLLIAVSRDGLPRLSLTGGF SHHHATDDVEDAAPE
TKEAVPESPRASGETAIHEPEPEAEQAVEDTA

>YDR073W, 1010 bp, CDS: 501-1010 (SEQ ID NO 91)

GTTAGCTTGCTTGCATTTCCCATGCGTCTCGAATAGGAATTATTCAAGATGGATTATT
GGCATTTACGAGTAACCAAGGATAACCCCGCTGTGCGTGAAACCACCCTCTTTTACAGTT
TCTTCAAGGCCAGTGCAAACGCGAATAAACATATCTACGCTATATATAGATATGACGTTT
CTCAAGCCAACAGAAGTAGATAAAGCAGCCAGGAGGGTAGAGAGTGTTCAAATTATAGCA
AGCCTTCTTCTACCTGTTTTTTTTTGTGATGATTGTTTTGCCGGGTAACAATCGACTTTCGG
GCAAATTTTTTTTCTTTTTTCTCCTAACAGTATATACGGAGTGAGAAACAGACTTCCCA
TAAAAGCATATTACGTGGGGTCGTAGTAAGATTGCCGTTTATGATACCTCTATTTCAGGG
CTCAGAGCGCATCACGATCGGGAGTGTAATTC AATGTGCATATAAGCAAAACACACAGA
TTTCTTTTTTTCCAGAAAAATGAGCAGTGAAATGCCTACTCGAATACGAACACCAACA
CTGAAAACGAGAACCGCAATACTGGCGCTGGCGTAGATGTAAATACAAATGCAAATGCAA
ATGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAGAGCTGA
ACCTCCCCACGGTCGATGAGCAAAGACAGTATAAGGTACAACCTGCTATTGCATATCAACA
GCATATTACTTGCTAGAGTTATTTCAGATGAATAATAGTTTACAAAACAATCTACAGAAC
ATATAAATAATAGCAATAACAATAACATCATCAGGATACAGCAACTTATATCTCAGTTCC
TTAAAAGGGTTTCATGCCAATCTTCAATGCATATCTCAGATAAACCAAGGAGTGCCCTCAG

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CGAAACCACTGATCCTCACGCCTCCTCAGCTAGCCAACCAGCAGCAACCTCCACAGGATA
TTCCTTCTAAACTCTATCTTCTCTTGGCAAGAGTGTTCGAGATATGGTAG

>YDR073W, 169 aa (SEQ ID NO 92)

MSSEIAYSNTNTNTENENRNTGAGVDVNTNANANANATANATANATANATAELNLPVDE
QRQYKQQLLHINSILLARVIQMNNSLQNNLQNNINNSNNNNIIRIQQLISQFLKRVHAN
LQCISQINQGVPSAKPLILTPPQLANQQQPPQDILSKLYLLLARVFEIW

>YDR178W, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)

ACGATTAGGCGTCAAGTCCTTAGACCCCAATGACAACAACACAGCCAACCGTATCATCGA
GGAATTGTTGAAGTGAATAGATAAAAAAAGCGACCAAGTAAGTAAGTAAATAAAGAA
TAAATAAACCTATATGAGTAAACACCAAGCGAGGATGTTTCATTGTGCATCCGTGTTCTT
GATGATCACATAACTGTAAAAGAATAATACGGCACGTTAAATGTTATTTTAGAATATATA
AACACCTTATGTGCCATAAGCATTGAGCCAATCGCTGCTGTTTTTTTTTATTCCGGGGCAC
CTTCGGAAGAACACAGGCGCAATTTAGTTATATAAGGAGAAGCCCTCGAGCGATCAGGGG
ACCGACTGCGGATCGCTTTAAGGCAAAGATAGAAGGATAAAATATCTGCTTTGGAAGATAG
TCGTATCTAATTTCCCATTTCTGTTGTTTTCTTGATCTTTCCCTACGCTTTTCGACTTTCCTC
CTACGCGCTTTATAATAGCTATGATGTTGCCAAGATCCATGAAATTTATGACTGGAAGGA
GAATTTTCCATACTGCCACAGTAAGGGCCTTCCAGTCTACCGCTAAGAAGAGCTTAACCTA
TCCCATTTTGGCCCGTATTACCCCAAGAACAGGTGGTGTAGGGGGCACCTCCAATGATG
CCTACGTCCCCCCCCCTGAGAATAAATTAGAGGGCTCATACCCTGGTATATGGAAGAAA
TCTTTGCGCTTGTCCGTCGTTCCATTGGCTACGACGGCTATGCTGACAACCGGTCCGTTAT
CCACTGCAGCTGATTCTTTCTTTCTGTCTATGCTTTTGGGATATTGTTACATGGAATTTA
ACTCTTGTATCACCGATTATATTTCTGAAAGAGTTTATGGTGTTTGGCACAAGTACGCCA
TGTATATGTTGGGCCCTGGTTCTGCGGTCTCCCTTTTGGGAATCTATAAACTAGAAACCG
AGAATGATGGTGTGTTGGTTTAGTAAAAAGTCTATGGGATCTTCCGAGAAAGACAACA
GTCAAAAGATTGAAGCCAAGAAGTAG

>YDR178W, 181 aa (SEQ ID NO 106)

MMLPRSMKFMTGRRIFHTATVRAFQSTAKKSLTIPFLPVLQKPGGVRGTPNDAYVPPPE
NKLEGSYHWMYKIFALSUVPLATTAMLTTGPLSTAADSFFSVMLLGICYMEFNSCITDY
ISERVYGVVHKYAMYMLGLGSAVSLFGIYKLETENDGVVGLVKSLWDSSEKDNSQKIEAK
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)

GAATTCCAACCGGAAATTGCAAACAGCAGCAATTTCTCGTACCGATGAAGGGGAACATGG
CCGTTGTACCGAGGTTCCATTGGCCGAGTATTAGCCAGGGCCCTAATACGTAACCTCGGTA
CGCTCTTCAGCTTCTTTTCGCATAATCAACGTTCTTGTATGTAACCTACCACGTTCCATG
GCATCCGCCAACCTTGCTTCCTTACCAAATATTAATGAGCCTAAGGTGTACATTGCCGCC
GCAGGTAATATTAGCCACGACGTTGGCATTCTCACTGGCAAAGTAGCTGTTGATCTCAGT
AAAGATAACCTCAACATACTCTTTTACTTGTCTTTTTTGTAGCTAATTGCTTTCTCTCC
CTTCTTTTCCACAAACCGCAACTATTTTCTCTCAAAAGTTATATGAAGTATATATACTG
AATGGAGCAATTCCGGGTTGAGTGAATTACAAAATTATAGTATCTGATCAAGCACACAGT
GGAAGTGCTCGAAAAGCAATATGAGTGTTGATTTGTTTCCAAATGATAGATTTGGTGCAG
AAGATAAATACGACAACCTTTAAGGATGCCGTAAGAAGATGCTCCTGGCTCATCGAAGAAA
TCGTCAAACCGCAATTACCCAACATTATTGACAACCTTTTCTAAATGCCTAGAGATGCTAG
AGAGTGACCAAATATTCAAATGCCTGTATCTAATGGTATTCCCAACGAAAGTAACAAAC
AAAACGACTCTCCGACGGTAAAGGGTGTATCACAAGACAAGGCCAATACATTGTTGACT
TTCACATTGTTGTCAGATTCCCACAATTTCAAAGGGGTAAACAAGTTATGTTCCGAATGA
ATACGGGACTGAATTTCTTACTTATTCAATTCAGTAAGATAATGACGCACTTGAAAAATA
TTTTGGAAATACTGAATCAACTTCAAGTAGCTACAGATGTCAGCGAATTCGTATCCAAAT
TTGGCGTGGCCATGGAACCTTTGAACCATCTCTAATACTTTTACAAAATCCTCCTAGAG
ACCTGGTATTCCCAGAAGATAACAACCTTTGCTATGAAGGAAATGTTCCAGGATTGTTACT
CAGTCTGCGAATCCACAGCTCACATCCTAGGACTGGAACCTTACGCTTTGTAGGAATGAGC
TTTGCATAGAATACTACGAAATCTAATTAAGGTGACTAAAAAACCTTGGTGGGAGATTGATA
GTAAACTGGCAGGTCATTTTGCACCAAAATAAGAAATCAAGTGACAAATGAAAGAAACA

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AAACTTTATCTAAGATCCTCTCAGAAAACGGTGTACAAGTCCAGGATTCCACATTACTTA
ACCACATAATTTCTTCTTTTCAAAGTGAAGCTATAACACTTCCAGAAGCTCAGGAATTAT
TAAGAAGGGGCGTTACTTTTCGATAATAGGGTAGTCATGGAATGTGAAAAGTTAATAGTAT
CTACAAGTGATCCAACCTTGTATCAGTATAAGCGCCAAATTGAACAGTCTCAAAGCTTCGA
TGGCGAACCATCAAGCAAATTTGGTAGCTAGCAAACAGTTAAGTACATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)

MSVDLFPNDRFGAEDKYDNFKDAVKECSWLIBEIVKPQLPNIIDNFSKCLEMLESQIFK
MPVSNGLPNESNKQNDSPVKGVITRQGYIVDFHIVVRFPQFORGKQVMFRMNTGLNFL
LIQFSKIMTHLKNILEILNQLQVATDVSEFVSKFGVAMELLNHSLLQLNPPRDLVPED
NNFAMKEMFQDCYSVCESTAHLGLELTLCRNELCIELRNLIKVKPWCEIDSKTGRSF
CDQIRNQVTNERNKTLKILSENGVQVQDSTLLNHISSFQSEAITLPEAQELLRRGVTF
DNRVMECEKLIVSTSDPTLISISAKLNSLKASMANHQANLVASKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)

GGGAAGAACTAAGAGATGTTATGGCTCGGAGAGTTTTGAAAAGCGAAATAGATTTCGCTGC
AAGTTTGTGAAGAAACCATCGACAAGAAATTACAAGGTTATTCCTGATGAAAAGCTGCTAA
CTAATATTTTAAAGAGAAAGTTGACAGAGGAAGAAAAAGCTCTGTCAAACGTCCTTGCG
TGAAGAAGTGAGCGGTTGTTCTAACCACTATTTAAAGCCGCAATTAGTAATGCAAAAAGT
TGGCCGGAATTAGCCGCGCAAGTTGGTGGGGTCCCTTAATCCGAAAAAGGACGGCTTTAA
CAAATATAAACCCGAAAAATCCCCACAGTGACAGAATTGGAGAAACAACCAAGTTTGTATA
TCGCCATACATATAAAGAGATGTAGAAAGCATTCTTCACTGTAATGTCCAAATCGTACAT
TTGAATTTCTTGTAGGTTTATTTAAAGGTAAGTTAAATAAATATAATAGTACTTACAAA
TAAATTTTGGAAACCTTAGAAGATGTGCAAAATTTGGGACAAGAAAAAAATGAAGTAAATTACT
CTGATGTAAGAGAGGATAGAGTTGTGACAACTCCACTGGTAATCCAATCAATGAACCAT
TTGTCAACCAACGTTATGGGGAACATGGCCCTTTGCTTTTGCAAGATTATAACTTAAATTG
ATTCTTTGGCTCATTTCAACAGGGAATAATTCCTCAAAGGAATCCACATGCTCATGGTT
CTGGTGCCCTTCGGCTATTTTGAAGTAACCGATGACATTACTGATATCTGCGGGTCTGCTA
TGTTTTAGTAAATTTGGGAAAAGAACGAAATGTCTAACAAGATTTTCGACTGTGGGTGGTG
ATAAAGGTAGTGCCGACACGGTTCTGTATCCAAGGGGGTTGCCACCAAATTCTACACTG
AAGAAGGTAATTTAGATTGGGTCTACAATAATACACCGGTATTCTTTATCAGAGACCCTT
CCAAGTTCCCTCACTTTATCCACACACAGAAGAGAAACCCACAAACCAACCTAAGGGATG
CTGACATGTTTTGGGATTTTCCTCACCCTCTGAAAATCAGGTGGCCATTTCATCAAGTAA
TGATCCTTTTTTCAGACCGTGGTACCCCTGCCAACTACCGTAGTATGCATGGTTATTCTG
GTCATACCTATAAATGGTCCAATAAAAACGGAGATTGGCATTATGTGCAAGTTCATATCA
AAACCGATCAAGGAATAAAGAAATTTGACCATAGAAGAGGCTACCAAAATTCGGGGATCCA
ATCCAGATTACTGCCAGCAGGATTTATTTGAGGCTATTGAGAAATGGAACTATCCTTCTCT
GGACAGTTTATATTCAAACAATGACCGAACCGGATGCCAAAAAATTACCATTTTCAGTCT
TTGATTTGACTAAAGTATGGCCTCAGGGCAATTCCCTTTACGGCGTGTGGGTAAGATTG
TTTTGAACGAGATACTCACTGAACCTTCTTCGCACAGGTGGAACAAGCTGCCTTCGCCCCCA
GTACCACGGTTTCCTTACCAAGAAGCAAGCGCTGATCCAGTATTACAGGCCCGTTTGT
CATATGCGGATGCTCATAGATACAGGCTAGGTCTTAACCTCCATCAAATACCCGTAAACT
GTCCATATGCATCTAAATTTTCAATCCCGCTATCAGAGATGGACCGATGAATGTAAACG
GCAACTTCGGCTCAGAACCTACATATTTGGCCAACGATAAATCGTACACGTATATCCAAC
AGGACAGACCCATTCAACAACACCAAGAGGTATGGAATGGGCCAGCTATCCCTTATCATT
GGGCAACATCCCCAGGTGATGTAGATTTTCGTGCAAGCAAGAAATCTCTACCGCGTTTGG
GTAAACAACCTGGACAGCAAAAGAACTTGGCATATAACATCGGCATTTCATGTAGAAGGCG
CCTGTCTCTCAAATACAGCAGCGGTTTATGATATGTTTGCTCGTGTGATAAGGGACTAT
CTGAGGCAATTAAAAAAGTAGCTGAGGCAAAACATGCTTCTGAGCTTTCGAGTAACTCCA
AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)

MSKLGQEKNEVNSYSDVREDRVVTNSTGNPINEPFVTQRIGEHGPLLLQDYNLIDSLAHFN
RENIPQRNPHAHGSGAFGYFEVTDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADT
VRDPRGFATKFYTEEGNLDWVYNNTPVFFIRDPSKFPHFIIHTQKRNPQTNLRLDADMFWDF
LTTPENQVAIHQVMILFSDRGTPANYRSMHGYSGHTYKWSNKNGDWHYVQVHIKTDQGIK

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NLTIEEATKIAGSNPDYCCQDLFEAIQNGNYPSTVYIQTMTTERDAKKLPFSVFDLTKVW
PQQGFPLRRVGKIVLNENPLNFFAQVEQAAPSTTVPYQEASADPVLQARLFSYADHR
YRLGPNFHQIPVNCPPYASKFFNPAPIRDGPMNVNGNFGSEPTYLANDKSYTYIQQDRPIQQ
HQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKQPGQQKNLAYNIGIHVEGACPQIQQ
RVYDMFARVDKGLSEAIIKVAEAKHASELSSNSKF

>YER103W, 2429 bp, CDS: 501-2429 (SEQ ID NO 145)

ACTATTGTCACCTTCTCCATTGAGATTGCAAAAACCCCTCGGGTCTTGTAGAACTAAATT
ACGTTTCATAGGGGTGGGATTTATATTGTAATTCGCGAGGTTTACACGAAAGATATCTCA
ACTCTAGCCGCACATCCATTCCGGTATGTACTCTCCACCATTGGGTATTATAGAATGTA
ATAGGTTTCAAAGCGGATATCTTTTGCCCGGTGAGTTGTTACTTTTTTCATTTCGAGCAATG
AAGTACATTCTAGAAGTTCTTAGAACCTTATGGAAGCACCAAGAAAAAGGAAGTTAAAC
AAAACACTGATTCAATAAGCAAGGGGGGAAGCTCCTTAGTTTGACGACAGTAACAAAATG
TTCGTATAAATTGAACGAACTCAAGCCAATAAAGGACTTTTCAGAGGCCATCTCTTCT
TTCTCCACAACCTTTGCAATAAAAACCACTAATAAAAAGTAAATAACAAAAACAAGAAAA
AAATAAACAAAACAATAATCATGTCAAAGCTGTTGGTATTGATTTAGGTACAACCTATT
CATGTGTTGCTCATTTTGCAAACGATAGGGTTGAAATTATCGCTAACGATCAAGGTAATA
GAACGACGCCTTCTTATGTGGCTTTTACTGACACAGAAAGGCTAATTGGTGACGCTGCGA
AGAATCAAGCTGCGATGAACCCACATAATACAGTATTGATGCTAAGCGTCTGATCGGAC
GTAAATTTCGATGATCCAGAAGTGACGAACGATGCTAAGCATTACCCATTCAAAGTGATTG
ACAAGGGAGGTAAACCGGTAGTGCAAGTGGAATATAAAGGCGAGACAAAGACATTTACTC
CAGAAGAAATTTCTCAATGATCTTGACAAAGATGAAGGAGACTGCTGAGAACTTTTAG
GAACAGAAGTGAAAGATGCTGTAGTAACGGTTCAGCCTATTTCAACGATTCACAAAGGC
AAGCAACAAAAGATGCCGGTACAATCGCGGGCTTGAACGTTCTTCGTATCATTAATGAAC
CTACAGCTGCCGCTATTGCGTATGGCTGGACAAGAAATCGCAGAAGGAGCACAAACGCT
TGATCTTTGATTTAGGTGGTGGTACTTTTGATGTCTCTCTGCTATCCATAGATGAAGGTG
TCTTTGAGGTTAAGGCTACTGCTGGTGACACTCACTTGGGTGGTGAAGATTTGATAGTA
GGCTGGTTAACTTTCTAGCCGAGGAGTTCAAAAAGAAAAATAAAAAGGATCTAACAACCTA
ACCAAAGGTCCCTAAGGAGGTAAAGGACCGCCGCTGAAAGGGCCAAGAGAACTCTGTCTT
CGTCTGCTCAGACATCTATAGAAATAGATTCATTATTTGAGGGTATCGATTTCTATACTT
CCATTACAAGGGCAAGATTTGAAGAATTATGTGCTGATTTGTTTAGATCTACATTGGAGC
CAGTGGAAGAAAGTTTGGCTGATTCAAAATTAGATAAGTCACAAATTGATGAAATTGTAC
TTGTTGGTGGTTCAACAAGAATTCAAAAGTACAAAACTGGTTTCTGATTTTTCATG
GTAAAGAACCAAACCGTTGATTAACCTGATGAGGCCGTCGCTTATGGTGCTGCCGTAC
AGGCTGCCATCTTAACGGGTGACCAGTCGTCGACGCCAAGATTTACTGTTGCTGGATG
TTGCACCATTATCTCTAGGTATTGAACTGCAGGTGGTATTATGACAAAGTTGATCCCAA
GAAATTCGACTATCCCAACAAAAAATCGGAAGTGTTTTCCACCTACGCTGACAACCAAC
CTGGTGTGTTGATACAAGTTTTTGAGGGTGAAAGGACAAGGACAAAAGACAACAATCTAC
TGGGTAAATTTGAGTTGAGCGGTATTCCACCCGCTCCAAGAGGCGTACCACAAATTGAAG
TTACATTTGATATCGATGCAAAATGGTATTCTGAACGTATCTGCCGTTGAAAAAGGTACTG
GTAAATCTAACAAGATTACAATTACTAACGATAAGGGAAGATTATCGAAGGAAGATATCG
ATAAAATGGTTGCTGAGGCAGAAAAAGTTCAAGGCCGAAGATGAACAAGAAGCTCAACGTG
TTCAAGCTAAGAATCAGCTAGAATCGTACGCGTTTACTTTGAAAAATTCTGTGAGCGAAA
ATAACTTCAAGGAGAAGGTGGGTGAAGAGGATGCCAGGAAATTGGAAGCCGCCGCCCAAG
ATGCTATAAATTGGTTAGATGCTTCGCAAGCGGCTCCACCGAGGAATACAAGGAAAGGC
AAAAGGAACTAGAAGGTGTTGCAAACCCATTATGAGTAAATTTTACGGAGCTGCAGGTG
GTGCCCCAGGAGCAGGCCAGTTCCGGGTGCTGGAGCAGGCCCCACTGGAGCACCAGACA
ACGGCCCAACGGTTGAAGAGGTTGATTAG

>YER103W, 642 aa (SEQ ID NO 146)

MSKAVGIDLGTTYSCVAHFANDRVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQAAMN
PHNTVFDKRLIGRKFDDEVTNDKHYFPKVIDKGGKPVVQVEYKGETKFTFPPEISSM
ILTKMKETAENFLGTEVKDAVVTVPAYFNDSQRQATKDAGTIAGLNLRLINEPTAAAI
YGLDKKSQKEHNVLIIFDLGGGTFDVSLLSIDEVFEVKATAGDTHLGGEDFDSRLVNF
EEFKRKNKDLTTNQRSLRRLRTAAERAKRTLSSSAQTSIEIDSLFEGIDFYTSITRARF
EELCADLFRSTLEPVEKVLADSKLDSQIDEIVLVGGSTRIPKVQKLVSDFNKGPEPNRS

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INPDEAVAYGA AVQAAILTGDQSSTTQDLLLLDVAPLSLGIETAGGIMTKLI PRNSTIPT
KKSEVFSTYADNQPGVLIQVFEGERTRTKDNLLGKFELSGIPPAPRGVPQIEVTFDIDA
NGIILNVSAVEKGTGKSNKIIITNDKGRLSKEDIDKMVAEAEKFKAEDEQEAQRVQAKNQL
ESYAFTLKNVSENNFKKVKGEEDARKLEAAAQDAINWLDASQAASTEYKERQKELEGV
ANPIMSKFYGAAGGAPGAGPVPAGAGPTGAPDNGPTVEEVD

>YER150W, 947 bp, CDS: 501-947 (SEQ ID NO 149)

ATACGGGGGAAGAAGAAATATCATATTCAAAGCTAATTCATTGAAATTAGTGCTTGTCTC
ATCTAGCCTTTAGTGCTTAATCTCTGGAGGAGCACATATGGGGTTAAAGCCATGCCGGGA
CTGGGGGCCCTATCGGGGCTCGAACCCGAATCCCGCGAGTATTTATTTGAAGGTCCGGG
ACGCAAGTTACCTAATCTGGTTAATTGATATCCCATTTAGGCGATGACGTTCTTCCCT
CACCCCTCGGCTTGTTAGAAGATCTATTGTTATAGCCTCCTCTGGAAGAATTTATGCCAG
ATGAAGAAAAAACTTCTCGAAGTTCCAGATGCCCAAATGAGGGCTTTCCATCCCTGTT
AGCTGGAAAAAGTGTAAGTATATCTATATAAAAAAGTCGGCCTACTTTTGCCAGGTTTCGTCT
TTCACTTGCACCTCTCTTGATCTTACTTTCTACTCAAAAAAGAATCCAATACACAAAAATAA
AATCAGTACTATTACTAATAATGTTGTCTAACGCTAAGCTCCTTCTATCATTGGCCATGG
CCTCTACGGCTCTCGGATTGGTATCTAATTCTAGTTCTCTGTAAATCGTGGTACCATCAA
GCGATGCTACTATTGCCGGTAACGATACAGCCACGCCAGCACCAGAGCCATCATCCGCCG
CTCCAATATTCTACAACCTCGACTGCTACTGCAACACAGTACGAAGTTGTCAAGTAAATTCA
CTACTTACTGCCCAGAACCAACGACTTTCGTAACGAATGGCGCTACATTCACTGTTACTG
CCCCAATACGTTAACAATTACCAACTGTCCTTGCACTATCGAGAAGCCTACTTCAGAAA
CATCCGTTTCTTCTACACATGATGTGGAGACAAATCTAATGCTGCTAACGCAAGAGCAA
TCCCAGGAGCCCTAGGTTTGGCTGGTGCAGTTATGATGCTTTTATGA

>YER150W, 148 aa (SEQ ID NO 150)

MLSNALLLSLAMASTALGLVSNSSSVIVVPSSDATIAGNDTATPAPEPSSAAPIFYNS
TATATQYEVVSEFTTYCPEPTTFVINGATFTVTAPTTLTIITNCPCTIEKPTSETSVSSTH
DVEITNSNAANARAIPGALGLAGAVMMLL

>YFR033C, 944 bp, CDS: 501-944 (SEQ ID NO 155)

ATCGAGCCATTTCGCGTCTGAGTAAGCGACGGTCATCGGGCGCGCTCGTGGACGATGA
CAAGCGGAATCACACAAGCATGCAGAGCAAGCACGGCGTAATCGATTAGCGGTTCGCGCT
GCACGAACTGGCGTCTTTAATCCCCGCGGAGTGGAAACAGCAAAATGTGTGGCGCGCGCC
GTCCAAAGCGACCACCGTGGAGGCGGCTGCCGGTACATCCGTACCTACAGCAGAACGT
GAGCACGTGACCGTGACCAATGGGAAGCACGTTCCGGGCATATCGGACTGGGGCGCGCC
TCCCTTGCGCGGTGCTTGTATAAGAGGCGCTTTGCTGGAAAGTGGCCACACCGGGTTT
TCGAGATTAGGACCTACTCAGTCTTAAGGGCAGTATTGGTTGGCGCTTATTTGCACATAT
TGTATACACGCACTCACATTAACAGAAGCACACATATACACTTACACCTACACACACGGA
TAAAGAAAAAGAAATAGAAAATGGGCATGTTGGAAC TAGTTGGTGAGTACTGGGAACAAC
TAAAGATAACCGTTGTGCCGTGTTGTGGCCGCGGCCGAAGATGACGATAACGAGCAGCATG
AAGAAAAGGCAGCAGAAGGAGAAGAAAAAGAAAGAAATGGGGATGAAGATGAGGATG
AAGACGAAGACGAAGATGATGATGATGATGACGACGAAGATGAGGAAGAAGAGGAAGAAG
TCACTGATCAGTTGGAAGATTTGAGAGAACATTTCAAGAACACGGAGGAGGGTAAGGCCC
TTGTGCACCACTACGAGGAGTGTGCTGAGAGAGTCAAGATACAGCAACAACAACCCGGCT
ACGCGGATCTTGAACACAAGGAGGACTGTGTGGAGGAGTTTTTCCATCTACAGCACTATT
TGGACACTGCCACGGCACCTAGATTATTTGACAAATTAAAGTAG

>YFR033C, 147 aa (SEQ ID NO 156)

MGMLELVGEYWEQLKITVVPVAAAEDDDNEQHEEKAAEGEKEEENGDEDEDEDEDEDD
DDDDDEDEEEEEVTDQLEDLREHFKNTEEGKALVHHYECAERVKIQQQPGYADLEHK
EDCVEEFFHLQHYLDTATAPRLFDKLLK

>YGR086C, 1520 bp, CDS: 501-1520 (SEQ ID NO 175)

GTTGAATATTTACCAATTGGGAAAAAGAACTCGTATTTTCATTCCCCTTTTTGGAAAGGGG
TGGGGAGAGACTGTTGTTTCAGCCACGTCAATTATTATTTTTTTCTTTGGCCCTGCGCTTGT
CTTATAAAATTCGCGAGCCGCCCTCTTATTTTTTTTTTTTTTCGATTTTTGGCCACAGGTC

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ATATTGCAAAAACCGAATGGCCGCGCCCCCTCACGCACGGGACGGAAGAAGGGCGGCGT
CCCCTGTTTTTCTGCTTTGGCTCATCTCTTTGGCTCCGACGGACGAAAGACGGGATTCCC
CCTCCCGTGTCTTTTTATAAATAACAAGTGCTCATTCTGCATCCTTCTTGTTCCTCGTC
GTTTGGGTACAATGCGTTGATTATCCCAACCCAAGAAAGAAAATTTGTCTCACATCTGCA
TCTGCACATTTATTTACCTATACTTTTCCATTGTTAGCAGTATTGCAAAGTGAAGAATAT
ATCAGCATCAAGTATATAGTATGCACAGAACCTTACTCTTTAAGAAATTCAGGGCACCTA
CCGCTCTCAATTACAGAACCCACCGCCACCACCATCTACAACCAAAGGTAGATTCTTTG
GGAAGGGTGGTCTAGCTTACAGCTTTAGGAGAAGTGCTGCTGGAGCTTTTGGCCAGAAAT
TATCCAGAAAGTTGTCTCAATTGGTTAAGATTGAAAAGAATGTTTGGAGGTCCATGGAAT
TGACAGCCAACGAAAGACGTGACGCTGCTAAGCAATTGTCTATTTGGGGTTGGAACG
ATGACGATGTTTCCGACATCACTGATAAATTAGGTGTCTTGATCTATGAAGTTAGTGAAT
TAGACGACCAATTTATCGATCGTTATGACCAATACAGATTGACTCTAAAGTCCATCAGAG
ATATCGAAGGTTCTGTTCACCATCTAGAGACCGTAAGGACAAGATCACCGACAAAATCG
CCTACTTGAAATACAAAGATCCTCAATCACCTAAGATTGAGGTCTTGAACAAGAATTGG
TGCGTGCTGAGGCTGAATCTTTGGTCGCTGAAGCTCAATTATCTAATATCACAAGGTCAA
AGTTGAGAGCTGCTTTCAACTACCAATTTGACTCCATCATCGAACATTCAGAGAAAATTG
CTTTAATCGCTGGTTACGGTAAGGCTCTCTTGGAACTATTGGACGACTCTCCTGTCTCTC
CAGGTGAAACCAGGCTGCTTACGATGGGTATGAAGCCTCTAAACAAATCATTTATTGATG
CTGAAAGCGCACTGAATGAATGGACACTAGACTCTGCCCAAGTCAAGCCTACTTTAAGTT
TCAAGCAGGATTACGAAGACTTCGAACCTGAAGAAGGCGAAGAAGAGGAAGAGGAAGACG
GTCAAGGCAGGTGGTCCGAAGACGAACAAGAAGATGGACAAATTAAGAACCTGAACAAG
AAGAAGAAGGTGCTGTTGAAGAACATGAACAAGTCGGACACCAGCAAAGTGAGTCTCTTC
CCCAACAAACAACAGCTTAA

>YGR086C, 339 aa (SEQ ID NO 176)

MHRTYSLRNSRAPASQLQNPPPPSTTKGRFFGKGGGLAYSFRRSAAGAFGPELSRKLSQ
LVKIEKNVLRSMELTANERRDAKQLSIWGLENDDDVSDITDKLGLVIYEVSELDQFID
RYDQYRLTLKSIRDIEGSVQPSRDRDKITDKLAIYLYKDPQSPKIEVLEQELVRAEAS
LVAEAQLSNITRSKLRAAFNYQFDSIIHSEKIALIAGYGKALLELLDDSPVTPGETRPA
YDGYEASKQIIIDAESALNEWTLDSAQVKPTLSFKQDYEDFEPEEGEEEEEDGQGRWSE
DEQEDGQIEEPEQEEGAVEEHEQVGHQQSESLEPQQTAA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)

TCCAGTATGCCACACATTATGCCCTTGCACACCTAAAGCACATATTTTCGTTATTTTTCAC
CACAATAGGTGGATCTCGAAAAGGATGGAAAATCAGGAAAAAGAAATGTTGAGAAAAAAA
TAAACCGATTCCCGTTTAGTTTTCTCCTATTTCCGTGTATATGCGTGGTTATTCGTTTTC
GAATCCTTTTATGAATGTCCGAGGAGGTGGTACAATCCGAAATAGACTAAAGAAAAGCGA
AAGCCGTAGTTTGTGATGATAGATGACTCGCAGCTTTGTCTATCAACGGGCCACCTTA
TTCCGAAGAAGGGAATGGAAAACGGACTGGCGTAGTCAATAAGCGTCTTCATATCTTAGCA
TTGTTGAGAGATACATAGTGTACTCCATATCGTTCTTTTTTTTTTGTATATATCAAGCCAC
ATATCCTGTTTCTTTAATCTTTTATACGCCGTAAAGAATCGGGTACTGACATAAGTGTAAAG
TAGCCGTACAGAGAACAATATGACTAAATCGGTTGGTGTGAAGAGTCACAGTACATTG
AGGACCTTAGTTTTCAGCAGCAGCTGCATTTACTGGCGGCAGGGACGGGGTTTCGTACA
GTAATCAGCGATTTGCTGAGGGTTCCGGCCATTCCTCTGACTTAGCAAAGTCATTAGAAG
ACTATCGGCCCTCCTGATGAAAAGCCGTCCCTCATTTGTCATCTGTGGGGGAAGGTGGCGCTA
ATGAGGAAGAGAAGGGCGGTAACGACGGCGGTCCCTTGGCAAGAATTCAAACAGGGCTTT
TTCTCCAAGACTGCGAAATCATAGGAAAAAGATTCTCTCGAAGTTTGTGTTTGAACAAC
TCTTCATGCTTGTGTGTGTATCGCTCATATCGATTTACTGGGGTGCCGTGTACGGAA
CAGATCGTTACTTTTCAAAGTGAAAAATATTGTTGTATTGCAGGATGCGCCATCTAATA
CTTCAGTTCAATCTATTTCCGCGATCATACCCCTATTGTTAGCGTCTGTCCCCGGGACAT
GGCATATATACAACGCAACATCATTTTCATAGGAAATTTGGTACGACGAACTCCACCGAAA
TTGACAGAAAGATAGTCGATTTAATTTACGATGAGAGATACTGGCTGGCGTTAAACGTTA
AACCTAATGCTACAGACACTTTGTATAATTTCTTTGATTAGCCAAGACGCAAACTCGGAGT
TCAATTCATCAATTTTTTTTTGAATCCGTGTTTGAAGTGGTCGTGACCCATCGAGTGTAA
AATCGACCATTTACCACATCATGCAACAATTGGAGGTCCGCCCTCAGAAATATTACGTCA
AGGAATATCTTCCCTCATTTGATGAGCAACATCACTTCTAATGACAGAGATCTTAATATAA

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ACATGGAGAACTGGGCGATTGCAGGACAGTTGTTGTTACCTACAACGATTATCGTCCTT
TTGCTGATCGTATTCTAATGGCCCTCTGCAGGTGGTCTGATTTATTGTTATTTTGTTAA
CCGTTTTACAACCTGTCATTATATGGTAAGTTGCACGGAGAAATGGCCAGAGTTCTGAAGC
CAAAGCATATTTTAATCTACAGGCTTCTAATTTCTGGGCAACTTATTTTCTTCTTTCCA
TTGGATTCTGTACCGTATCTGCAATTTTAGGATCGATTTACCCCCGCCTTTGGCAGAG
GAGGATTCTGTAGTATATTGGATGTCTACGTGGTTGGTAATGATGGCTGTTGGTGGTGCCA
ATGAAAACGTTCTCAGCTTAGTTATAGCTTACTGCCCTCCATACCTGAGTATTTGGTTGA
TGACGTGGATCATATTAATATTTCTGCTTCATTCTACCCAATGGTTTTGAACAACGAAT
TTTACAGGTACGGCTACATAAATGCCAATCCATAATGCCGTGGATATCTATAAAGTGATTT
TTTTGAATTTAACCAGAAAGAAAAATGGGAAGAAATTACGGTATTCTCGTGGCATGGGTTG
CCCTCAATACATCCTTGATGCCATTTTGTTATGAAGTTGCAGGTAAAAAATGCAAAAAA
ATGCTATGCAAGCAGCAGAAGCCGCTGTCGCAGCAGCTACCCAGCGTGCTAGCCGCCCGG
CAGAGGCCAATACTGATAAAAAATAACAACCCGCCCGGAAATTAA

>YGR197C, 547 aa (SEQ ID NO 186)

MTKSVGDEESQYIEDPSFAAAAAFTGGRDGVSYSNQRFAEGSGHSSDLAKSLEDYRPPDE
KPSSLSSVGEAGANEEKGGNDGGPLARIQTGLFSPRLRNHRKKILSKFVLNNFFIACVC
VSLISIWGACYGTDTRYFFKVKNIIVLQDAPSNTSVQISAIIPSLLASVPGTWHIYNAT
SFHRKFGTTNSTEIDRKIVDLIYDERYWLALNVKPNATDTLYNSLISQDANSEFNSSIFF
ESVFESGRDPSSVKSTILPLMQQLEVRLOKYYVKEYLPSLSMNTSNDRLNINMENWAI
AGQLLFYNDYRPFADRILMAPLQVGLIYCILLTVLQLSLYGLKHGEMARVLKPKHILY
RLLSIWATYFLLSIGFCTVSAIFRIDFTPAFGRGGFVVYWMSTWLVMMAVGGANENVLSL
VIAYCPPYLSIWLMTWIIILNISASFYPMVLNNEFYRYGYIMPIHNAVDIYKVI FLNLTKR
KMGRNYGILVAWVALNTSLMPFCMKFAGKKMQKNAMQAAEAAVAAATQRASRPAEANTDK
NNNPPGN

>YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)

TCTTGTGTACGTACGATGTTTCTCCCGCTGATCCGATTACTAGCCGAAGACGTAAAATTG
GCGCTTGATTCAATTTATGCCCTTCCCGGAATAGTTGACCAAAGGGCAAAAAAATTCAG
TCGGAGATTCCCTATTGGGCGGAATTTAGTAGATCTCTTTCCGTGCATAACGCCTGCCCG
TTAGTCGTTATTTTACGTTAACATTTTCTTGGCCACTGCGCTATATAAATAAATACATAT
ATATATGTCAAGCACAATAAAGAACTTCCCTTAAATATTGAATAAGTAAATAATAGTTG
AAAAGTGCCTTTTGTTCGAAGGATTAGAGTGTTCTTAATTTTAGTTTCGTTCAACGGTCTC
AAAAAAAGTGTGAACAAGTAAAGCATAGCACATCCCAAATTACAAGGCACCCTGATTA
AAAATCCAAAAATAAACCATAGTTTATTTTACTAAAAACATTATACGTGAAAGACAAA
CCGCATCAGAAGTTTCGAGGATGAATATTGCAGAAGAACCATCAGATGAAGTAATATCTA
GTGGCCCCGAGGATACAGATATCTGCAGCCAGCAGACATCAGCGAGCGCAGAAGCTGGAG
ACCAATCAATAAAAAATTGAAAGGAAAACTTCCACTGGTCTTCAACTGGAACAATTGGCCA
ACACAAATTTATTAACCATAAGAATAAAATGGCAGTTACAAGAAGAAGAAGATGATCACT
GCAACTCTAGAATAACCGATCAAATAATGGACACAATACAGCACTACAAAGGTATCTCCG
TTAACAACTCTGATACAGAAACATATGAATTTCTTCCGGATACAAGGAGGTTACAGGTTT
TCGAACAAAATAAAGACATCTATCTTTACGAGCATGGAAGTCAAGAGTATGAGAAATCTT
ACAAAGATAACGAAGAGGAAGATGATTGGAGATACGATACCGTTTTGCAAGCACAATTCA
AGTACCCCAAGTCATTAGAAAATGCATGTACAGATATCTCGGAATTACTCAAGAGCGAAC
CTATTGGTCAGCATATTGATAAATGGTCTATCGGTGTGAACAAGCATGCACTAACCTATC
CTGGAATATTTTTGTGCGGGGAATAGCAAAGAGCCTTTCTATTGGTGAACATAAGTTTCT
TATTTTCAAAATATGGACCAATTTTATCAATGAAATTGATATATGATAAAACGAAAGGCG
AACCTAACGGATACGGGTTTCTCTTACCCCTTGGGTTCTCAAGCTTCACTTTGCATCA
AGGAACCTAATGGAAGGACGGTAAATGGCTCCACACTATTTATCAACTATCACGTTGAGC
GAAAGGAGAGAGAAAGAATCCATTGGGACCATGTCAAAGAAAACAACAAATGATGATAATT
TCAGGTGTCTCTTTATAGGCAACTTGCTTATCACAATCCTGAAAAAGTAGAGACTTTGA
TTACACCTAAAGAAGTCATAGAAGTAATCAAGAAGGAGTTATCAAAAAAGTTTCCGGACT
TTGATATCATTTTCATATTACTTTCCGAAGAGAAAGTAATACAAGAAGCAGTAGTTTCAGTAA
GTTTCAATGAGGAGGGGTCAGTAGAATCAAAACAAATCTTCCAATAATACTAATGGAAATG
CCCAAGATGAAGATATGTTGAAGGGTTATGGTTTCATCAAGCTTATCAACCATGAACAAG
CACTAGCAGCCATCGAGACCTTCAATGGGTTTCATGTGGCATGGAAACAGGCTCGTTGTTA

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ATAAGGCGGTTCACATAAAGTTTACAACAACCAATAGCCATGACAGGCACCCCTTCCA
TCAGTAACCACAATGATATGGAGGTTTTGGAATTTGCAAATAACCCAATGTATGATTACA
ATAATTATACATATGATAGATATTACTTCAACAATAAAAAACGGGAACAGCAACGATA
CCTCCAATGTACGGTATTTTGATTCTGTAAGATCAACCCCTGTGGCAGAGAAAATGGATC
TGTTCTATCCTCAAAGGGAATCTTTCAAGTGAAGGTCGTGGTCAACGTGTGCC'TAGATTCA
TGGGCAACAAGTTTGACATGTACCAGTACCCATCAACTTCTTACAGCTTACCTATACCAA
TGAGTAATCAGCAAGAATCAAACCTATATGTCAAGCACATCCCTCTTTCTTGGACAGATG
AAGATTTATATGATTTCTACAAATCTTTCCGGTGAAATAATCAGCGTTAAGGTCATTACTG
TTGGGGGTAGTAAGAACAAGTATCGTCAACAATCGAATGATAGCTCATCAGATAATGATC
TGCCAGTGGGATCATCAAGAGGTTATGGTTTTGTTTCTTTTGAAAGCCATTAGATGCTG
CTAAGGCAATTTTGAATACAGACGGGTATCAAGTGAGCAAAGATCAAGTGTATCTGTTT
CTTTCCGCTCAGAAACGTGGTAATTTATCTTCAAGTGATGATGATGATCAATCCCAAACCTG
ATAACTCATCAAAGTTCCAAAATTTTCAGCCACATAATGATTATCATAAGGCTTATCCAA
CAAAGTATAATAAGAAATTTATCAATGCCTTGATGACTCAGAACCAATCGCAACAGCAAG
TCTCGAGGGAAAATTATTTTCATACCACTGCAGTACCCTAATACCAACACAAAGCCCGTGA
ACAGTTACAACCTAATAAGTGCAAACCAAATAACGCTAACTGGATGATGCCAATGTTCC
CATCATTTGGGTTTATTCCACAGGTGCCGCCAGTGCCCTATATAATACCTCCGCAGAATC
CTGCAGCAAATCATATTCTTATAATGGCAAACGGTAGTAATGAAGAGGAAGAATTTTCTA
GTGGTGATTATTCTATGGACTACTAG

>YGR250C, 781 aa (SEQ ID NO 192)

MNIAEEPSDEVISSGPEDTDICSQOTSASAEAGDQSIKIERKTSTGLQLEQLANTNLLTI
RIKWQLQEEEDDHCNSRITDQIMDTIQHYKGISVNNSDTETYEFLPDTRRLQVLEQNKDI
YLYEHGSQEYKSYKDNNEEDDWRYDTVLQAQFKYPKSLENACTDISSELLKSEPIGQHID
KWSIGVNHKHALTPGNIFVGGIAKSLSIGELSFLEFSKYGPILSMKLIYDKTKGEPNGYGF
ISYPLGSQASLCIKELNGRTVNGSTLFINYHVERKERERIHWDHVKENNDDNFRCLFIG
NLPHYHNPEKVETLITPKEVIEVIKKELSKKFPDFDIISYFPKRSNTRSSSSVSFNEEGS
VESNKSSNNTNGNAQDEDMKGYGFIKLINHEQALAAIETFNGFMWHGNRLVNVKAVQHK
VYNNHNSHDRHPSISNHNDEMEVLEFANNPMYDNNNTYDRYFNNKNKGNNSNDTSNVRYF
DSVRSTPVAEKMDLFYPQRESFSEGRGQVRPRFMGNKFDMYQYPSTSYSLPIPMNSNQES
NLYVKHIPLSWTDEDLYDFYKSFGEIISVKVITVGGSKNKYRQQSNDSSSDNDLPVGSRR
GYGFVSFESPLDAAKAILNTDGYQVSKDQVLSVSFAQKRGNLSSDDDDQSQTDNSSKFQ
NFQPHNDYHKAYPTKYNKKFINALMTQNQSQQQVSRENYFIPLQYPNTNTPKPVNSYNLIS
ANQNNANWMMPMFSPFGFIPQVPPVPYIIPPQNPAANHIPIMANGSNEEEEFSFGDYSMD
Y

>YHR001W-A, 797 bp, exon1: 501-506, intron1: 507-569, exon2:
570-797 (SEQ ID NO 195)

TTCTATTCGGCCTTATAAAAAGCATGGAATCCAAAAGAATTAGGCTTCTCATTCTATTTT
AATTATACTAGTACGATTTCTCACTCTGTAATTTAATATCAGTGTAATATGCACCTAGTT
ATGGGTAGTTTTGCTAACGTTACGAGCCGCGAAACTGTCCTCAATCTTACCACCTACCT
CTAATGACTGAAGAATGCTATGCGATATAACGCTGTGCGCACTTTGAATATATAC'TTATAT
TTACATAGTTTTCAAGTGCGTATTACTATTGCAAAGTAGTATTTTGTACCGTGATTTTGA
TCCAATTA AAACTAAAATATGGTTCAACCCGTTGTTTCCGCATCAAAAAACCATACCATTT
ATCAAGGGGACGGGATATATCACATAACAGTTTGAATGCATAATTTGTTATAGATATCTT
CTGGAATAATCTTCACAGCAAAAGCGCAAGTCGAATAATATATCGATAAAATACAATCCAT
AAGACTTAAAACCTAACCTCAATGGCGGTAAGTATCCTATCATATTATGTGAGCTAGAACC
GAATTAGTATACTAACATTTATAATACAGTACACTTCTCATCTGCTTCAAAAACCTGGTC
TACATTTCCGTAGACTTTCTTTAAGAAGTTTAAACAGCTTATGCTCCGAATTTAATGTTAT
GGGGTGGTGCTAGCATGCTTGGGC'TATTTGTATTACAGAAGGATGGCCTAAGTTTCAAG
ATACGCTATACAAAAAGATTCCGTTGTTAGGACCTACATTGGAAGATCATACTCCACCAG
AAGATAAACCTAATTGA

>YHR001W-A, 77 aa (SEQ ID NO 196)

MAYTSHLSSKTGLHFGRSLRSLTAYAPNMLWGGASMLGLFVFTEGWPKFQDTLYKKIP
LLGPTLEDHTPPEDKPN

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>YJL142C, 893 bp, CDS: 501-893 (SEQ ID NO 225)

TGCTGAATTATTTTGGGTATACCGATCTTCCCAGGCGCTTCTGAATATAACCAATTAAC
AAGAATAATAGACACGCTTGGATATCCTCCATCGTGGATGATAGATATGGGTAAAAACTC
TGGAAAAATTATGAAGAAATTGGCACCAGAAGAAAGTTCTTCTTCTACACAAAAGCATCG
TATGAAAAC TATTGAAGAGTTTTCAGAGAATACAATATAGTGGAAAAGCCCAGTAAACA
ATATTTTAAGTGGAGAAAGTTACCAGATATTATTAGAACTACAGGTATCCTAAAAGCAT
ACAGAACTCCCAAGAACTTATCGACCAAGAAATGCAGAATAGGGAGTGTGTGATCCACTT
TTTAGGCGGTGTGCTAAATTTGAACCCGTTAGAAAGATGGACACCACAACAAGCTATGCT
ACACCCCTTCATAACAAAGCAGGAGTTTACAGGTGAGTGGTTTCTCCAGGATCGTCTTT
ACCGGTCTTCAGAAAAACATGACGATGCAAAAGGCCAGCAAAGTGAATATGGAAGTGC
GAACGACTCTAGTAACAATGCAGGCCACAACATGTCTATAATCCTAGCTCTGCCACTGG
TGGTGTGATAGCGTGCACATTGGTGTCTAGTAAAGGAAGGAGAATACATCTGGCGA
CATCTCCAATAATTTTGTCTGTTACTCATTCTGTTCAAGAAGGGCCAACAAGCGCGTTCAA
TAACTTTCACATTGTGCGAAGAATAAATCGTTATTTTGTCTGACTTTTCTTAACTACCCAT
TTCATTTTATTACGGCTTGGTGCCATAATGATATACTAAATAAATATGAATTTTGCCTTT
TCTTAATTTTCTTATACGTATAGTCATTACAATTAATAAAGTAACATTATAA

>YJL142C, 130 aa (SEQ ID NO 226)

MTMQKASKVNMEVRTTLVTMQATTMSIILALPLVVLIAS TLVLSVKGRRIHLATSPIILL
LLILFKKGQARSINFTLSKNKSLFCLTFLNYPHFITAWCHNDIILNKYEFCLFLIFLIR
IVITINKVTL

>YJL144W, 815 bp, CDS: 501-815 (SEQ ID NO 227)

AGAAAGAAGTTCTGTTGTTATTAACCGACGGCAGCAAGTTGGGTCAATACTTGAAGGATTGC
CCATATGAAGGTATGGCGGGAAAGATAAGAAGAAACAATCTGACCAAGCAAAATGTCACA
AATGTCCATCCAACAGAATACGGCCTTTACATTTTACAAAAACAAATCATCGAGGACGTT
GAGTGATTTGTTGGCATGATCTAATAATAGTCTCTTATATAAACCCCTATAATAATTTCTT
ATTTTTCGCTTATATTACAGGTAAATCACCATCTAAGTATTATCTCTCACGTATCTTCA
CTTATATGGCTCAGAAAAACCCGTACGAAACGAAGGGGCTGCGAAAAATGTTTCTAGAAG
TAATGGCAATAATAGGGATACAGATCGATCCGCCTATATAAAAGACAACGCACCG
AAGGTGAACAAGATCGCAGATAAAGGTATTTACAAGGGAAGGAAAGTCAGCAAAAAACAAGA
GATAAGATAACAAGAAGAAGATGTTAAGGAGGGAAGCTTCAACAATATACAGGACACACA
AAAAAAGCAACAGTAGTATACTCAGGAGCCAGCGGACCAGACTAGAGTGGATTCTTGG
TAGAGGAGTCTCCCATGGCGATTTTCGGGATCAATAACCAGCCTACACAGCCTGGCGTGA
TATACTACTTTGTAGAGCTGACTAATTTAGGCATACAGGAAAACACAAGCAGTAATAATA
ACAACAACAATAATCATGGTGACGATGAAAACGGCAGTCGATACGGCCACGGCAGCAGTC
TGGGTGGAGACGTTCACTCTCGCCGTTGTTTCATGA

>YJL144W, 104 aa (SEQ ID NO 228)

MLRRETSTIYRTHKSNSSILRSQRDQTRVDSLVEESPMGDFGINNQPTQPGVIYYFVEL
TNLGIQENTSSNNNNNNHGDDENGSRYGHGSSLGGDVHSRRCS

>YJL166W, 785 bp, CDS: 501-785 (SEQ ID NO 231)

TGAACAGCTATACCACGAATATGAAGAGTCTATTGCCAAGGATTTGAAGGCCAAAAATTC
TCAGGTGATGAGTCTCGTGGCTTCAAAGCTGATGTCTTAAGTGGCTTCTTGAACAAAGT
TTACAAGAGAAGCAAAATAGAACTAACGCTAATCGATAAAACATTAGATTTCAAAC TAGAT
AAGGACCATGTATAAGAACTATATACTTCCAATATAATATAGTATAAGCTTTAAGATAGT
ATCTCTCGATCTACCGTTCCACGTGACTAGTCCAAGGATTTTTTTTAAAGCCAATGAAAAT
GAAGAAATGCGTGATCGGAAATTACGGGTAGTACGAGAAGGAAACTTGAGCCACCCCCCA
AATTTTATTTCATATAATAATAGGAAAAGCAACGACCTCATCTCTCGAACATTGTTTACTT
GAGCAAGTCCGATTAAGAGTAAGTTGTTCGTACGTTAAATACAAATAATCAACAAAACACT
ACACAAAAACTTCTACGATAATGGGTCTTCCAAGCGGTAAACCTTACATGGGATGGTGGG
GTCACATGGGTGGTCCAAAGCAAAAAGGTATAACCTCATATGCTGTGTCTCCATATGCTC
AAAAGCCATTACAAGGTATTTTCCATAACGCTGTATTCAATAGTTTTAGAAAGATTTAAGT
CTCAATTTCTATATGTATTAATACCTGCGGGAATTTATTGGTACTGGTGGAAGAACGGTA
ACGAGTATAATGAATTTCTGTACAGCAAAGCTGGTAGAGAAGAGCTGGAAAGAGTTAATG

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TTTAA

>YJL166W, 94 aa (SEQ ID NO 232)

MGPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGFHNAVFNFRFKSQFLYVL
IPAGIYWYWWKNGNEYNEFLYSKAGREELERNV

>YKL117W, 1151 bp, CDS: 501-1151 (SEQ ID NO 247)

TTATAGAACTGTTTTATTGTTTAAAGAGCTTGTTATAGTAATCTAAGTGGAAATACACT
AACAGTAAATAGGGCGTGTGGCGTAGTCGGTAGCGCGCTCCCTTAGCATGGGAGAGGTCT
CCGGTTCGATTCCGGACTCGTCCAATCTTTTTATACTTATTAATAATTTTTTCTGCGG
TTACTTGCTTTTAAATAACTGCCTTTTATGAATACAGAGTATAATTTTGTATATACAAA
GAGGTTGACTGTGATAATCAATACTTAATTTGTGGTTATTGGTACACATATACCTACAAA
AGTTACCAACAACTGTTGACTTTTAATGCTACCCGCTTCCGAGTGTTTTGAAGGGG
CGGAGAGGAGCGGCAAGAATTAGCATGGAAAAAGCATAAAAAGACGAAATGGGTGGCAA
TGTATTAACTTGTTGAGAAACCTAGTGGACTCAATTCATTACAACAACAAGTTCCCAAG
ATCATCGATTCAATAAGTCATGTCCGATAAAGTTATTAACCCCTCAAGTTGCATGGGCTC
AAAGGTCTAGTACTACTGATCCAGAAAGAAATTATGTCTTAATAACTGTGTCAATTGCAG
ACTGTGATGCCCCCTGAGTTAACCATTAAAGCCATCATACATCGAATTAAGGCTCAATCAA
AGCCTCATGTTGGCGATGAAAATGTCCATCATTATCAATTACACATTGATCTATACAAGG
AAATTATACCTGAAAAACAATGCATAAGGTTGCTAATGGCCAGCACTACTTTTGAAT
TGTATAAAAAGGATTTAGAATCTGAATACTGGCCACGTTTGACAAAGGAAAAGGTGAAGT
ACCCTTACATCAAACTGATTTGATAAATGGGTTGATGAAGATGAACAAGACGAAGTTG
AAGCTGAAGGTAATGATGCCGCTCAAGGAATGGATTTGAGCCAAATGATGGGAGGTGCTG
GAGGTGCTGGAGGTGCTGGAGGCATGGACTTCAGCCAAATGATGGGAGGTGCTGGTGGCG
CTGGTTCTCCAGATATGGCTCAATTCAGCAATTATTGGCTCAAAGCGGTGGTAATTTGG
ACATGGGAGATTTCAAAGAAAACGATGAAGAAGATGAAGAAGAGGAAATAGAGCCGGAAG
TGAAAGCTTAA

>YKL117W, 216 aa (SEQ ID NO 248)

MSDKVINPQVAWAQRSSTDPERNYVLITVSIADCDAPELTIKPSYIELKAQSKPHVGDE
NVHHYQLHIDLYKEIPEKTMHKVANGQHYFLKLYKKDLESEYWPRLTKEKVYPYIKTD
FDKWVDEDEQDEVEAEGNDAAGMDFSQMMGGAGGAGGAGMDFSQMMGGAGGAGSPDMA
QLQQLLAQSGGNLMDGDFKENDEEDEEEIEPEVKA

>YKR075C, 1424 bp, CDS: 501-1424 (SEQ ID NO 257)

TTCAACAGAAATGCCGTAGCCGGAACCAAGCGGGGACAGTGAAGCGTGAGAGGG
GCGAGACAGGGGGAACCTGAATGGGGTATTTTGCTTTTGCTGCATTTTTTCCGCTGGTAC
CTCTATCTTTAGGCGACCGGAAAAATTCATTTCTCATCTTTTTTTTTTTTCTCGTTCCG
ACTCGATACTTTTACAAAGAAACCCCGCGGGGAAATGTTAGATTTGAGCTTTTTCCGC
CAGGAAAAGAAAAACCTGGGGACATTAATCTTGTTTTTTTCTTTCTTCTTTGTCTCCC
TTGGATGACTGCAGAAAAAGTACAGTTACCGGGTCTTAGCAAAAACAAACATATATATAT
ATATATATGAAAGCGTATGGTCAACACGGTTTTATAGGTTTTACTTTTTGCATTCAGTTC
AACTTTGGCCCTTTCTCTTATCGCATTCAGATACTACACACAAGTGTTTCATACACACACA
AATAGATACATATACAGAAATGACTAGTTTGGACGATACAATAATTTTCGTACCAGAATA
TAATGTTACTGGATAACATGACCAACTACAACAAGCCTGCGATTGACTATTTCCATCATG
AATTTAATGATGCAAGCTTGGAATATCGGCTTCATGGACACTACTATTGAAGATGCGCA
AACATAAACTACTTCGATTACCAAGTTGCTCTTCAGAGGACGTGCTAGATTACAACATGT
ACCTCGTTAGGCTACATCATTTGCCCTGAGGCGTTGGTCCATAAATCACTATGGTTTAC
AGAACTCCAAATCCAATCCACTGTCCATCAACTGGAACAAAGAAACCGATGTAACGGTGT
TGTAACGGTCCAGATTTGACTAACATAGATAGTAATGAAAACGAAATATCGCCGGTCCAGA
ACCAAAATTGACCAGAAACAAACAAAAATCTAAATCTGCTTTAAAGAAAAATACGGAAT
GCTGGGTAAACCGAGGAGGTGGATGAGATTAACGCTTCTATAGAGAGCAATGACAACGCTT
TGGTGAATTAGAAGACATTTTCATGCCCATCGTCTGTTGATTCTCACACGCTTTCATTTT
TCGACCAGCATTTACATGCACTAAATTTCTCCATAGATGAAGATTCTGAAGACCTTA
TGAACGAAAAGAAGGAACAATTTCCCAGGAAGTTGAAGTTTAACCAAGCCGTGATGAAGA
GGGAGATCGACTCAAAGGGGACTATCCGCGAATCCCTCATCAACATAAACGATATCCAAC

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ATTCCCCGCCACCATCGCCGTCACCATCGTCGCCATCATCACCATCACCATCAAAATAGTT
CTCATTTCTGATGAAACAATAAAAGAAGCTCATTATGAGTTTACAGCAACTATACATTTGGCA
CTATGGAAGAAGACATTTTTTTATAGGAACCAGGTTGTTTTTTAA

>YKR075C, 307 aa (SEQ ID NO 258)

MTSLDDTIISYQNIIMLLDNMTNYNKPAIDYFHHEFNDALEISASWTLLKMRKHKLRL
PSCSSEVDLDYNMYLVRLHHCLWRRWSINHYGLQNSKNPLSINWNKETDVTVLYGPDLT
NIDSNENEISPQVQNIQKQTKNLKSALKKNTECWVTEEVDEINASIESNDNALVKLEDI
SCPSSVDNHTSSIFDQHSTCTKISSIDEDSEDLNNEKKEQFPRKLKFNQAVMKREIDSKG
TIRESLININDIQHSRHHRRHRRHHHHHHQNSSHSDETIKEAHYEF SNYTFGTMEEDIF
YRNQVVF

>YLR216C, 1616 bp, CDS: 501-1616 (SEQ ID NO 279)

GAAGAATACAAAGAGGTCCAAGAAGACGAAGACCCGGATGTGTGGGACACGAGAATATCC
AAGACCGGATGCTACGTAGAGAACCTCGCATTACAGCTGTGCCATGCCGAAACAGGTGAC
TGGAGGCAGTGCCTCAACGAGATGGCGTTATTTAGGAAGTGTGGGAAAAGAATGGTAAT
AGAGAGCGCGTAAGCACAGTGGACGTGGATGGGACGACCAGTAAGGATTCGGAAAAGAAG
AAATGAAAATCTAAATGTCTGTATATAACTGTATATAATAGACAGCTGCAGTGATCG
AAACACATTTGTTTCCCTTTATAGAACATAACTGTTACGCTTTTGAACGGCATTTCATGA
GCTTCTAGAAATATTTTTCCGCCCTAGCTGGAGAAAGTTCAGACAGAAAATTATTTAAATA
AGTCGAATATCAGAGGTGCTGATGCGCTCACATCAGTAACTGGTAAGACAATATT
CAGGCGATCAAGGAGTAAAAATGACTAGACCTAAACTTTTTTTGATATTTCTATTGGAG
GTAAACCCCAAGGCCGTATAGTTTTTGTAGTTGTACAATGACATAGTGCCTAAACGGCTG
AAAATTTTTTGAAGTTGTGTGAAGGAAATGCTGGTATGGCAAAGACTAAACCTGATGTAC
CATTTGTCGTAAAGGTTCCATTTTCCACAGAGTGATCAAAGACTTCATGTGTCAATTTG
GTGATTTTACCAATTTTAATGGTACTGGCGGTGAGAGCATATACGATGAAAAATTCGAGG
ATGAAAATTTCACTGTTAAACATGATAAACCATTCCTTCTATCCATGGCCAACGCCGGTC
CAAATACCAATGGATCTCAAGCTTTCATAACCTGTGTTCTTACACCTCATTGACGGGA
AGCACGTTGTGTTTGGTGAAGTGATTCAAGGTAAGAAATTTGTTGTTGATTGAAAACC
AACAATGTGACCAAGAAAACAACAAGCCATTGCGTGATGTAAAGATTGATGACTGTGGCG
TGTTACCTGACGATTATCAAGTGCCAGAGAATGCCGAAGCTACACCAACAGATGAGTACG
GCGATAATTATGAAGATGTTTTAAACAAGACGAAAAGTTGACTTGAAGAATTTTCGACA
CCGTCTTGAAAGCTATCGAAACGGTAAAGAACATTGGTACTGAACAGTTCAAGAAACAGA
ACTATTCGGTGGCTTTAGAAAAATATGTCAAATGTGATAAATCTTGAAAGAGTATTTCC
CAGAAGATTTGGAGAAGGAACAAATGAAAAAATCAATCAATTGAAAGTGTCTATTCCAT
TGAATATTGCCATCTGTGCTCTTAAATTAAGGATTACAAGCAAGTATTAGTAGCCTCAT
CGGAGGTGTTATATGCCGAAGCGGCTGACGAAAAGCCAAGGCCAAAGCTTTGTACCGTC
GTGGCCTGGCCTATTACCATGTTAATGACACAGATATGGCTCTCAATGACCTAGAAATGG
CCACTACTTTCCAGCCAAATGACGCTGCCATTTTGAAAGCTATTTCATAATACTAAATTA
AAAGAAAGCAACAAAACGAAAAGCTAAAAAGTCTCTTTCGAAGATGTTCTCTCTGA

>YLR216C, 371 aa (SEQ ID NO 280)

MTRPKTFFDISIGGKPQGRIVFELYNDIVPKTAENFLKLCEGNAGMAKTKPDVPLSYKGS
IFHRVIKDFMCQFGDFTNFNGTGGESIYDEKFEDENFTVKHDKPFLLSMANAGPNTNGSQ
AFITCVPTPHLDGKHVVFGVEVIQKRIVRLIENQQCDQENNKPLRDVKIDDCGVLPPDDYQ
VPENAEATPTDEYGDNYEDVLKQDEKVDLKNFDTVLKAIETVKNIGTEQFQKQNYSVALE
KYVKCDKFLKEYFPEDLEKEQIEKINQLKVSIPLNIAICALKLKDYQVQLVASSEVLYAE
AADEKAKAKALYRRGLAYYHVNDTDMALNDLEMAITTFQPNDAAILKAIHNTKLKRKQONE
KAKKSLSKMFS

>YLR346C, 806 bp, CDS: 501-806 (SEQ ID NO 289)

CTTATCTCAGGGTACCCATAATTTCAACCATCCTTAGCTTCCATTAAAAACACAATGAGT
TGCCTTACTAGCGAAGCGGCTTATCTGTTAATTTCTTGTGCAAACATCTTAGCTGAAAG
TGAAAAGGCACAGCGCACCTGCTGAATGCTCAACGTTTGTAAATAATCCGCCTATTTCCGC
GGAATCAATAGGGCTCCTAGCAGGCCGCCATCAATTTTTCAGCGTGCCGATTAATAATTAT
ATTACCAAGATTTCCATTTCCGCGGCTGATTCTATCAATATTAAGTAATCAATCTTTTC

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CTCGTGATTCTTTGTGATGCTCATTACAGAGGACTAATTAAGACATGTAGCACAAATATA
TTCATATAAAAGTTGGTGCAGTTAATGATTAATTGCATTGTTTTCCTTGTTCTTTCTGT
TATACCTGTGCAATTAACATAAAGTGTATATGAATTTTAAGGGGCACAAATAACAAAGG
ATTATTTATCACCTTTAATAATGCAATCGATCAGTAATTGTCCCATCGGGTTAGTTTCAA
AAAACACAATCAATTCAGCTTCCACTATTGCAGAGTGGGTAGCATGTCCATGGAAATATA
TCAACGTTGTTGGTTCAGGCAGATATGTGAGCAATAAACCTGATAAAATTACCAGATATG
ATTTACTCAAGGCTGCCAGGAAGCGGAAATGCAGGAGTTGCTTACAAGAAATGATATGA
AAGGTAGACATAAACGTAATAAGAAAAGTAAGATAGCATTGGAGACTATAGCGGAAGAAA
ACTCTTCAACTGAAAGCCTTTTTTAA

>YLR346C, 101 aa (SEQ ID NO 290)

MQSISNCPIGLVSKNTINSASTIAEWVACPWKYINVVGSGRYVSNKPKITRYDLLKAAQ
EAEMQELLTRNDMKGRHKRNKSKIALETIAEENSSTESLF

>YML129C, 713 bp, CDS: 501-713 (SEQ ID NO 297)

TAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTCCGGCACTGTTAAGGAGCCTGCTT
ACAAGAGGTACCTACATAACGTTAAAACTGGTCGAAAAGCATATTAGGGTTCAACTAAT
GATTGGGGTGTCAACGTAATGTACTTTTCTCCCAATTTTTCTTTTCATCCGTATATTTT
ACCGTAAAATGGACAAGCTAATAGCAAAACGAAAAACACGTTGTCACTTCTATATAACT
TTGCTTAAGTAAGTATTTTGTCTTTTATAATGTTACATACTGTGAAATACACTCTTTAGAA
AACACTATTTCTCTACTCTCGGAAGCAGATTTCGAAGTTCTTCCTTACTTCTGAGCTTTG
CTTCTCCTTTCCTTGCGATTAATGTTACCCGGTATACGAAATCGGAGAGGATCAGAATAAA
TGCATTGAAAGGAGCATAAATCTATACAGCGGTTTGGCAATGGTGAGAGGAAGAGAACAA
AAAATAGAACGCAGATAGTCATGTCCAAATACGCTTGGTATACCAGAGTTACAGATACAT
TACATCGTCTAACGGTACTGACGTTGGTGGTGGTACGTTATACATGTCGGGTGGCTTAG
CTTACACTTTTATACATGAACGGTAAGAAGTACGAACAACAAGTGACCCAACAAAAGGCAC
TTGAAGAAGACAATCAACAACCTGCAAAGTCCTACTGCACCTCCTACCGAGTAA

>YML129C, 70 aa (SEQ ID NO 298)

MSKYAWYTRVTDLHRLTVLTLVGGTLYMSGGLAYTLYMNGKKYEQQVTQQKALEEDNQ
LQSP TAPPTE

>YML132W, 1640 bp, CDS: 501-1640 (SEQ ID NO 299)

GTAACCTGGTTCATGAATCTTCATGTCAGATACGTAGGACAGACTCTTTCCTGTGTAAA
TATTTGTGACAGCTACGTCTATTTTCTACTAGATGTTTACACAGTTTGTACACAGGAAAT
CTACGCTTAAATATGTATTTTCATTCAAGCGGTAACCGCTGTACGAGCAGTGACATTGCT
GGTTCGACCCCTAAATGTGAACCAACGTTACGGCACACCGTGATGTACCCGCATTAAGTT
TTGTAAATTCGTTATTACGATTATCGAGTTGGCTAGATAGAAAACCGGAAATGTAATGGA
TGCCCTTTTCGAATAGCTGAGTTTCTTTTGCCATAAATAGCCCAATATTGTTGCCCTTTT
CTATCACGAGGTTACTGAGCCATTCATGAACGCGCGCGCTCGGCGGCTTTTTTTTTCT
GCTGTGCTGTATAAAAGCGAAAAGCCAGAAGTTACTATCTCGAATAAAAAACCCCTCGAA
CTGCCATCTCACTACCGAAAATGAAAGAGAATGAACCTAAAAATGAGAAGAGTGTAGATG
TATTATCCTTCAAACAGCTCGAATCCCAAAAGATTGTTCTACCTCAAGATCTTTTCAGAA
GCAGCTTTACCTGGTTTTGTTATGAAATTTACAAGTCCTTAGCGTTTCGCATCTGGATGC
TATTATGGCTACCCTTAGCGTCTGGTGGAAACTTTCCAACAATTTGATTTTACCCACTTA
TAGTTTCACTTCTGGTCCGTGTTCTGGGACCAATATTGTCTCTGTTATTGTTGGACTTT
CTCGTAAGCGTTCCCTTATCGAAACAACCTCATTCAAGTTTTCGAAAAGAGATTACTGAAAACA
CACCAAGTTCTGATCCTCATGATTGGGAAGTTGTTGCAGCAAATCTAAATTCGTACTTAT
ATGAAAATAACGTTTGGAAATACCTAAGTACTTTTTTTTCAATGCCATGGTCTGTCAAGAAG
CGTTCAGAACCAACCTTCTCGAACCATTTTCTTTGAAAAAAGATAAAGCTGCCAAGGTTA
AGTCATTTAAGGATTCCTGCTCCCTTACATTGAAGAAGCATTGGGAGTTTATTTTACAGAAG
TTGAAAAACAATGGAAATTTGTTTAATACTGAAAAATCATGGAGCCCTGTTGGCCTGGAAG
ATGCTAAACTTCCCAAGGAAGCTTACCGATTTAAGCTTACTTGGTTTTTAAAGAGGATTT
CCAATATTTTTATGTTGATACCATTCCTTAATTTTTTGTGCTGCATATATGTGTCACGGG
GAATGTGCCCTTCTATTACGCACCTTGTATCTCGGGTGGATTCTTTTCATGTTGGTACAAG
GTTTCCAAAATATAAGGGTTTTGATTATGAGCATGGAACACAAGATGCAGTTCTTGTCGA

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CTATTATAAATGAGCAAGAAAGTGGTGCGAATGGGACGAAATTGCAAGGAAAATGA
ATAGGTACTTGTGAGAAAAAGCCTGGAAGAATGAAGAGTTTTCTTCGACGGGATTG
ACTGTGAATGGTTTTTAACCACTTCTTCTACCGCGTTCTATCTGCGAAGAAATCTATGT
GGCCTTTACCATTGAATGTGGAATATGGCCATACATTAAAGAAGCGCAATTATCCCGCA
GTGAGGTGCTCTTAGTGTAG

>YML132W, 379 aa (SEQ ID NO 300)

MKENELKNEKSVDVLSFKQLESQKIVLPQDLFRSSFTWFCYEIYKSLAFRIWMLLWLP
VWWKLSNNCIYPLIVSLLVFLGPIFVLVICGLSRKRSLSKQLIQFCKEITENTPSSDPH
DWEVVAANLNSYLYENNWNKYFFFNAMVCQAFRTTLLPEPFLKKDKAAKVKSFKDSV
PYIEEALGVYFTEVEKQWKLNFTEKSWSPVGLEDKLPKEAYRFKLTWFLKRISNIFMLI
PFLNFLCCYVSRGMCLLLRLTYLGWILFMLVQGFQNIIRVLIMSMEHKMQFLSTIINEQE
SGANGWDEIARKMNRYLEKKAWKNEEFFFDGIDCEWFFNHFFYRVLSAKKSMWPLPLNV
ELWPYIKEAQLSRSEVLLV

>YMR009W, 1040 bp, CDS: 501-1040 (SEQ ID NO 301)

ACCGGTATTTTCATCTCTTCTAGATCAAGACTAAGTCTCGTTCAGTACAAGTATTTTAC
GATAGTCCATATTACTCTTCAATTAATATTTTTTTTTTATATTCTGGCCCGTTTTTGACA
CAATTTTTTCTCTCTTTTTCTCCCTATAAACTATGCAGAAGTAGCGATAATCACGATC
TTGTTAATGATTACATGTGCGCAAGTCGTATTGTCTGTCTAGATAGTGAGATGCCTTCT
AAATAACAGGAGAGAGGCAAGATAGCATAACGGCGCAATGAAGGTAATTTCTGCCAGTTT
TCTTTGCAATTGACGACTGAAAGGGCCCTTGTAAGAGCCGCTCGACAGGGCGACGCCACAG
TAGAGTCGCTAACACCGAAATATGCATATTGAAAAACATCAAAGTATAAAAAGAACAAAGA
GGGTGGCATCTGCAGATCAAAAAAACAAATAACCACCAAACAAGACACTAAAAAAGGTGCG
TAAAAAGGTCAAAAGTTAGAATGGTTAAGGTATATATTCATGACAACAAGGTTGACTCCG
ATTATCGCGCACCCCAACAATTCGGAACAGAACTTTCCCTGGATGAATTAGCCAAGTTAG
GAGTGATTTATAAATACTGTGCAAAATGAGGAAGAAGTGAATGAAATTGCTAGGCAAAGAG
AATATAAAAATAGAGATGTGGTCAACATCTGCGAAGGTTCTTCAAAGTGAAGCAGAGT
TTAATGAAAACTAGCAACATTTTACCAAGAGCATTTACATGAAGACGAAGAAATAAGAT
ACTGTCTCGAGGGTGTGGTACTTTGACGTCAGGGATGCTTCCACACCAGAGAACTGGA
TTAGGTGTTTGGTAGAGTCAGGTGATTTACTGATTCTTCCACCAGGCATCTATCATCGTT
TCACCTTGACAACCTAGCAACCACATCAAGGCCTTGAGACTGTTTAAGGACGAGCCCAAAT
GGCAAGCTATCAACAGGTCAAATCAGGCTGATTTCATGCTGTACGCAAGGACTACATTG
CCCTGATCAATCAGTACTAA

>YMR009W, 179 aa (SEQ ID NO 302)

MVKVYIHDNKVSDYRAPHNSGTLSLDELAKLGVYKYCANEEVNEIARQREYKNRDV
VNICEGSFKSEAEFNEKLATFYQELHEDEEIRYCLEGAGYFDVRDASTPENWIRCLVES
GDLILPPGIYHRFTLTSSNHIKALRLFKDEPKWQAINRSNQADSLPVRKDYIALINQY

>YMR011W, 2126 bp, CDS: 501-2126 (SEQ ID NO 303)

GCAGCTTCACTTTTAAGTTTCTTTTTCTCTCACGGCGCAACCGCTAACTTAAGCTAATC
CTTATGAATCCGGAGAAAAGCGGGTCTTTTAAGTCAATAAAATTTCCGAAATCCTTTT
TCCTACGCGTTTTCTTCGGGAAGTAGATAGGTGGCTCTTCCACCTGTTTTTCCATCATTT
TAGTTTTTTCGCAAGCCATGCGTGCCTTTTCGTTTTTTCGATGGCGAAGCAGGGCTGGAAA
AATTAACGGTACGCCGCCTAACGATAGTAATAGGCCACGCAACTGGCGTGGACGACAACA
ATAAGTCGCCCATTTTTTATGTTTTCAAACCTAGCAACCCCCACCAAACCTGTGCATCGT
TCCCGGATTACAAATGATATAAAAAGCGATTACAATTCTACATTCTAACCAGATTTGAG
ATTTCTCTTTCTCAATTCCTCTTATATTAGATTATAAGAACAACAAATTAAATTACAAA
AAGACTTATAAAGCAACATAATGTCTGAATTCGCTACTAGCCGCGTTGAAAGTGGCTCTC
AACAAACTTCTATCCACTCTACTCCGATAGTGAGAAATTAGAGACGGATGAATCTCCTA
TTCAAACCAAATCTGAATACACTAACGCTGAACTCCAGCAAAGCCAATCGCCGCATATT
GGACTGTTATCTGTTTTATGTCTAATGATTGCATTTGGTGGGTTTGTCTTTGGTGGGATA
CTGGTACCATCTCTGGTTTTGTAAATCAAACCGATTTCAAAGAAGATTTGGTCAAATGA
AATCTGATGGTACCTATTATCTTTCCGACGTCGGACTGGTTGATCGTTGGTATCTTCA
ATATTGGTTGTGCCTTTGGTGGGTTAACCTTAGGACGCTGGGTGATATGTATGGACGTA

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GAATTGGTTTGATGTGCGTCGTTCTGGTATACATCGTTGGTATTGTGATTCAAATTGCTT
CTAGTGACAAATGGTACCAATATTTTCATTGGTAGAATTATCTCTGGTATGGGTGTCGGTG
GTATTGCTGTCTATCTCCAACCTTTGATTTCCGAAACAGCACCAAAACACATTAGAGGTA
CCTGTGTTTCTTTCTATCAGTTAATGATCACTCTAGGTATTTCTTAGGTACTGTACCA
ACTATGGTACTAAAGACTACTCCAATTCAGTTCAATGGAGAGTGCCCTTTGGGTTTGAAC
TTGCCTTCGCTATTTTCATGATCGCTGGTATGCTAATGGTCCAGAATCTCCAAGATTCT
TAGTCGAAAAAGGCAGATACGAAGACGCTAAACGTTCTTTGGCAAAATCTAACAAAGTCA
CCATTGAAGATCCAAGTATTGTTGCTGAAATGGATACAATTATGGCCAACGTTGAAACTG
AAAGATTAGCCGGTAACGCTTCTTGGGGTGAGTTATTCTCCAACAAAGGTGCTATTTTAC
CTCGTGTGATTATGGGTATTATGATTCAATCCTTACAACAATTAACGGTAACAATTACT
TCTTCTATTATGGTACTACTATTTTCAACGCCGTCGGTATGAAAGATTCTTTCCAAACTT
CCATCGTTTTAGGTATAGTCAACTTCGCATCCACTTTCGTGGCCTTATACACTGTTGATA
AATTTGGTCGTCGTAAGTGTCTATTGGGTGGTTCGCTTCCATGGCCATTTGTTTTGTTA
TCTTCTCTACTGTCCGTGTCACAAGCTTATATCCAAATGGTAAAGATCAACCATCTTCCA
AGGCTGCCGGTAACGTCATGATTGTCTTTACCTGTTTATTCATTTTCTTCTTCGCTATTA
GTTGGGCCCCAATTGCCTACGTTATTGTTGCCGAATCCTATCCTTTGCGTGTCAAAAATC
GTGCTATGGCTATTGCTGTTGGTGCCAACTGGATTGGGGTTTCTTGATTGGTTTCTTCA
CTCCCTTCATTACAAGTGCAATTGGATTTCATACGGGTATGTCTTCATGGGCTGTTTGG
TATTTTCAATCTTCTACGTGTTTTCTTTGCTGTGAAACCAAGGGCTTAACATTAGAGG
AAGTTAATGAAATGTATGTTGAAGGTGTCAAACCATGGAAATCTGGTAGCTGGATCTCAA
AAGAAAAAAGAGTTTCCGAGGAATAA

>YMR011W, 541 aa (SEQ ID NO 304)

MSEFATSRVESGSQQTSIHSTPIVQKLETDESPIQTKSEYTNAELPAKPIAAYWTVICLC
LMIAFGGFVFGWDTGTISGFVNQTDKRRFGQMKSDGTYLSDVRTGLIVGIFNIGCAFG
GLTLGRLGDMYGRRLGMLCVLVYIVGIVIQIASSDKWYQYFIGRIISGMGVGGIAVLSP
TLISETAPKHIRGTCVSFYQLMITLGIPLGYCTNYGTDYSNSVQWRVPLGLNFAFAIFM
IAGMLMVPESPRFLVEKGRYEDAKRSLAKSNKVTIEDPSIVAEMDTIMANVETERLAGNA
SWGELFSNKGAILPRVIMGIMIQLQLTGNVYFFYYGTTIFNAVGMKDSFQTSIVLGIV
NFASTFVALYTVDFKRRKCLLGSSASMAICFVIFSTVGVTSLYPNGKDQPSKAAGNVM
IVFTCLFIFFFAISWAPIAYVIVAESYPLRVKNRAMAIAVGANWIWGLIGFFTPTFITS
IGFSYGYVFMGLVFSFFYVFFVFCETKGLTLEEVNEMYVEGVKPKWKSWSISKEKRVSE
E

>YMR099C, 1394 bp, CDS: 501-1394 (SEQ ID NO 307)

AACAGTTCACCTCGATCTACATATATTTCAATGCGAGAATGATTAATCTTGCCATTGAC
AAACAACCCTTTTACTGCCAGCGCCTTTTCATAACCATGTAGTTTTATATGCCAATTATA
ATAAAGCATGACATATAATGCCAACCCCATATTTATATAGTTAACTTGAAACCGAGATTC
ATCTATTGCACCAGGAAAAAGTGCCCTTCTTCTTAAAAACATAAGTTACGTCCCGACCATTC
TCTAAACGGCATCAATCATTCAGCAGAAGAAATAGTGTGTAGATGTCTCGTTCGCTAG
ACGCAGTCAATGATAACAAGGTCTTTCTTCAAGCTGTCTTTCCATAAAAAGGTATCGCAA
ATGGGGTCACCAATGCGCCTTTTATTTTTTACGCCGAAAGAAACTTAGTAGGTCCCTAG
AAATGAATAAAGAGGTGATTCTGAGGTTCATTATAAGCCTTTGGTAAAACTTGAACCAAG
AAAGATTAAAAACACAAAGCCATGCCTATCAAAGAACTGATAAAGAAAGTTGTTTGTACTC
ATCCAGCTGATGAGACCACCAGCGTTCATATTTCTAAAGTACGGTGCTACAGTTTATTCCT
GGAAATTGAAATCTGAAGAACAGTTGTGGTTGTCTACTGCTGCTAAATTGGATGGTAGCA
AACCTGTGAGAGGTGGTATACCTTTTGGTCTTTCTGTATTTCGGGAAAAATAGCACCAGATG
AACATTTGAGTAAATTACCTCAACATGGTCTTGCAAGAAATTTCTACTTGGGAGTTTTTGG
GTCAAACTAAGGAAAAACCCACCGACCGTACAATTTGGCTTGAAACCAGAAATTGCTAACC
CAGAATTGACCAATTTGTGGCCAAATGGATTATCTTTTGATTTTGACTGTTGAATTAGGCT
CCGATTATTTGAAAACTGCCATAGAAGTAGAAAACACATCTAGTTCCAAGGAATTAAAGT
TCAACTGGTGTTCATACATACTTCCGTATCGAAGATATTGAAGGAACAATGGTCTCTA
ATTTAGCTGGCATGAACTTTATGACCAACTGTTGAAGGAATCCTACGTCGACAAGCACC
CAGTCGTTACCTTCAATCAAGAAACCGATGTAATTTATCAGAAATGTCAGCGCCGAACGGG
CCATTCAAATAGTTGACAAAGGGCTTCAAATTCACACTCTAAAAAGATACAACCTGCCCCG
ACACTGTTGTTTGGAAATCCATGGATTGAGAAGTCTCAAGGGATGGCCGATTTTCAACCAA

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AAACTGGTTACCAACAAATGATATGTATTGAACCTGGTCATGTTTCATGATTTTATTTTCCT
TGGCTCCTGGTAAAAAATGGAATGCTTATCAATTACTTTGCAAAGAAGAATTGAAATATC
AAGCTATTCAATAA

>YMR099C, 297 aa (SEQ ID NO 308)

MPIKETDKEVVLTHPADETTSVHILKYGATVYSWKLKSEQLWLSTAAKLDGSKPVRGGI
PLVFPVFGKNSTDEHLSKLPQHGLARNSTWEFLGQTKENPPTVQFGLKPEIANPELTKLW
PMDYLLILTVELGSDYLKTAIEVENTSSSKELKFNWLFHTYFRIEDIEGTMVSNLAGMKL
YDQLLKESYVDKHPVVTFNQETDVIYQNVSAERAIQIVDKGVQIHTLKRYNLPDVTVVWNP
WIEKSQGMADFEPKTYQQMICIEPGHVHDFISLAPGKKWNAYQLLCKEELKYQAIQ

>YMR110C, 2099 bp, CDS: 501-2099 (SEQ ID NO 311)

AAGAGAGAGAAGCTAGATTATCATTACAGCAGCCACATAGTATACCAAATTCAGTACAG
GCACACCAGAACATGATCAAGACACTTAGAGGAAATGGAACAACGAATTTCCAGCCAAAA
ATTCCGAGTAGTTTCATGATGAAAGATTTTACATGCATTTTATATATAAATATATACCGT
CCTATATGGATTTTCATGCCAACAGGGTATATAATAGACAATTACCGGTGTACTGATATAT
CAACTATCGACTCCAAGCCTTTTATCTATCAGTCAATTTTACATCAAGATCCCACTTTTA
GATAGGTTTCGAAAATTCATCTAATATTAGTGATTTAATTAGATGGTGGATTGCTTACCC
TTTTTTTTTGTCGTTTTAGGAGGAGATTCTTCGGATTTTAGGGATAAACGGGATACTCCATA
TATAAAAAACAAAACCTCAGGCATATTGATTATCTAAAAGGAATATTCTAAAACCATAGC
CATAGTAATTTATCACCAACATGTCAAACGACGGCTCAAAAATATTGAATTATACCCCAG
TGTCTAAAATAGATGAAATAGTTGAAATCTCAAGAAATTTCTTCTTTGAGAAACAATTGA
AATTGTTCCACGAAAATAACCAAGGAAAAAAGATCTAGAATTCAGGCAGTTGCAGTTGA
AAAACTCTATTATGCCGTCAAAGATCATGAGGAAGAACTGATCGATGCTATGTACAAGG
ACTTTTCATCGGAACAAAATTGAATCGGTTCTGAATGAAACGACCAAACCTTATGAACGATA
TACTTCACCTAATTGAGATTTTACCAAATTTGATCAAACCTCGGAGAGTATCTGATTCTT
CTCCTCCATTTATGTTTGGTAAAACAATCGTGAGAAAATATCAAGGGGCAGTGTCTTGA
TTATTGCTCCTTTCAATTTTCCCCTACTTTTAGCATTTGCCCCATTTGGCAGCAGCTCTTG
CTGCAGGTAACACCATTGTTCTGAAGCCAAGTGAACCTAACACCACACACTGCTGTAGTTA
TGGAAAATTTGTTAACCACAGCTGGTTTCCCTGATGGATTGATTCAAGTAGTTTCAGGGAG
CTATAGATGAAACTACAAGACTACTAGATTGTGGAATAATTTGACCTAATATTCTACACAG
GTTCTCCCCGTGTCGGATCAATAGTTGCTGAGAAAGCAGCAAAAAGTCTAACACCTTGTG
TACTTGAACCTGGTGGTAAATCACCTACCTTTATTACAGAAAATTTCAAAGCAAGTAACA
TAAAAATTGCTTTGAAAAGGATTTTTTTTTGGTGCTTTCCGAAATTTCTGGCCAGATTTGTG
TTTACCAGATTATTGTTAGTACATAAATCTATCTATCCAAAAGTCATTAAAGAGTGTG
AATCAGTACTAATGAATTTTATCCAAGCTTTGATGAACAAACAGATTTCACTCGTATGA
TTCATGAGCCTGCTTACAAAAAGGCCGTTGCAAGTATAAACTCAACTAACGGCTCCAAGA
TGTGCTTCAAAAAATTTCTATCAATTCAGATACTGAGGATCTATGCCTTGTACCACCAA
CCATAGTTTATAACATTGGTTGGGATGATCCTTTGATGAAACAGGAAAACCTTTGCTCCTG
TATTGCCCATCATTGAGTACGAGGATCTTGATGAGACCATTAAACAAGATAATAGAAGAAC
ATGACACTCCATTGGTGCAATACATATTCTCTGATAGCCAACTGAAATAAATCGTATCT
TGACGCGCTTAAGATCTGGTGAATGTGTTGTCGGTGATACAGTGATTTCATGTAGGAATTA
CCGACGCTCCATTTGGAGGGATCGGTACTTCAGGTTATGGTAATATGGTGGATATTATG
GATTCAATACCTTTAGTCATGAAAGAACAATTTTTAAACAACCATATTGGAATGATTTTA
CCCTTTTTTATGAGATACCTCCAAATAGCGCACAAAAGGAAAAGCTCGTCCGTTTTGCGA
TGGAAAGAAAACCTTGGTTTGACAGAAATGGCAATAACAAGTGGGGGTACGCCAATATT
TTTCATTATCTGCCGCCGTTATTTTAATTAGTACCATTTCAGCTCATTGTTCTTCTGA

>YMR110C, 532 aa (SEQ ID NO 312)

MSNDGSKILNYTPVSKIDEIVEISRNFEEKQLKLSHENNPRKKDLEFRQLQLKKLYYAV
KDHEEELIDAMYKDFHRNKIESVLNETTKLMNDILHLIEILPKLIKPRRVSDSSPPFMFG
KTIVEKISRGSVLIIAPFNFPLLLAFAPLAAAALAAGNTIVLKPSELTPHTAVVMENLLTT

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AGFPDGLIQVVQGAIDETTRLLDCGKFDLIFYTGSPPRVGSIVAEKAAKSLTPCVLELGGK
SPTFITENFKASNIKIALKRIFFGAFNSGQICVSPDYLLVHKSIIYPKVIKECESVLNEF
YPSFDEQTDFTMRIHEPAYKKAVASINSTNGSKIIVPSKISINSDTEDLCLVPPTIVYNIG
WDDPLMKQENFAPVLPPIEYEDLDETINKIEEHDTPLVQYIFSDSQTEINRILTRLRSG
DCVVGDTVIHVGITDAPFGGIGTSGYGNYYGGYGFNTFSHERTIFKQPYWNDFTLFMRYP
PNSAQKEKLVRFAMERKPWFDRNGNNKWGLRQYFSLAAVILISTIIYAHCSS

>YMR173W-A, 1685 bp, CDS: 501-1685 (SEQ ID NO 691)

AAAAAACCACCTCCGAAGGTTTCGAGGATGACAAATCGCCCCCTTAGCTGTGGCCATACAAGC
TTGGCACCCGACGAAAAAGGGAAAAAGGAAAAAGAAATGTCGTACAAGAACTCTTACAACCAC
GTTGAGATTTTCATTTAACAACGCCCCCTTTCCATTATATAAGAAGGCATTAATTTTTTAT
GTAATAAAAAAAGAATTTCTCGAAAATGTCTTACAATTAATTTTTTTCTTTTGTAGAGTAG
GGCTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCAATGGGTTT
ATTTGATAAAGTGAAGCAATTTGCTAACAGCAATAATAACAACAATGATTCTGGCAATAA
CAATCAAGGCGATTATGTTACCAAAGCTGAGAATATGATCGGCGAAGATAGAGTCAATCA
ATTCAAAAGCAAAATCGGAGAGGACAGATTTGATAAGATGGAGTCCAAGGTTTCGTCAACA
ATTTTCTAATACCTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTTCTAA
TAACAACGATTTCATATGGTTCTAACAACAATGATTTCATATGGCTCTAACAACAATGATTC
ATATGGCTCCAACAACAATGATTTCATATGGCTCTAACAACGATGATTCCTACGGTTCTTC
CAACAAGAAGAAGAGCTCTTATGGTTCTAACAATGACGATTTCGTACGGCTCCAGCAACAA
CAATGACTCTTACGGTTCCAACAACAATGACTCTTACGGTTCCAACAACAATGACTCTTA
CGGTTCCAACAATGACGACTCTTACGGTTTCGTCAACAAGAATAAGAGCTCTTACGGTTC
CAACAATGACGATTCTTATGGCTCTAACAATGATGATTTCATATGGTTCTTCCAACAAGAA
GAAGAGTTCTTATGGTTCCAGCAACAACGATTCGTATGGTTCTAACAACGATGATTTCATA
TGGTTCTAACAACAATGATTTCATATGGCTCTAACAACGATGATTTCCTACGGTTCTTCCAA
CAAGAAGAAGAGCTCTTATGGTTCTAACAATGACGATTTCGTACGGCTCCAGCAACAACAA
TGACTCTTACGGTTCCAACAATGACGACTCTTACGGTTTCGTCAACAAGAATAAGAGCTC
TTACGGTTCTTCTAGCAACGATGATTCTTACGGATCTTCCAATAACGACGACTCTTACGG
TTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCCAACAATGACGATTCTTATGGCTCTAA
CAATGATGATTTCATATGGTTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCCAGCAACAA
CGATTTCGTATGGTTCTAACAACGATGATTTCCTACGGTTCTTCTAACAAGAAGAAGAGTTC
TTATGGTTCCAACAACGATGATTTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTC
CAACAATGACGACTCTTACGGTTCTCTAATAGAAACAAGAATCCTATGGGTCTTCCAA
CTACGGTTTCATCCAACAATGATGACTCTTATGGTTTCATCTAATAGAGGCGGTGTAATCA
ATACGGTGGTGACGACGATTACTAAGTTTTTGGATGCTTCGATAAAAAAATATATATAT
TGTGTTTAGACTTAAGTATGAAAATTTTATGTATGAGCTGTGGCTATGTATCCGCTGGCA
AATAG

>YMR173W-A, 394 aa (SEQ ID NO 692)

MTTTPTTTTTHMVLITTIHMLVLTMIHMLTMIHMAPTTMIHMLTMIPTVLPTRRRAL
MVLMTIRTAPATMTTLTVPTMTTLTVPTMTTLTVPTMTTLTVRQTRIRALTVPMTILM
ALTMIMHMLVLPTRRRVLMVPATTIRMVLTMIHMLVLTMIHMLTMIPTVLPTRRRALM
VLTMTIRTAPATMTTLTVPTMTTLTVRQTRIRALTVLLATMILTDLPIITTLTVLPTRRR
VLMVPTMTILMALTMIMHMLVLPTRRRVLMVPATTIRMVLTMIPTVLLTKRRVLMVPTM
IHTAPATMTTLTVPTMTTLTVPLIETRTPMGLPTTVHPTMPLMVHLIEAVVINTVVTTI
TKFLDVFDKKNILLCLDLSMKILCMSCGYVSAGK

>YNL031C, 911 bp, CDS: 501-911 (SEQ ID NO 325)

CAACAGCCCAGGCGGAGTGAACAACATATTAATTAACGCCTTCTGTGTCAGTTGTTTT
GTTCTGGTCTGGTCTGCATTTTCGCGCCCGAAAAAGCTTGAGACGCGAAGCTCCCAGAACG
TCCTGCCATACAAATGCGAACTCTCGGTCTAGTACCACCTTCCCGGTGCCAAACGACCA
CAGTTGTCCGTTCCGAGCACTTCGCATTAAGCGCGTGAACCTATGGCACGCCCTAAGGG
GCTCCTACGGATGGGAGTTGGTCATTTAGCGTTCATTATCGCCCAATGTGACGCACAATC
ACGGCTATGGCTCGGTGTCAAAACATAGTTTGGCGTGATAACAGCGTGTGTGTCTCTCG
CGTTGCTTCTTGTGACCGCAGTTGTATATAAATAATCTTTTTCTGTCTCTTTATATAGG
ACCACTGTTTTGTGACTTCCACTTTGGCCCTTCCAACCTGTTCTTCCCCCTTTTACTAAAGG

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ATCCAAGCAAACACTCCACAATGGCCAGAACTAAACAAACAGCTAGAAAAATCCACTGGTG
GTAAAGCCCCAAGAAAAACAATTAGCCTCCAAGGCTGCCAGAAAATCCGCCCCATCTACCG
GTGGTGTTAAGAAGCCTCACAGATATAAGCCAGGTACTGTTGCCTTGAGAGAAATTAGAA
GATTCAAAAATCTACTGAACGTGTGATCAGAAAGTTACCTTTCCAAAGATTGGTCAGAG
AAATCGCTCAAGATTTCAAGACCGACTTGAGATTTCAATCTTCTGCTATCGGTGCTTTGC
AAGAATCCGTCGAAGCATACTTAGTCTCTTTGTTTGAAGACACTAATCTGGCTGCTATTC
ACGCTAAGCGTGTACTATCCAAAAGAAGGATATCAAATTGGCCAGAAGACTAAGAGGTG
AAAGATCATGA

>YNL031C, 136 aa (SEQ ID NO 326)

MARTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVLREIRRFQKSTE
LLIRKLPPQRLVREIAQDFKTDLRFSQAIGALQESVEAYLVSLFEDTNLAAIHAKRVTI
QKKDIKLARLRGERS

>YNL134C, 1631 bp, CDS: 501-1631 (SEQ ID NO 331)

AAACTCGGAAACTCTTTTTCTATTCTATCTTCCCTTCTCGTACGTGCCCACGGAAGCAATA
AAAAGAACCGAAATAACCAACACCCGTAACGTCAAAGCATTTCATGCTTAGAATGGAAACC
ATTTCTGTGAATGAAATGGCAAATTGATCACATTGATTGCTCGTTCCACTACCTGTGTCC
GCAATTTTTTAATGGTCATCACAGCCCCTGCTGACTAAAGTTCTTCGGATCCGCTTACGG
TTGTGCGCGCGTTCCGCCCCCTGCGTACTCTTAGTACCTAGCATATGGGCTCCCTCCGTTG
GATTGGCATCGATTAGTAAGGACAGATGTTAAGGATTAAAGACCGTTTTTAAGGTATTTTC
GGCAATGCTTCGATTTAAAGGAGAGAGTTTTTTTTTTTGGCGTTTTCTTCTCTCACTTC
TTGATTAGTACTGTAATTCTAGTTGAAAAAAAATCGTTAACTATACACAGCAAAAAGCAA
TATCATACTGCATATCAAGCATGTCCGCCTCGATTCCAGAAACCATGAAAGCCGTTGTCA
TTGAAAATGGCAAGGCTGTAGTCAAACAGGACATTCCAATTCTGAATTAGAAGAAGGAT
TTGTTCTAATTAAGACTGTGCGCGTTGCGGTAACCTACCGATTGGAAACATATTGATT
TCAAGATTGGTCTCAAGGTGCCCTCTTAGGCTGTGATGCAGCCGGCCAAATCGTAAAGT
TGGGCCCAAATGTTGATGCTGCACGCTTTGCCATTGGTGATTACATTTATGGGGTTATTC
ACGGTGCTTCAGTGAGGTTCCCTCAAACGGTGCCTTTGCTGAGTACTCTGCCATTTTCAT
CCGAGACTGCTTATAAACCAGCCAGAGAGTTTAGATTGTGCGGTAAAGACAAGCTACCAG
AAGGCCCGTAAATCTTTAGAAGGGGAGTATCCCTCCAGTCTCATTGACCACGGCTG
GTATGATCCTTACACATAGTTTTGGCTTGGACATGACATGGAAGCCCTCCAAAGCGCAA
GAGATCAACCCATCTTATTTTGGGGTGGTGCCACTGCTGTTGGCCAGATGCTTATTCAAT
TGGCAAAAAAACTAAACGGTTTCAGCAAGATCATCGTCGTTGCTTCTCGTAAACATGAAA
AATTGTTGAAAGAGTACGGTGCAGATGAACTTTTTGACTACCACGATGCTGACGTTATCG
AACAGATAAAAAAGAAGTACAACAACATTTCCTTACTTGGTGGACTGTGTCTCCAACACAG
AACTATTCAACAGGTGTACAAATGTGCCGCTGATGACTTAGACGCTACGGTCGTTCAAT
TGACCGTTTTTAACCGAAAAAGATATCAAGGAGGAAGACAGGAGGCAAAACGTCAGTATTG
AAGGAACCTTCTATATTTGATAGGAGGTAACGACGTCCCATTTGGCACGTTTACTTTGC
CAGCAGACCCTGAATACAAGGAAGCCGCATAAAATTTATTAAGTTCATCAATCCAAAAA
TCAATGATGGTGAAATCCACCACATCCAGTGAAAGTTTACAAGAACGGGTTAGATGATA
TCCCACAGTTACTTGATGATATTAAGCACGGGAGGAATTCTGGCGAAAAGTTGGTTGCCG
TCTTGAAATAA

>YNL134C, 376 aa (SEQ ID NO 332)

MSASIPETMKAVVIENGKAVVKQDIPIPELEEGFVLIKTAVAVAGNPTDWKHIDFKIGPQG
ALLGCDAAAGQIVKLGPVNDAAARFAIGDYIYGVHIGASVRFPSNGAFAEYSAISSETAYKP
AREFRLCGKDKLPEGPVKSLEGAVSLPVSLTTAGMILTHSFLDMTWKPSKAQRDQPILF
WGGATAVGQMLIQLAKKLNGFSKIIVVASRKHEKLLKEYGADELFDYHDADVIEQIKKKY
NNIPYLVDCVSNTEIQQVYKCAADDLDATVVQLTVLTEKDIKEEDRRQNVSIETLLYL
IGGNDVPFGTFTLPADPEYKEAAIKFIKFINPKINDGEIHHIPVKVYKNGLDDIPQLDD
IKHGRNSGEKLVAVLK

>YNR002C, 1349 bp, CDS: 501-1349 (SEQ ID NO 339)

ATGGACAATTTGAAGTTCCTTGACTACCCCTATCTCACACTAGTACGTAATTCAATGTATC
ATTCTGATTGTAAGTAGATAGAGACGCAATACAGGAAAGCTGACCTTCCTTCCAATCACC

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ACGGCTGAAATGCTTTTGTGACCAATTACGGACGCTTAAGAGCGGACGCGGCTGGAACGG
CTCCATCCTAAATCGGCCGAGGGAGAACTCCGATACCAGCCGACATGGCAATAATAGTGA
CAGTAGATGCTACCAGCCCCGCAATAATTTACAGTAGATCATCAACAGTCTCCTCATTT
CTGGAAATGATCAGCAACTTCGACGGATTTAACTCTCAAGCAGTTACGCACTCCGAGAAC
AGCCGTGATCATCTTTGAACAAGCAAAATATATAAAGCAGGAGAACTGTCTTACCTAGAG
CTAGAATAGCCATAACTAACTATGTAAACATTTCTACAGATCAATCAAAAACAACTTTCAAT
CACAGAAAAAATAAAAGGCAATGTCTGACAGAGAACAAAGCAGCGGCAACACCGCTTTTG
AGAACCCCTAAGGCACCTCGATTCTTCCGAGGGTGAGTTTCTCTGAAAACAACGATCAGA
GCCGCCACTCGCAAGAGTCCATATGCAAAATATATACTGCGGGCAAAAACAACGAGTATA
TTTACATCGGCCGCTCAAAAATTTTTAAGGGATGATTTGTTGAGGCATTCGGTGGTACTC
TGAATCCCGGTTTAGCCCCCGGCCAGTCCATAAATTCGCAAACTCCTGCTCCACTAGGAC
TTTCCGGTTTTTGCCCTCACTACGTTTGTCTTATCCATGTTCAATGCAAGAGCCCAAGGCA
TCACTATCCCTAATGTTGTTGTTGGGTGTGCCATGTTTTACGGTGGCCTCGTTCAACTCA
TTGCTGGTATTTGGGAAATCGCTTTAGAGAACACTTTCCGGTGGTACAGCCCTGTGTTCTT
TCGGCGGTTTTTGGTTAAGCTTCGGTGCTATATACATCCCTTGGTTTGGAAATCTAGATG
CCTATAAGGACAAGGAATCCGACCTTGGAAATGCGCTAGGGTTTTACCTCCTAGGATGGG
CACTCTTCACCTTCGGTCTTTCCGCTGTCACCATGAATCAACTATAATGTTTTTGCCT
TATTCTTCTCTTAGCAGTGACCTTCTTACTTCTATCCATTGCAAACTTCACAGGCGAAG
TTGGCGTCACTAGAGCTGGTGGGGTCTTGGTGTGATAGTAGCCTTCATTGCCTGGTACA
ACGCTTACGCAGGTATTGCCACAAGACAAAACCTCGTACATTATGGTCCATCCATTGCGAT
TACCTAGCAATGATAAGGTGTTCTCTAA

>YNR002C, 282 aa (SEQ ID NO 340)

MSDREQSSGNTAFENPKALDSSEGEFISENNDQSRHSQESICKIYTAGKNNEYIYIGRQK
FLRDDLFEEFGGTLNPG LAPAPVHKFANPAPLGLSGFALTTFVLSMFNARAQGITIPNVV
VGCAMPFYGGVLQLIAGIWEIALENTFGGTALCSFGGFWLSFGAIYIPWFGILDAYKDKES
DLGNALGFYLLGWALFTFGLSVCTMKSTIMFFALFLLAVTFLLLSIANFTGEVGVTRAG
GVLGVIVAFIAWYNAYAGIATRQNSYIMVHPFALPSNDKVFF

>YOL139C, 1142 bp, CDS: 501-1142 (SEQ ID NO 347)

ACAAGTTTGGATACTGGTATTGTGACTCTTGTAAGAAGAAGAATACATCTTGTGTTCTAT
GTGAAAGACCATTAAAGAAACTGACCATGGTCATCCTCCCCTGTGGACACGAAGGTCACT
TCCAGTGCATACAAGAATGGTTTCTCGATGAGAATGAACAAGAATGTCCCGGCGGTTGCC
CCGGTGTGCAATTCATCTAGGTTCTCCACATAATGTATAGTTTAAACATATCATCACCATT
GTTTAGTTAAATCGTTTAGAGTAATATTACCCGTCAAAAGGTGCGGTAATAATTTATTA
CCCTCTCCGAAAAGAAAATTTTTTTCGTCGTCATAGAGTTTAAATGCAATACCTGATAAA
GAGAGTTTTACATTGCAAGAGGTAGTGTTAATTCTGGATTATATTGTACATATGTGTTT
AGTTTAGTGCTTGGTACTTCTAGGAGTTTACGAAAATAAAAGCATTTTTGTCTGAA
AAGCTAGTGAAGGAAGAAAATGTCCGTTGAAGAAGTTAGCAAGAAGTTGAAGAAAACG
TTTCAGTCGATGATACCACAGCTACTCCAAAGACTGTTTTAAGTGACAGTGCTCACTTCG
ATGTCAAGCACCCATTGAACACCAAATGGACTTTATGGTACACAAAGCCAGCCGTCGATA
AATCTGAGTCGTGGTCTGATCTATTACGTCCCGTCACTTCATTCCAAACTGTTGAAGAAT
TTTGGGCTATCATTCAAAATATTCTGAGCCACACGAACCTACCATTGAAATCAGATTACC
ACGCTCTTCCGTAATGACGTTAGACCTGAATGGGAAGATGAAGCCAATGCTAAAGGTGGTA
AATGGTCTTTCCAACCTTAGAGGAAAAGGTGCTGATATTGATGAATTATGGCTAAGAACTT
TACTAGCAGTTATTGGTGAAACAATTGATGAAGACGACTCCCAAATTAACGGTGTCTGTTT
TAAGCATTAGAAAAGGTGGTAACAAGTTTGCCTTATGGACTAAATCTGAAGACAAAGAAC
CACTATTGAGAATTGGTGGTAAATTCAAGCAAGTTTTAAAATTAACCGATGACGGGCATT
TGGAATTCTTTCCACATTCCAGTGCCAATGGTAGACACCCTCAACCATCAATCACCTTGT
AA

>YOL139C, 213 aa (SEQ ID NO 348)

MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHFDVKHPLNTKWTLWYTKPAVDKSESWS
LLRPVTSFQTVEEFWAI IQNIPPEHELPLKSDYHVRNDVRPEWEDEANAKGGKWSFQLR
GKGADIDELWLRLTLLAVIGETIDEDDSQINGVLSIRKGGNKFALWTKSEDKEPLLRIGG
KFKQVLKLTDDGHLEFFPHSSANGRHPQPSITL

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>YOR120W, 1439 bp, CDS: 501-1439 (SEQ ID NO 353)

TGTC TTACATATTGCAATGGATATGCTTGGGTGATCATACTTCCTGGCTTTAGATATTTG
AAACTTAACTCTTGTCAACAAACTTCCTATGGAGTGATATAAGAATTGTAAGTTATAACAC
CGGCGAACAATCGGGGAGACATTTCCGGGGAAGAACAAGGAAGGGCGGCTTTTCTCCC
TCATTGTCATAGCAAGGTCATTTCCGCTTCTCAGAAAGGGGTAGAATCAATCTAGCACGC
AGATTGCAAACACGGCTTAATAATATGCCATCAGGCATTCACCCGTGTGACGAATCGCA
CACCGCTGCTCTCTTAATTTCCCTAGAGTAGAAACCGAGCTTTCAGGAAAAGACTACGGC
AGTAAAGAATTGCTTTACTGGGCGTATAAAACCGGAGAATCAAGACATTTCTAATGACTT
GATTCAGGATGAGAGCTTAATAGGTGCATCTTAGCAAGCTAAAATTTGGACAGCTCTCAT
TACTAAATTAAGATAGAAAAATGCCGTGCTACTTTACATGATTCTACGAAAATCCTTTCTC
TAAATACTGGAGCCCAAATCCCTCAAATAGGTTTAGGTACGTGGCAGTCGAAAGAGAACG
ATGCTTATAAGGCTGTTTTAACCGCTTTGAAAGATGGCTACCGACACATTGATACTGCTG
CTATTTACCGTAATGAAGACCAAGTCGGTCAAGCCATCAAGGATTCAGGTGTTCTCGGG
AAGAAATCTTTGTTACTACAAAGTTATGGTGTACACAACACCACGAACCTGAAGTAGCGC
TGGATCAATCACTAAAGAGGTTAGGATTGGACTACGTAGACTTATATTTGATGCATTGGC
CTGCCAGATTAGATCCAGCCTACATCAAAAATGAAGACATCTTGAGTGTGCCAACAAAGA
AGGATGGTTCTCGTGCAGTGGATATCACCAATTGGAATTTTCATCAAAACCTGGGAATTAA
TGCAGGAAC TACCAAGACTGGTAAACTAAGGCCGTTGGAGTCTCCAAC TTTCTATAA
ATAACCTGAAAGATCTATTAGCATCTCAAGGTAATAAGCTTACGCCAGCTGCTAACCAAG
TCGAAATCACTCATTACTACCTCAAGACGAATTGATTAAATTTTGTAAAAGTAAAGGCA
TTGTGGTTGAAGCTTATTCTCCGTTAGGTAGTACCGATGCTCCACTATTGAAGGAACCGG
TTATCCTTGAAATTGCGAAGAAAAATAACGTTCAACCCGGACACGTTGTTATTAGCTGGC
ACGTCCAAAGAGGTTATGTTGTCTTGCCAAATCTGTGAATCCCGATCGAATCAAAACGA
ACAGGAAAATATTTACTTTGTCTACTGAGGACTTTGAAGCTATCAATAACATATCGAAGG
AAAAGGGCGAAAAAAGGGTTGTACATCCAAATTGGTCTCCTTTTCAAGTATTCAAGTAA

>YOR120W, 312 aa (SEQ ID NO 354)

MPATLHDSTKILSLNTGAQIPQIGLGTWQSKENDAYKAVLTALKDGYRHIDTAAIYRNED
QVGQAIKDSGVPREEIFVTTKLWCTQHHEPEVALDQSLKRLGLDYVDLYLMHWPARDPA
YIKNEDILSVPTKKDGSRAVDITNWNFIKTWELMQELPKTGKTKAVGVSNFSINNKLKDLL
ASQGNKLTAAANQVEIHPLLPQDELINFCKSKGIVVEAYSPLGSTDAPLLKEPVILEIAK
KNNVQPGHVVISWHVQRGYVVLPKSVNPDRIKTNRKIFTLSTEDFEAINNISKEKGEKRV
VHPNWSPFVFK

>YOR122C, 1090 bp, exon1 : 501-513, intron1: 514-722, exon2:
723-1090 (SEQ ID NO 357)

AGGAAGAGGAGGCTGCGTTTGACGACGAAGAGGATGATAATGAGGAAGAAGAAGAAG
AGGACGCGGATGAAGAGAACGCCTCTCGTCTAAGAAATTTAAAAAGAGAAGGAGCAGCAA
TGTACAGAGAAGAGGAAGAAGAAGAAAAAGATAGGAGCGAGACAAAAAGAAGAGGGTTG
CGGTCATCGAGGACGACGAAGACGAGGATTAGAGGAGACGTTACTTTGTTTATATATATT
AGTATGTACAATCGCAAAGAAATGGAGTGATGACATGTTGTAGTATTTAGTATGAGGTTA
CTGTGTGGGAGGTTTTACCATGATTTTTGGCGAGAACACGCCATGAAATGCTTTGTACG
AAACTCATTACCCGCATTAATATTTTTTTCTTTTAAAGCTCAGTTGACCCTTTCTCAT
TCCCTTCTTAAACAACACTGTGTGATCCTTGAGAAAAGATAAATTACATACACAACATAAA
CCCAACTACGATCGCAAATATGTCTTGCGAAGGTATGTGAACGAGACAATTTATCAATTG
ATTAAGAAAAGAAATGAGTCGGAGGTTAGCTTTGTGTGACAATGTTTGGCAATGCCCGATTT
TTGTTGATGCGCGTAATTTTCAAGATTAAACCACTCAGAGTAAATTTACTAACTGGAATATC
AAAAACATATGAAATTTCAACATGAATTTCTTTCCGTTTTTTTCTCTACTTTTAAAC
AGCATACACTGATAACTTAATAGGAACCGGTAAAGTCGACAAAGCTGTCTACTCGAG
AGCAGGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAACGAAATTGG
TGAAATTGTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCAATGGTTTGCATATTCA
AGGCCAAAAGTTCATGTTGTTGAGAGCTGACGATAGAAGTATCTACGGTAGACATGATGC
TGAGGGTGTGTTTGTGTAAGAACTAAGCAAACCGTTATTATTGCTCATTTATCCACCAAC
CGTACAAGCCGGTGAGGCCACCAAGATTGTCGAGCAATTGGCTGACTACTTGGTTGGTGT
TCAATACTAA

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>YOR122C, 126 aa (SEQ ID NO 358)

MSWQAYTDNLIGTGKVDKAVIYSRAGDAVWATSGGLSLQPNEIGEIVQGFDPAGLQSNGLHIQGGQKFMLLRADDRSIYGRHDAEGVVCVVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLIGVQY

>YOR261C, 1517 bp, CDS: 501-1517 (SEQ ID NO 361)

GTAAGGTAAGGCATCATTAGCAGGATCCATATTTACTACCTGGGAATGTCTTCCGATGGCATTGAAGAAGTGTGAGCAGCCGTTGCAATAGGTTGACTTCCCTGAACCTGGTGGACCAATAACAATCTGAGCGAAGGGCATTATTGTACTCTCTAGTAGAAAATCAAACTATTGACACAACAACAATCAAATGAAAAACAACTTCTATTACGGTAAGTAGTGAAGACTCACAATGCAATCTTTCAATGAGCATCACTTACTTTAAGTAGCAATATTCCTAATCACTTATTACGAAATTGATTTTACTAAAGTTCGGGGATACCTCAGTGGCAAATCGTTACTCAAGTTGCACGTAA CGTAGAATCTACAATGAAATAATTGTGAAGCCAACAGCTAAGCAATCTATAGTGTAAACGT TGGCTTTCTGTACAACCTGCTACTGATTGAGGGCATTTCGAATTTAAAAAAGAAAGAAA GAAAGGAAAATCAAATTACAATGTCTCTACAACACGAGAAAGTTACCATTGCACCACTAG TTTTGCTATCTGCTTTGGATCATTATGAGCGTACGCAGACAAAAGAAAACAAAAGATGCG TTGGTGTATCTTTAGGTGATGCTAACAGTTCCACTATCAGAGTCACTAATTCCTTTGCCT TACCGTTTGAAGAAGATGAGAAAACTCTGACGTGTGGTTTTTAGACCATAATTATATTG AAAACATGAATGAAATGTGTAAAAAGATTAAATGCCAAGGAAAACTCATTGGATGGTATC ATAGTGGTCCATAAATTAAGGGCTTCTGACCTCAAGATTAATGAGCTGTTTAAAAAATATA CTCAGAATAATCCGCTATTATTAATTGTTGATGTCAAACAACAAGGTGTTGGTTTACCAA CAGATGCATATGTCCGCTATTGAGCAAGTTAAGGATGATGGTACGTCTACAGAAAAGACGT TTCTTCATTTGCCTTGTACTATTGAGGCCGAAGAAGCTGAAGAAATTGGTGTAGAACACT TATTGAGAGACGTACGTGATCAAGCAGCAGGTGGCTTATCTATCCGGTTGACCAACCAAT TAAAATCTTTGAAAGGATTACAAAGCAAACTAAAAGACGTTGTGAGTACTTAGACAAAG TCATTAATAAGGAATTACCGATAAACACACTATATTGGGCAAGCTACAAGATGTTTTCA ACCTTTTACCAAATCTGGGAACACCTGATGATGACGAAATAGATGTGGAGAATCATGACA GAATTAATATTTCAAATAACTTACAAAAGGCTTTAACTGTGAAAATAATGATGAATTAA TGGTTATATATATAAGCAATTTGGTTAGGTCAATTATCGCGTTTGATGATTTGATTGAAA ACAAATTCAAAATAAAAAAATTCAGAACAAGAGTAAAGGACAAACAATCAAAAGTCT CTGATGACAGTGAGAGTGAGAGTGGTGACAAAGAAGCAACTGCGCCATTGATCCAACGAA AGAACAAGAAAAATTAA

>YOR261C, 338 aa (SEQ ID NO 362)

MSLQHEKVTTIAPLVLLSALDHYERTQTKENKRCVGVILGDANSSTIRVTNSFALPFEEDENKSDVWFLDHNHYIENNMCKKINAKEKLIGWYHSGPKLRASDLKINELFKKYTQNNPLL LIVDVKKQQVGLPTDAYVAIEQVKDDGTSTKTFLLHLPCTIEAEAEIEIGVEHLLRDVRD QAAGGLSIRLTNQLSKLQSLKLDVVEYLDKVINKELPINHTILGKLQDVFNLLPNLGT PDDDEIDVENHDIRINISNNLQKALTVKTNDELMVIYISNLVRSIIAFDDLIENKIQNKK IQEQRVKDKQSKVSDDSESESGDKEATAPLIQRKNKK

>YPL271W, 689 bp, CDS: 501-689 (SEQ ID NO 391)

CAGCAGCGACAAGTCAGAGTGCTTACAAAAAAGAGTTGATCCGGCTAAAGAAAGTC TGATTTACGTATTTATCCAGGTTCAAACGGATTGCCAAAAATAGTCGATAACCTCGGAGT AAGCAAAGCAACAATATATTTGTTCTTCGAAAAGGTAACTTCTTAACTTCTATAGAAGC ATGTACTAGTTCTCTCGAAGAAAAAACTAAGAAAGCTATAGCTGTATCTTACCAAGCC ATGAACTTGAGGAATTTGGTAATCCCTATTAGGAAATACGCTAAACTAGGTAATAGCAGAT GATTTACTAGCTTACTATCTCACACTAAGTCTGGCAACGCGCTTATTTTTAATACTTTT ATACGAACCAATGAAATTTGATCCTCCCCCTTTTCGTCTAGTTAAATGAAGAGATACAAG TAGGCCTTTCTATTGAGTACTTAGCAAGATATGTATTTCTAAGAAACATCAACAGTTTCA GCCACAACCGATTCAAAAATGTCTGCCTGGAGGAAAGCTGGTATATCATATGCTGCAT ATTTGAATGTGGCCGCTCAGGCTATCCGTTCTTCATTGAAAACCTGAATTACAAACCGCTA GTGTTCTTAACAGATCGCAAACAGATGCTTTTTATACCCAATATAAAAAATGGCACTGCAG CTTCTGAACCCACTCCAATAACAAAATAG

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>YPL271W, 62 aa (SEQ ID NO 392)

MSAWRKAGISYAAAYLNVAQAIRSSLKTELQTASVLNRSQTDAFYTQYKNGTAASEPTPI
TK

>YPR035W, 1613 bp, CDS: 501-1613 (SEQ ID NO 395)

TAGTGCCATTGTGGTCATTATTATTCGCCAAATATGCGAAAATAGTACACTATTTTGG
CAGGAGAGTAGGCTGATATGCCGCATTGATGTCTGTGTAGCGAAACACAAACAAAAA
GAAAAAGTAGGATGAAAAAAGAAAAGTAATATGAAAAAGAGTGAAAAATTAATTCATT
TGTTAGTGTAAAGCGGTGAGGTGTAAGTAGTAGGCTTGATAATGAATTAAAGATGACTCCG
ACGCATATTGTTGCCATGTTTTATTTTAGTTTGTAGATTTCTTTTTTTGTAAATATATA
AGGGAGTGATTCTATATATCGAATTCTCAGGCTTGGTTGGTTCGTAGGTTGTTCTGTCTT
TGTTTTCGTTAGGTAAGAACATCACACAAAGATAACTATAGAATCACATACATATTTGTG
AGAAATTAACCTTCATTTTATAGAAGAAGTTCAACCGAAACAAAAATTAAACATAAT
ATAATATAATATAATCAAAAATGGCTGAAGCAAGCATCGAAAAGACTCAAATTTTACAAA
AATATCTAGAAGTGGACCAAAGAGGTAGAATAATTGCCGAATACGTTTGGATCGATGGTA
CTGGTAACTTACGTTCCAAAGGTAGAAGTTTGAAGAAGAGAATCACATCCATTGACCAAT
TGCCAGAATGGAAGTTCGACGGTTCTTCTACCAACCAAGCGCCAGGCCACGACTCTGACA
TCTATTTGAAACCGTTGCTTACTACCCAGATCCCTTCAGGAGAGGTGACAACATTGTTG
TCTTGGCCGCATGTTACAACAATGACGGTACTCCAACAAGTTCAACCACAGACACGAAG
CTGCCAAGCTATTGCTGCTCATAAGGATGAAGAAATCTGGTTTGGTCTAGAACAAGAAT
ACACTCTATTTGACATGTATGACGATGTTTACGGATGGCCAAAGGGTGGGTACCCAGCTC
ACAAGGTCCTTACTACTGTGGTGTGGTGCCGGTAAGGTTTATGCCAGAGACATGATCG
AAGCTCACTACAGAGCTTGTGTTGTATGCCGGATTAGAAATTTCTGGTATTAACGCTGAAG
TCATGCCATCTCAATGGGAATTCGAAGTCGGTCCATGTACCGGTATTGACATGGGTGACC
AATTATGGATGGCCAGATACTTTTGCACAGAGTGGCAGAAGAGTTTGGTATCAAGATCT
CATTCCATCCAAAGCCATTGAAGGGTGAAGTGAACGGTGCCGGTTGTACGCTAACGTTT
CCACCAAGGAAATGAGACAACCAGGTGGTACGAAATACATCGAACAAGCCATCGAGAAGT
TATCCAAGAGACACGCTGAACACATTAAGTTGTACGGTAGCGATAACGACATGAGATTAA
CTGGTAGACATGAAACCGCTTCCATGACTGCCTTTTCTTCTGGTGTGCGCAACAGAGGTA
GCTCAATTAGAATCCCAAGATCCGTCGCCAAGGAAGGTTACGGTTACTTTGAAGACCGTA
GACCAGCTTCCAACATCGACCCATACTTGGTTACAGGTATCATGTGTGAAACTGTTTGGC
GTGCTATTGACAATGCTGACATGACGAAGGAATTTGAAAGAGAATCTTCATAA

>YPR035W, 370 aa (SEQ ID NO 396)

MAEASIEKTQILQKYLELDQRGRIIAEYVWIDGTGNLRSKGRITLKKRITSIDQLPEWNFD
GSSTNQAPGHDSDIYLPVAYYDPFRRGDNIIVLAACYNNDGTPNKFNRHEAAKLFAA
HKDEEIWFGLEQEYTLFDYDDVYGWPKGGYPAPQGPYYCGVGAGKVYARDMIEAHYRAC
LYAGLEISGINAEVMPSSQWEFQVGPCTGIDMGDLWMARYFLHRVAEEFGIKISFHPKPL
KGDWNGAGCHANVSTKEMRQPGGTYIEQAIEKLSKRHAHEHIKLYGSDNDMRLTGRHETA
SMTAFSSGVANRGSSIRIPRSVAKEGYGYPEDRRPASNIDPYLVTGIMCETVCGAIDNAD
MTKEFERESS

YBR133C, 2984 bp, CDS: 501-2984 (SEQ ID NO 53)

AACCTTACGACAGAGTTGTAATGAATGCTACTGATGTCTGCTCTACTGCCA
TCCGCTGTCTTTTATGCATAAAAGCTCCATTCTTTATTTATCTCATAACC
ACGAGAAAAAAAATCACCTGACATATTTTATAACCCGCCTTTTAGACC
CTAAAACAGATCTCAGGGCTCGAGTACTGTTTATCTGAAAATCTTTCGA
GCCCTCGTTTTGCACTGAGCTAAACCAAAAAGAAAAATAACAATCACAAA
TGGAACCCGAAACAGCAGCTGCCGAGTGTGTTTATATTTTTTTGAAACA
AATGGCTTTATACAATGTGTATGTGTGATAGAAAAATGGTATATTTTGA
GTGACTTGTGATCCTATTCCCAAGCCCTATAGGAGCTATTTCAAATTGCG
TGTGTGAAAGCGTGTGTGTGTGTGTGTGTGGAATTGTGCGGACGTTCC
TCTTCTTTTATACATATAATTTTATATATACAAAGGGTTCAGTTTGCAT
ATGCATAGCAACGTATTTGTTGGTGTCAAACAGGCTTTAATCATAAACA
GCACAGCAAAAAGTCACGTTTCCTAGAAAATGTCTCTAGTCATTACACCAG

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AACTGCCTAGTAACCTATGATTACGTTTTGCTTCCTATAACAACGCCAAGA
TATAAGGAAATAGTTGGGCAAGTTTTCAAAGATTTCCAAAGACAATCCAT
ACAGAACTGGAAACCGCTTCAAATTCCTGAACCGCAGTTGCAGGATATCT
GTATACCCCGTTCAACGTCAAGAAGCTAGACAATGACGATACGCCGTCT
TACATAGGGCTGTTATCCTCTTGGCTGGAGCTGGAGAGTCGCGATCCAAA
TGTAAGAGATCTTGGCTTAAAGGTCCTTCTAAACGAATGTAAGTACGCGA
GGTTTGTGGAATCAATAAGCTAATATTGGCGCTCCACGGGACCTGTCC
AACCTGCAATTGTATGGACAGATGATTTACAGGCTCCTGCAAAATCGCAT
CGTCTTTGCTGCGCCTGCGTTAACCATATCCATTTCTCTGCCACTTTACG
AAGACAGCGATCCATTGGCCACTTGGGAAGTGTGGAATACCGTGCGGAAA
CAATGCGAATATCATCCCTCTTTGACTATCTCTTTGGCTTTGCCAAGAAC
CAGGACTCCTTCGTATGTGCTGAATAGATGGTTAGCCGAACCGTCTCGT
GTCCTTTGGTATCTTCATCCATCTTTGCCAGTAATCAGTACGATTATCCC
GTTTTACACAAGTTTAACCAGAATTTGATTTTAAAGTTCCAAAAGGTTAA
TGGAGATTACAAATTTTGGGTAATGAATTATGCGTGATATTGCATGGGA
TGGAGAAATATGCCAATAATGTTAAGGGCGGAGAATCTGCCTATTTGGAA
TATATAAACTACTTATTGAAAAAGGGCGACAAAGTATTAAATTCCAATAG
TAATCACCAATTTTGTCTCCAAGAGGACTCTCGGATAATGCCGCCTCTGA
AACCTCATTAGATAATTTATTAAATTCACATATTTGACTTTTGAAAAA
GATTTGGTGAAGTACGATCTTTACGAATCTGCCATATTAGAGGCGCTTCA
AGATCTTGCTCCTCGAGCGAGTGCCAAGAGACCGTTGGTGATCCTAGTAG
CCGGTGCGGGAAGAGGACCTTTAGTGGATCGAAGTTTAAAGATAATATCA
ATGTTGTTTATGGATAGTAAGGTTTCTATAAATTGCCATTGAAAAAATCC
ACAGGCATATCTGTACTTGCAAAAAAGAAATTTGACTGTTGGGATAATA
GAGTGAAATTAATCAAGGAGGATATGACCAAAATGGCAAATCAACGAGCCG
TCGGAAAAGCGTATTCAGATAGATCTGTGCATAAGTGAAGTCTGGGTTT
GTTTCGGTTGCAATGAATTATCACCAGAATGTCTCTGGTCTATTGAAAAAT
ATCATTTCCACAATGACACAATTTTCATACCGAGGTCATACTCTTCATAC
ATAGCACCATTTCGTACCATTTATTCTACCAAAAACCTCTCACAACAAA
TCGCTCTTTGGAGGCGCCCTGGATAGTCCATAGAGTGCCATACTGTATAT
TATCCTCAAGGGTAAATGAAGTGTGGCGGTTTCGAGCATCCCATGGCCCCA
AAAGATACTGTCCAAGACGAAGATGATTTTACAGTTGAATTTTCTCAAAG
TTCATTAAATGAGTTCAAGATAAAGCACCGCGGCGAAATCCATGGCTTTA
TCGGATTCTTCTCGGCAACCTTATATAACAATATATTCTTGTCAACTTTG
CCCAATGACAGCACAGTCCGTTTAAATTTAGCGAAGAAACGTTGATGAA
TACCAGACGAGAAGAAAATCTAATCAAGAAATGTGACCATACACCAATA
TGACCTCGTGGTCTCCAATTATCTTTCTTTGAAGCAACCAATATCCTTT
ATAGATGACTCCGAACCTTCTGTGCTGATGTCTCGGATACACTCCGATAC
AGAACAAAAAGTTTGGTATGAATGGTCTTTGGAGAGTTTCATATACCTTA
TGTTGTCAAATTACACTTCGGCGGTAAGTGTGCAAGCATGACTATTCCG
AGGTCATATAGTTACAGATGACACTAAAACCTTTAGCCCATATCGACATTA
TTCAGCGACTACCAATCAAAGCTAGATAATCAAATTGATCTTGACCAAG
ACATTGAAAACGAAGAAGAACAGGGATTCCATCCAATCTAGAAACTGGT
TGGCAAAGCGTACAAGATATTCACGGACTCAGCGAAACCGCCAAACCGGA
CCATTTAGATTCTATCAATAAGCCTATGTTTGATCTCAAATCTACTAAAG
CGCTTGAACCTCTAACGAATTGCCAAGGCACGAAGACCTCGAGGAAGAT
GTTCCAGAAGTTCATGTGAGAGTCAAGACTAGTGTTCACGCTACATAA
TGTCGTGTGGCAGAGCCTTTTCCCTGCCTCTGTGA

YBR133C, 827 aa (SEQ ID NO 54)

MHSNVFVGVPKPGFNHKKQHSKSRFLENVSSHSPELPSNYDYVLLPITTPR
YKEIVGQVFKDFQRQSIQNWKPLQIPEPQLQDICIPIPFNVKKLDNDTPS
YIGLLSSWLELESRDPNVRDLGLKVLNCKYARFVGINKLILAPPRDLS
NLQLYGQMIYRLLQNRIVFAAPALTIISLPLYEDSDPLATWELWNTVRK
QCEYHPSLTISLALPRTRTPSYVLNRWLAEPVSCLLVSSSIFASNQYDYP
VLHKFNQNLILKFQKVNQDSQILGNELCVILHGMKEYANNVKGESAYLE

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YINYLKKGDKVLNSNSNHQFLQEDSRIMPPLKPHSDNLLNSTYLTFEK
DLVKYDLYESAILEALQDLAPRASAKRPLVILVAGAGRGPLVDRTFKIIS
MLFMDSKVSIIEKNPQAYLYLQKRNFDWDRVVKLIKEDMTKWQINEP
SEKRIQIDLCESELLGSFGCNELSPECWLSIEKYHSHNDTIFIPRSYSSY
IAPISSPLFYQKLSQTNRSLEAPWIVHRVPYCILSSRVNEVWRFEPMAQ
KDTVQDEDDFTVEFSQSSLNFEKIKHRGEIHGFIGFFSANLYNNIFLSTL
PNDSTVRLKPFSEETLMNTRREENLIKCDHTPNMTSWSPIIFPLKQPISF
IDDSLSVLMSRIHSDTEQKVWYEWLSLEFIYLMLSNYTSAVTAASMTIP
RSIVTDDTKTLAHRHYSATTNQKLDNQIDLQDIENEEEQGFLSNLETG
WQSVQDIHGLSETAKPDHLDKSTKALEPSNELPRHEDLEED
VPEVHVRVKTSTVSTLHNVCGRFSLPL

YBL085W, 3443 bp, CDS: 501-3443 (SEQ ID NO 31)

AAAGGGAAGTATGGCATGCCTAGAAATCTTTTCTGGAAACTTGAAGCAT
ATCATATAATTGTATGAACTTGTCTTCAAAGATGTTACCAAATATTCA
AGAGTATGTGAGCTTTCTATTCTATTGACGCGTAAGAAAGGCTATCACGT
GTGGGGGGGAGAGCTCAGCCACATTGCACTACTTTGAAACCGCGTAGTC
GGAAACGACATTCCCCGTACCAAAACAAACGAAAGGACGTGAAAGGTAA
ATGAATAACATGGCACTAAAAATTTGGCAGAAAACGAAAAAAAAGGAA
AAAGAACTGAAACTATACGCTTCCCTTAGGATACTTTCTGATTTACAT
CCGAAGAATTGGGTGCGTCAATTAAAGGCAATTCTTCGCTCTATCAAGCA
GTTTTACTGCGTCTGTCTAAAGAAACAATTGTTTTACTGAATTTCAACAA
AGTTCTAACTCGAGGTGACCGGAGGCCACTGTAATAATAAAAAATAGAAG
ATGAGTCTCGAAGGAAATACCCTAGGCAAAGGGGCCAAATCTTTTCTCT
GTATATTCCGGTAATCAGTACTCTAAACGAATGGAGGACGAGCTCAATA
TGAAACCAGGTGATAAAATTAAGTCATTACTGATGATGGGGAGTACAAT
GACGGCTGGTATTATGGGCGCAATTTGAGAACCAAAGAGGAAGGTTTATA
CCCAGCGGTATTTACCAAAAAGATAGCAATAGAAAAACCAGAGAACCTGC
ACAAATCACCAACCAAGAGAGTGGAAATTTCTGGTGTTAAATATGGAAAT
TTAAATGATTCTGCGAGTAACATAGGTAAAGTCTCTCGCATCAACAGGA
GAACAGATATACATCATTTGAAAAGTACAATGAGCGATATAGACAAAGCCT
TGGAAGAGCTAAGAAGTGGTTCAGTTGAACAAGAGGTATCAAATCGCCC
ACACGCGTGCCCGAAGTTAGCACTCCACAGTTGCAAGATGAACAGACTTT
GATTCAAGAAAAAACAGAAATGAGGAAAAACAGACACATGACTCGTTAT
TTTCTAGCACAGCGGATTTAACTTAAGTTCTGAATCTTTGAAGAATATA
AGTAAGTCAAATATATCAACAAAATCCCTAGAACCGAGTTCGGAATCAGT
TCGTCAATTAGATTTGAAAATGGCTAAAAGTTGGAGCCAGAAAGAGGTTA
CTGATTACTTTAGCTTGGTTGGATTGATCAATCCACTTGCAATAAATTC
AAAGAGCATCAAGTCTCCGGAATAATACTACTGGAATTAGAACTGGAACA
CCTAAAAGAATTGGAATAAATCTTTTGGTATAAGATTTCAGATATTCA
AAGAAATAAGGAACATCAAGTCTGCAATTGATTGCTCGTCAAATAAAGT
GACGCCGACTACTCTACCTTTTGCTTTTGAAAACCAAGCTGCCCAACTAAT
GCCTGCAGCCACTGTAAATAGAGACGAAATCCAACAACAAATTTCTCCA
AGTGTAACAAGTTGTCAAGTGAAAGCTCTGATAGAAAATCATCTTCGGTC
ACCACAGAATTGCAAGACCAAGCTCGGTTGTTGTTAATCCCAATTTTAA
ACTTCACGACCCAGCTGAGCAGATCCTAGATATGACAGAAGTTCTAAT
TGTTTGCTGTAAAGATATTTTCGAATCACCGGGAAGGGCTCCAAAACCA
CCATCATATCCAAGTCCAGTTCAACCTCCACAATCGCCCTCTTTTAATAA
CAGGTACACAAATAATAACGCAAGGTTTCTCTCAAACAACATATCCAC
CTAAAAACAAGAACCAACCGTTTATTCAAATGGGCTAATTCCAAATCT
TCGACATCTTCCGATAATTCACGGGCAAGTTCAAATTCCTGCCATGAA
TGGTCATGACTCGAACTCTAGGAAAACAACACTGACATCTGCTACTATAC
CTTCTATTAAACCGGTTAACACAGATGAATCTCTACCCGCAATTTCAAAT
ATATCTTCAAATGCTACATCTCATCATCCGAACAGAAATTCGGTTGTTA
CAATAACCATAAGAGGACGGAATCCGGAAGCTCATTGTTGATTTGTTCA
ACAGGATTTCAATGCTATCGCCAGTCAAGTCAAGTTTCGACGAAGAAGAA

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ACGAAACAACCTTCAAAAAGCTAGCAGAGCAGTTTTTGGACTCAGCACGCAG
AAAGTCGCTTTACGGACATTCAAGAGATGCCCTACTTTCTGAAATGAAAA
AGCATAGGAGAAACTCTTCTATATTATCTTTTTTTCTTCAAAAAGTCAG
TCTAATCCAACGTCACCAACCAACAAACTTTCACTATCGATCCCCGCAAA
GATGACTTCCCATTCTCGTTCTCAGTCGAATTCCTATTTCGCATGCAAGAT
CACAACTTACTCCCATAGTAGAAAAACACTCGTTAGTTACCAGCCCCCTTG
AAAACCTCTTTAAGCCCTATAAAATCCAAATCCAATATTGCTTTAGCGCA
TAGCGAAACTCCTACTAGTAGTAATAATAAGGAGGCAGTATCACAACCAA
GTGAAGGGAAGCACAAAGCACAAAGCACAAAGCAAGCACAAACAC
AAGAACAGTAGCTCCAAAGATGGCTCTTCCGAAGAAAAAGCAAAAAGAA
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GATCTCCCAGTGAACCTACCCAAAAATCTACCAAATCGATACTTCCCAGG
TCGAATGCTAAAAAGCAACAAACATCTGCTTTTACCGAAGGTATACGCTC
TATCACAGCAAAGGAATCTATGCAAACCTGCGGACTGTTTCAGGCTGGATGA
GCAAAAAGGTACCGGTGCTATGGGGACTTGGAAACAACGGTTTTTTCACA
CTTCATGGAACAAGGCTTTCTTATTTTACGAATACCAATGATGAGAAGGA
GCGTGGCCTGATAGATATAACGGCACATAGGGTCTTACCTGCCAGTGATG
ATGATAGGCTCATTTTCCTTATACGCTGCGAGCTTAGGAAAAGGAAAATAC
TGTTTCAAATTTGGTCCCTCCGCAACCGGGGTCCAAAAGGGGCTAACCTT
TACAGAACCTCGCGTTCACTATTTTGCAGTTGAGAATAAATCTGAAATGA
AGGCATGGCTGTTCAGCCATAATAAAGGCCACTATTGATATTGATACAAGC
GTCCCTGTCTATTAGTTTCATATGCCACACCAACGATACCTCTAAGCAAGGC
ACAGACGCTATTGGAAGAAGCTAGGTTACAAACCCAGTTAAGAGATGCTG
AAGAGGAAGAGGGAAGAGATCAATTTGGATGGGATGACACCCAAAATAAA
AGAAATTCTAATTATCCAATCGAACAAGATCAATTTGAGACCAGCGATTA
CCTGGAAAGTTTACGATTTGAATACCCCTGGTGGCAGACTTTGA

YBL085W, 980 aa (SEQ ID NO 32)

MSLEGNTLGKGAASFPLYIAVNQYSKRMEDELNMKPGDKIKVITDDGEYN
DGWYYGRNLRTEEGLYPAVFTKRIATIEKPENLHKSPTQESGNSGVKYGN
LNDASASNIGKVSSHQENRYTSLKSTMSDIDKALEELRSGSVEQEVSKSP
TRVPEVSTPQLQDEQTLIQEKTRNEENTTHDSLFSSTADLNLSSSLKNI
SKSNISTKSLEPSSSVRQLDLKMAKSWSPVEVTDYFSLVGFQDSTCNKF
KEHQVSGKILLELELEHLKELEINSFGIRFQIFKEIRNIKSAIDSSSNKL
DADYSTFAFENQAAQLMPAATVNRDEIQQQISSKCNKLSSSESSDRKSSSV
TTELQRPSSVVVNPFLHDPAEQILDMTEVPNLFADKDIFESPGRAPKP
PSYSPVPQPPQSPSFMNRYTNNNARFPPTTYPPKNKNPTVYSNGLIPNS
STSSDNSTGKFKFPAMNGHDSNSRKTTLT SATIPSINTVNTDESLPAISN
ISSNATSHHPNRNSVVYNHNRTESSSFVDLFNRISMLSPVKSSFDEEBE
TKQPSKASRAVFDASARRKSSYGHSRDASLSEMKHRRNSSILSFFSSKSQ
SNPTSPTKQTFITIDPAKMTSHSRSQSNSYSHARSQSYSHSRKHSVLTSP
KTSLSPIINSKNIALAHSETPTSSNNKEAVSQPSEGKHKHKKHKSXKH
KNSSSKDGSSEEKSKKLFSSSTKESFVGSKEFKRSPSELTQKSTKSILPR
SNAKKQQTSAFTEGIRSITAKESMQTADCSGWSKKGTGAMGTWKQRFPT
LHGTRLSTYFTNTNDEKERGLIDITAHRLVPASDDRLISLYAASLGKGY
CFKLVPQPGSKKGLTFTEPRVHYFAVENKSEMKAWLSAIKATIDIDTS
VPVISSYATPTIPLSKAQTLLLEEARLQTLRDAEEEEGRDQFGWDDTQNK
RNSNYPTEQDQFETSDYLESSAFEPGGRL

YDR545W, 5891 bp, CDS: 501-5891 (SEQ ID NO 137)

TTCTATTATATTGGTCTTTTCGAGAGCGGAAGAAGTTGTAGGCTAAGCGC
AGGCTAAGCGTAGGTCCATATTTAAAGTATCCAAGAGAATATCCACGAAG
CGGCTGAGCAACGAACAGAATCCTGGTTCTCCTCGACTAAGCAGATAGTT
AAGATACTGTGCACCATGGAAATTGAAAACGAAAGTACGTACCGACTACT
TTATTTTTGCAGGCCGGAATCAAGCGATGAATGAGACATCCTTCTGT
TCTATGTTGGGACAGACAGTCGCTTATCTTAGTGAGATTTCTTATTA

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GAATTTTCTTTGCTGCTGCTGGAGATTTCACCTGCATAGCGCAGATTCT
GCTTCTTCTCAATAGAGTAGCTTAATTATTACATTCTTAGATGATGATAA
GACGGAACTCGACAATCTTTTGTATTATATTGATGGATTCTTGTCAAAA
AGCATAACAATCAACATACTATTGTAAATTCGAACTTACAAAAATAAA
ATGAAAGTTTCCGATAGGCGTAAGTTTGAAAAAGCAAACTTTGACGAGTT
TGAGTCGGCTCTAAATAACAAAAACGACTTGGTACATTGTCCCTCAATAA
CTTTATTTGAATCGATCCCCACGGAAGTGGGTACATTCTACGAAGACGAA
AAGTCTGGCTTAATCAAAGTGGTAAATTCAGAACTGGTGCAATGGATAG
GAAAAGGTCCTTTGAAAAAATTGTCAATTCCTGTCATGGTCGGGAAAAATG
TACAAAAGTTCTTGACATTGTGTTGAAGACGAACCAGATTTCAGGGCGGA
CCAATCCCCTCAAAGTATCTTATTCCTCAAGAAAAATCAACTTGATGGTCTA
CACGTTGTCTCAAAGTGCATACCTTGAAATTCATAGAAAAGGATTACGATA
CCCTTTCTCTTTTACCTCAACAGAGGATACTATAATGAGTTGAGTTTC
CGTGTCTCGGAACGTTGTACGAAATAGCGAGTGCCAGGCCGAACGACAG
CTCTACGATGCGTACTTTTCACTGACTTTGTTTCTGGCGCACCTATTGTAA
GGAGTCTTCAGAAAAGCACCATAAGGAAATATGGGTACAAATTTGGCACC
TACATGTTCTTGTACTACACGTAGATGAGCTATCGATTCTTCTGTCATA
CCAAGCAAGTTTACCTGGCGAAAAGAAAGTCGACACAGAGCGGCTGAAGC
GTGATCTATGCCACGTAAACCCATTGAGATAAAGTACTTTTCACAGATA
TGTAACGATATGATGAACAAAAAGACCGATTGGGTGATATTTTGCATAT
TATCTTGGCAGCATGTGCGCTCAATTTGGGGCGGGTCCCCGTGGTGGCG
CTGGTGACGAAGAGGATCGATCTATTACGAATGAAGAACCCTATTATCCC
TCTGTGGACGAGCATGGCTTGAAAGTATGTAAGTTGCGTAGTCTAACAC
TCCACGAAGACTCAGAAAAACACTAGATGCCGTGAAAGCTTTATTGGTGT
CGTCTTGTGCTTGTACTGCAAGGGATTAGATATATTTGATGACACCAAC
GGCGTTGCAATGTGGAAATGGATCAAATTTCTGTACCACGAAGTAGCGCA
GGAAACCACGCTGAAGGACTCTTATAGAATAACTTTGGTACCTTCTCTG
ATGGTATATCAGTATGTGGAAAACCTTTTAAATCGCGAGTATGTCCGCGGC
TTTTACTTTGCATGCAAGGCTCAGTTCGATAACCTTTGGGGAGAGTTGAA
CAACTGCTTTTATATGCCCTACAGTGGTTGATATTGCCAGCCTCATTTTGC
GTAATCGAGAAGTTTGTTCAGAGAGCCAAAGCGAGGAATTGACGAGTAT
CTGGAACACGATTCTTTTCTTCAAATGATACCTGTAAATATCGTGAAT
TGTGCTGCCCAAGTTGAGAAGAGATACTAACAAAATGACCGCGGCTCTTA
AAAATAAAGTCACTGTTGCAATTGACGAGCTTACGGTGCCACTTATGTGG
ATGGTCCATTTTGCCGTAGGATACCTTACCGTTATCCAGAGCTTCAGCT
ACTCGCTTTTGCCGGTCTCAGCGCAACGTATACGTCGATGATACAACAA
GACGCATCCAACGTACACTGATTACAACAAGAACGGTTTCATCGGAGCCT
CGACTTAAGACGCTTGACGGACTCACTTCAGATTACGTGTTTTATTTTGT
CACTGTGCTAAGGCAAATGCAAATATGTGCGCTTGGTAACAGTTATGACG
CTTTTAATCATGATCCTTGGATGGATGTGGTGGGATTTGAGGATCCAGAT
CAAGTAACAAATCGAGACATTTGAGGATAGTTTTGTATTCTTACATGTT
TCTGAATACCGCGAAGGGCTGTCTGGTTGAATACGCAACTTTTCGGCAGT
ACATGAGGGAACCTCCGAAGAATGCACCTCAGAAGCTGAATTTTCGGGAG
ATGCGTCAGGGGTTGATTGCCCTAGGACGGCACTGCGTAGGTAGCAGATT
TGAAACAGATTGTACGAGTCGGCGACGAGTGAACCTCATGGCCAATCATT
CCGTTCAAACAGGGCGAAATATTTACGGTGTGGATTCTTTTCGTAACT
AGTGTCAAGTGGGACGACCGCCACTTTATTGCAGGAACGAGCTTCCGAGCG
CTGGATTCAATGGTTAGGCCCTTGAAAGCGACTACCATTGTTTCTCTA
GTACTCGGAATGCGGAAGACGTAGTGGCAGGTGAGGCGGCGAGTTGAGAT
CATGATCAAAAATTTCAAGAGTAACGCGAAAAAGGCCCCGAGAGCCCAA
GAGTACAAACGATATCTCGTCCGAGGCCAGAACTCTTTGGCAGCTCCT
TTGAATTCAGGACTTGCATCAGTTGCGCTTATGTCATGAAATATACATG
GCAGACACACCCTCTGTGGCAGTACAGGCCCCACCGGGCTATGGTAAGAC
GGAGTTATTTCTCTCCCTTGATAGCACTGGCGTCTAAGGGCGACGTGA
AATATGTGTGCTTTCTGTTGTACCGTACACAGTGTGCTTGCTAATTGC
ATGATCAGGTTGAGCCGATGCGGTTGCTTGAATGTGGCCCCTGTAAGAAA

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CTTTATTGAAGAAGGTTGCGATGGCGTTACTGATTTATACGTGGGGATCT
ACGATGATCTTGCTAGCACTAATTTACAGACAGGATAGCTGCGTGGGAG
AATATTGTGTGAGTGACCTTTAGGACCAACAACGTAAAATTGGGTACCT
CATTGTAGATGAGTTTCACAACTTTGAAACGGAGGTCTACCGGCAGTCGC
AATTTGGGGGCATAACTAACCTTGATTTTGACGCTTTTGAGAAAGCAATC
TTTTTTGAGCGGCACAGCACCTGAGGCTGTAGCTGATGCTGCGTTGCAGCG
TATTGGGCTTACGGGACTGGCCAAGAAGTCGATGGACATCAACGAGCTCA
AACGGTCGGAAGATCTCAGCAGAGGTCTATCCAGCTATCCAACACGGATG
TTTAATCTAATCAAGGAGAAATCCGAGGTGCCTTTAGGGCATGTTTCATAA
AATTTGGAAGAAAGTGGAATCACAGCCCGAAGAAGCACTGAAGCTTCTTT
TAGCCCTCTTTGAAATTTGAACCAGAGTCGAAGGCCATTGTAGTTGCAAGC
ACAACCAACGAAGTGGAAGAAATGGCCTGCTCTTGAGAGAAAGTATTTAG
GGTGGTATGGATACACGGGAAGCTGGGTGCTGCAGAAAAGGTGTCTCCCA
CAAAGGAGTTTGTCTACGTGACGGTAGCATGCGAGTTCTCATCGGAACGAAA
TTAGTGACTGAAGGAATTGACATTAAGCAATTGATGATGGTGATCATGCT
TGATAATAGACTTAATATTTATGAGCTCATTCAAGGCGTAGGGAGACTAA
GAGATGGGGGCCCTCTGTTATCTATTATCTAGAAAAAACAGTTGGGCGGCA
AGGAATCGTAAGGGTGAATTACCACCGATTAAAGGAAGGCTGTATAACCGA
ACAGGTACGCGAGTTCTATGGACTTGAATCAAAGAAAGGAAAAAAGGGCC
AGCATGTATGGATGCTGTGGCTCCAGGACAGACCCTGCTGCTGACACAGTG
GAATGTATAGAAAGAATGGACAGATTGGCTGAAAAACAGGCGACAGCTTC
CATGTCGATCATTTGCGTTACCGTCTAGCTTCCAGGAGAGCAATAGCAGTG
ACAGGTGCAGAAAGTATTGCAGCAGTGATGAGGACAGCGACACGTGCATT
CATGGTAGTGCTAATGCCAGTACCAATGCGACTACCAACTCCAGCACTAA
TGCTACTACCAC TGCCAGCACCAACGTCAGGACTAGTGCTACTACCAC TG
CCAGCATCAACGTCAGGACTAGTGCGATTACCAC TGAAAGTACCAACTCC
AGCAC TAATGCTACTACCAC TGCCAGCACCAACGTCAGGACTAGTGCTAC
TACCAC TGCCAGCATCAACGTCAGGACTAGTGCGACTACCAC TGAAAGTA
CCAACTCCAACACTAGTGCTACTACCACCGAAAGTACCGACTCCAACACT
AGTGCTACTACCACCGAAAGTACCGACTCCAACACTAGTGCTACTACCAC
TGCTAGCACCAACTCCAGCACTAATGCCACTACCAC TGCTAGCACCAACT
CCAGCACTAATGCCACTACCAC TGAAAGTACCAACGCTAGTGCCAAAGGAG
GACGCCAATAAAGATGGCAATGCTGAGGATAATAGATTCCATCCAGTCAC
CGACATTAACAAAGAGTCGTATAAGCGGAAGGGAGTCAAATGGTTTTGC
TAGAGAGAAAGAACTGAAAGCACAAATTTCCCAATACTTCCGAGAAATATG
AATGTCTTACAGTTTCTTGGATTTCGGTCTGACGAAATTAACATCTTTT
CCTCTATGGTATTGACGTATACTTCTGCCAGAGGGAGTATTCACACAAT
ACGGATTATGCAAGGGCTGTCAAAAGATGTTGAGCTCTGTGCTGTGTTGG
GCTGGCCAGAAAGTATCGTATCGGAGGATGGCTTGGGAAGCACTAGCTGT
GGAGAGAATGCTGCGAAATGACGAGGAATACAAAGAATACTTGGGAAGACA
TCGAGCCATATCATGGGGACCCTGTAGGATATTTGAAATATTTTAGCGTA
AAAAGGGGAGAGATCTACTCTCAGATACAGAGAAATTATGCTTGGTACCT
GGCCATTACTAGAAGAAGAGAAACAATTAGTGTATTGGATTGACAAGAG
GCAAGCAAGGGAGCCAAGTTTTCCGCATGTCTGGAAGGCAGATCAAAGAG
TTGTATTATAAAGTATGGAGCAACTTGGCTGAATCGAAGACAGAGGTGCT
GCAGTACTTTTTGAACTGGGACGAGAAAAAGTGCCGGGAAGAATGGGAGG
CAAAAGACGATACGGTCTTTGTGGAAGCGCTCGAGAAAGTTGGAGTTTTT
CAGCGTTTTCGTTCCATGACGAGCGCTGGACTGCAGGGTCCGCAGTACGT
CAAGCTGCAGTTTAGCAGGCATCATCGACAGTTGAGGAGCAGATATGAAT
TAAGTCTAGGAATGCACTTGCGAGATCAGCTTGGCTGGGAGTTACCCCA
TCTAAAGTGCCGATTGGACGGCATTCTGTGATGCTGATAGGGCTGTT
CTACAATAAAACATTTCCGCAGAACTGGAATATCTTTTGGAGCAGATTT
CGGAGTGCAGTTGTTTACCACATTGGCTTGATTGGCAAACGTTGAAGTT
CTCGCTGCAGATAACACGAGGTACCGCTGTACATGCTGATGGTAGCGGT
TCACAAAGAGCTGGATAGCGATGATGTTCCAGACGGTAGATTTGATATAA
TATTACTATGTAGAGATTTCGAGCAGAGAAGTTGGAGAGTGA

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YDR545W, 1796 aa (SEQ ID NO 138)

MKVSDDRRKFEEKANFDEFESALNNKNDLVHCPSTLTFESIPTEVRSFYEDE
KSGLIKVVVKFRTGAMDRKRSFEKIVISVMVGKNVQKFLTFVEDEPDFQGG
PIPSKYLIPIPKINLMVYTLFQVHTLKFNRKDYDTLSLFYLNRGYYNELSF
RVLERCHEIASARPNDSSMTMRTFTDFVSGAPIVRSLQKSTIRKYGYNLAP
YMFLLHVDLSIFSAYQASLPGEKKVDTERLKRDLCPRKPIEIKYFSQI
CNDMMNKKDRLGDILHIILRACALNFGAGPRGGAGDEEDRSITNEEPIIP
SVDEHGLKVCKLRSPNTPRRLRKTLDVAVKALLVSSCACTARDLDIFDDTN
GVAMWKWIKILYHEVAQETTLKDSYRITLVPSSDGISVCGKLFNREYVRG
FYFACKAQFDNLWGELNNCFYMPVVDIASLILRNREVLFREPKRGIDEY
LENDSTLQMIPIVKYREIVLPKLRRDTNKMATAALKNKVTVAIDELTVPLMW
MVHFAVGYPYRYPELQLLAFAGPQRNVYVDDTTRRIQLYTDYNKNGSSEP
RLKTLDDLTSYVYFVTVLRQMICALGNSYDAFNHDPWMDVVGFEDEPD
QVTNRDISRIVLSYMFNLNTAKGCLVEYATFRQYMRELPKNAPQKLNFRE
MRQGLIALGRHCVGSRFETDLYESATSELMANHSVQTGRNIYGVDSFSLT
SVSGTTATLLQERASERWIQWLGLSDYHCSFSSTRNAEDVVAGEAASSD
HDQKISRVTTRKPREPKSTNDILVAGQKLFSSFEFRDLHQLRLCHEIYM
ADTPSVAVQAPPGYGKTELFHLPLIALASKGDVKYVSFLFVPPYTVLLANC
MIRLSRCGLNVPVRNFIEEGCDGVTDLYVGIYDDLASTNFTDRIAWE
NIVECTFRTNVVKGLYLIVDEFHNFETEVYRQSQFGGITNLDFAFEKAI
FLSGTAPEAVADAALQRIGLTGLAKKSMIDINELKRSEDLRGLSSYPTRM
FNLIKEKSEVPLGHVHKIWKKVESQPEEALKLLALFEIEPESKAIIVVAS
TTNEVEELACSWRKYFRVWVWVHGLGAAEKVSRTKEFVTGSMRVLIGTK
LVTEGIDIKQLMMVIMLDNRLNIIELIQGVGRLRDGGCLCYLLSRKNSWAA
RNRKGELPPIKEGCITEQVREFYGLSKKGGKQHVGCCGSRDLSADTV
ELIERMDRLAEKQATASMSIILPSSFQESNSSDRCKYCSSDESDTCI
HGSANASTNATNSSTNATTTASTNVRTSATTTASINVRTSAITTESTNS
STNATTTASTNVRTSATTTASINVRTSATTTTESTNSNTSATTTTESTDSNT
SATTTTESTDSNTSATTTASTNSSTNATTTASTNSSTNATTTTESTNASAKE
DANKDGNADNRHFPVTDINKESYKRKGSQMVLLERKKLKAQFPNTSENM
NVLQFLGFRSDEIKHFLYGLIDVYFCPEGVFTQYGLCKGCQKMFELCVCW
AGQKVSYYRMAWEALAVRMLRNDEEYKEYLEDIEPYHGDVPVGYLKYFSV
KRGEIYSQIQRYAWYLAI TRRRETISVLDSTRGKQGSQVFRMSGRIKE
LYYKWSNLRESKTEVLQYFLNWDEKKCREWEAKDDTVFVEALEKGVF
QRLRSMTSAGLQGPQYVKLQFSRHRQLRSRYELSLGMHLRDQLALGVTP
SKVPHWTAFLSMLIGLFYNKTFRQKLEYLLEQISEVWLLPHWLDLANVEV
LAADNTRVPLVYMLMAVHKELDSDDVDPGRFDIILLCRDSSREVGE

YCR005C, 1883 bp, CDS: 501-1883 (SEQ ID NO 71)

AGAGTTGTTGCCACAACATAAGCCGCTTTGGAGTGTGAACAAATCCGTC
CTTGGGTCAATCAATCAATGGCTTGGCGGTATCTCAAAGAGCGCAAAC
AATAGCGCGCACATTCGACGCATTTATCCGGTGGTCATCGACTAGGGGCG
AAGAGGTCACGACCTATTTTTCTTGCAGAAAAAAGTGTGACCTTTTCC
GTAGCTAGACGCTATCAGGGCGTCAGCAATGGGAGGCACAGCGGAAAA
CAATAACAATGGTAAGCGCAATTACCTTTTGAGCGTTACATTCGTATGAA
ATTGGTGACGTTAATCTAAAGATAGTCATGCTCTCAAAGGGCCCATAT
TCTCGACGTTGAGCGTATATAAGACTATTAAAACTTGGTTCTTTAGATAT
GGTGTTCGTTCCCTCATTATTAAGTTTCAGGGAACAATATCAACACATATC
ATAACAGGTTCTCAAACCTTTTTGTTTTAATAACTAGTAACAAGAAAA
ATGACAGTTCCCTTATCTAAATTCAAACAGAAATGTTGCATCATATTTACA
ATCAAATTCAGCCAAGAAAAGACTCTAAAAGAGAGATTTAGCGAAATCT
ACCCCATCCATGCTCAAGATGTAAGGCAATTCGTTAAAGAGCATGGCAA
ACTAAAATTAGCGATGTTCTATTAGAACAGGTATATGGTGGTATGAGAGG
TATTCAGGGAGCGTATGGGAAGGTTCCGTTTTGGACCCAGAAGACGGTA
TTCGTTTCAGAGGTCGTACGATCGCCGACATTCAAAGGACCTGCCCAAG
GCAAAGGAAGCTCACAACTACTACAGAAGCTCTCTTTTGGTTATTGCT

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AACTGGCGAGGTTCCAACCTCAAGCGCAAGTTGAAAACCTTATCAGCTGATC
TAATGTCAAGATCGGAACCTACCTAGTCATGTCGTTCAACTTTTGGATAAT
TTACCAAAGGACTTACACCCAATGGCTCAATTCTCTATTGCTGTAAGTGC
CTTGGAAGCGAGTCAAAGTTTGCTAAGGCTTATGCTCAAGGAATTTCCA
AGCAAGATTATTGGAGTTATACCTTTTGAAGATTCAGTACTTGCTGGGT
AAATTGCCAGTTATTGCAGCTAAAATTTATCGTAATGTATTCAAAGATGG
CAAAATGGGTGAAGTGGACCCAAATGCCGATTATGCTAAAAATCTGGTCA
ACTTGATTGGTTCTAAGGATGAAGATTTCTGGACTTGATGAGACTTTAT
TTAACCATTCATTCCGATCACGAAGGTGGTAATGTATCTGCACATACATC
CCATCTTGTGGGCTCAGCACTATCATCACCTTATCTGTCCCTTGCATCAG
GTTTGAACGGGTTGGCTGGCCCACTTCATGGGCGTGCTAATCAAGAAGTA
CTAGAATGGTTATTTCGACTTAAAGAAGAGGTAAATGATGACTACTCTAA
AGATACGATCGAAAAATATTTATGGGATACTCTAAACTCAGGAAGAGTCA
TTCCCGGTTATGGTCATGCTGTGCTAAGGAAAACCTGATCCTCGTTATATG
GCTCAGCGTAAGTTTGCCATGGACCATTTTCCAGATTATGAATTATTCAA
GTTAGTTTCATCAATATACGAGGTAGCACCTGGCGTATTGACTGAACATG
GTAAACTAAAAATCCATGGCCAAATGTAGATGCTCACTCTGGTGTCTTA
TTACAATATTATGGACTAAAAGAATCTTCTTTCTATACCGTTTATTTTGG
CGTTTCAAGGGCATTGTTGTTATTCTTGCTCAATTGATCACTGATAGGGCCA
TCGGTGCTTCCATTGAAAGGCCAAAGTCCTATTCTACTGAGAAATACAAG
GAATTGGTCAAAACATTGAAAGCAAACCTATAG

YCR005C, 460 aa (SEQ ID NO 72)

MTVPYLSNRRNVASYLQSNSSQEKTLKERFSEIYPIHAQDVRQFVKEHGK
TKISDVLLLEQVYGGMRGIPGSVWEGSVLDPEDGIRFRGRTIADIQKDLPK
AKGSSQPLPEALFWLLLTGEVPTQAQVENLSADLMSRSELP SHVVQLLDN
LPKDLHPMAQFSIAVDTALESESKFAKAYAQQGISKQDYWSYTFEDSLDLLG
KLPVIAAKIYRNVFKDGKMGVEVDPNADYAKNLVNLIGSKDEDFVLMRLY
LTIHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEV
LEWLFALKEEVNDDYSKDTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYM
AQRKFAMDHFPDYELFKLVSSIYEVAPGVLTEHGKTKNPWPNVDAHSGVL
LQYYGLKESSFYTVLFGVSRAFGILAQLITDRAIGASIERPKSYSTEKYK
ELVKNIESKL

YOL126C, 1772 bp, CDS: 501-1772 (SEQ ID NO 345)

ATCCCTCATACTTTTCCGTTTGTATCTCCTACTTTCTTACTTCCTTTTT
TTCTTCTTTATTTGCTTGGTTTACCATTGAAGTCCATTTTTACTACAGAC
AATAGCTAGTCATTGCTATCTTCCGTTTGTCACTTTTTTCAAATTTCT
CATCTATATAGCGAAGTACGGAAAAGATGTCACTTGCCGGCATCTCGGCC
TTCCCGGCCAAATGGACTCATCATCTACGATACGGCCCCCTTAAATCCGC
AATTACTTTGCCCATTGCGCCGTAGCCGTTCTAAAGCCGCGTGCCTTGC
CCCCAATACTCCCCTAATGATCCGGGAAGTTCCGGTTTTTTTCTTTGTT
TAGTGGCATTTTGTGTTGCCCAAGGTGGGAAGGTCCGATTGACTTTAA
GGAACACGGAAGGTATCTAAGGTTTCTAAAAACAATATACACGCGGTG
CGTAGATATATAAAGATAAAGATTTATCGATATGAGATAAAGATTGCTGC
ATGATTCTCCTTCTGATTCTTTTCCCTGTATATATTTCTCCCCCTCTG
TATAAATCGTACAGTCAGAAAGTAGTCCAGAATATAGTGTGCTGAGACTATT
ACAAAAGTTCAATACAATATCATAAAAGTTATAGTAACATGCCTCACTCA
GTTACACCATCCATAGAACAAGATTCGTTAAAAATTGCCATTTTAGGTGC
TGCCGGTGGTATCGGGCAGTCGTTATCGCTGCTTTTGAAAGCTCAGTTGC
AATACCAGTTAAAGGAGAGCAACCGGAGCGTTACCCACATTCATCTGGCT
CTTTACGATGTCAACCAAGAAGCCATCAACGGTGTACCGCCGACTTGTC
TCATATAGACACCCCCATTTCCGTGTCGAGCCACTCTCCTGCAGGTGGCA
TTGAGAAGTGTGTCATAACGCTTCTATTGTTGTCATTCCTGCAGGTGTT
CCAAGAAAACCTGGCATGACTCGTGATGACTTATTTAACGTGAATGCTGG
TATCATTAGCCAGCTCGGTGATTCTATTGCAGAAATGTTGTGATCTTTCCA

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AGGTCTTCGTTCTTGTCAATTTCCAACCCTGTTAATTCCTTTAGTCCCAGTG
ATGGTTTCTAACATTCTTAAGAACCATCCTCAGTCTAGAAATTCGGGCAT
TGAAAGAAGGATCATGGGTGTCAACAAGCTCGACATTGTGAGAGCGTCCA
CTTTTCTACGTGAGATAAACATTGAGTCAGGGCTAACTCCTCGTGTTAAC
TCCATGCCTGACGTCCCTGTAATTGGCGGGCATTCTGGCGAGACTATTAT
TCCGTTGTTTTACAGATCAAACTTCCTATCGAGATTAAATGAGGATCAAT
TGAAATATTTAATACATAGAGTCCAATACGGTGGTGATGAAGTGGTCAAG
GCCAAGAACGGTAAAGGTAGTGCTACCTTATCGATGGCCCATGCCGGTTA
TAAGTGTGTTGTCCAATTTGTTTCTTTGTTATTGGGTAACATTGAGCAGA
TCCATGGAACCTACTATGTGCCATTAAAAGATGCGAACAACTTCCCCATT
GCTCCTGGGGCAGATCAATTATTGCCTCTGGTGGACGGTGCAGACTACTT
TGCCATACCATTAACTATTACTACAAAGGGTGTTCCTATGTGGATTATG
ACATCGTTAATAGGATGAACGACATGGAACGCAACCAATGTTGCCAATT
TGCGTCTCCAGTTAAAGAAAAATATCGATAAGGGCTTGAATTTCGTTGC
ATCGAGATCTGCATCATCTTAA

YOL126C, 423 aa (SEQ ID NO 346)

MILLLLILFPCIYFLPFCINRTVRSSPEYSAADYKSSIQYHKSYSNMPHS
VTPSIEQDSLKIAILGAAGGIGQSLSLLLKAQLQYQLKESNRSVTHIHLA
LYDVNQEAINGVTADLSHIDTPISVSSHSPAGGIENCLHNASIVVIPAGV
PRKPGMTRDDLNVNAGIISQLGDSIAECCDLSKVFLVISNPVNSLVPV
MVSNIKLNHPQSRNSGIERRIMGVTKLDIVRASTFLREINIESGLTPRVN
SMPDVPVIGGHSGETIIPLFSQSNFLSRLNEDQLKYLIIHRVQYGGDEVVK
AKNGKGSATLSMAHAGYKCVVQFVSLLLGNIEQIHGTYVPLKDANNFPI
APGADQLLPLVDGADYFAIPLTITTKGVSYVDYDIVNRMNDMERNQMLPI
CVSQLKKNIDKGLEFVASRSASS

YBR019C, 2600 bp, CDS: 501-2600 (SEQ ID NO 39)

ATCGCTTCGCTGATTAATTACCCAGAAATAAGGCTAAAAAACTAATCGC
ATTATCATCCTATGGTTGTTAATTTGATTCTGTTAATTTGAAGGTTTGTTG
GGCCAGGTTACTGCCAATTTTTCCTCTTCATAACCATAAAAGCTAGTATT
GTAGAATCTTTATTGTTTCGGAGCAGTGC GGCGCGAGGCACATCTGCGTFT
CAGGAACCGCACCGGTGAAGACGAGGACGCACGGAGGAGAGTCTTCCGTC
GGAGGGCTGTGCGCCGCTCGGCGGCTTCTAATCCGTACTTCAATATAGCA
ATGAGCAGTTAAGCGTATTACTGAAAGTTCCAAAGAGAAGGTTTTTTTAG
GCTAAGATAATGGGGCTCTTTACATTTCCACAACATATAAGTAAGATTAG
ATATGGATATGTATATGGTGGTAATGCCATGTAATATGATTATTAACTT
CTTTGCGTCCATCCAAAAAAGTAAGAATTTTGGAAAATTCATATAA
ATGACAGCTCAGTTACAAAGTGAAAGTACTTCTAAAATTTGTTTTGTTTAC
AGGTGGTGCTGGATACATTTGGTTTACACACTGTGGTAGAGCTAATTGAGA
ATGGATATGACTGTGTGTTGCTGATAACCTGTGCAATTCAACTTATGAT
TCTGTAGCCAGGTTAGAGGTCTTGACCAAGCATCACATTCCTTCTATGA
GGTTGATTTGTGTGACCGAAAAGGTCTGGAAAAGGTTTTCAAAGAATATA
AAATTGATTTCGTAATTCACTTTGTCTGGTTTTAAAGGCTGTAGGTGAATCT
ACACAAATCCCGCTGAGATACTATCACAATAACATTTTGGGAACGTGTCGT
TTTATTAGAGTTAATGCAACAATACAACGTTTCCAAATTTGTTTTTTCAT
CTTCTGCTACTGTCTATGGTGATGCTACGAGATTCCCAAATATGATTCCCT
ATCCCAGAAGAATGTCCCTTAGGGCCTACTAATCCGTATGGTCATACGAA
ATACGCCATPGAGAATATCTTGAATGATCTTTACAATAGCGACAAAAAAA
GTTGGAAGTTTGTCTATCTTGGCTTATTTTTAACCCTAATTGGCGCACATCCC
TCTGGATTAATCGGAGAAGATCCGCTAGGTATACCAAACAATTTGTTGCC
ATATATGGCTCAAGTAGCTGTGGTAGGCGCGAGAAGCTTTACATCTTCG
GAGACGATTATGATTCCAGAGATGGTACCCCGATCAGGGATTATATCCAC
GTAGTTGATCTAGCAAAAGGTCATATTGCAGCCCTGCAATACCTAGAGGC
CTACAATGAAAATGAAGGTTTGTGTCTGTGAGTGGAACTTGGGTTCCGGTA
AAGGTTCTACAGTTTTTGAAGTTTATCATGCATTCTGCAAAGCTTCTGGT

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ATTGATCTTCCATACAAAGTTACGGGCAGAAGAGCAGGTGATGTTTTGAA
CTTGACGGCTAAACCAGATAGGGCCAAACGCGAAGTGAATGGCAGACCG
AGTTGCAGGTTGAAGACTCCTGCAAGGATTTATGGAAATGGACTACTGAG
AATCCTTTTTGGTTACCAAGTTAAGGGGTGTCGAGGCCAGATTTTCCGCTGA
AGATATGCGTTATGACGCAAGATTTGTGACTATTGGTGCCGGCACCAGAT
TTCAAGCCACGTTTGCCAAATTTGGGCGCCAGCATTTGTTGACCTGAAAAGTG
AACGGACAATCAGTTGTTCTTGGCTATGAAAATGAGGAAGGGTATTTGAA
TCCTGATAGTGCTTATATAGGCGCCACGATCGGCAGGTATGCTAATCGTA
TTTCGAAGGGTAAGTTTAGTTTATGCAACAAAGACTATCAGTTAACCGTT
AATAACGGCGTTAATGCGAATCATAGTAGTATCGGTTCTTTCCACAGAAA
AAGATTTTTTGGGACCCATCATTCAAAATCCTTCAAAGGATGTTTTTACCG
CCGAGTACATGCTGATAGATAATGAGAAGGACACCGAATTTCCAGGTGAT
CTATTGGTAACCATACAGTATACGTGTAACGTTGCCCAAAAAAGTTTGGGA
AATGGTATATAAAGGTAATTTGACTGCTGGTGAAGCGACGCCAATAAATT
TAACAAAATCATAGTTATTTCAATCTGAACAAGCCATATGGAGACACTATT
GAGGGTACGGAGATTATGGTGCGTTCAAAAAAATCTGTTGATGTCGACAA
AAACATGATTCCTACGGGTAAATATCGTCGATAGAGAAATTGCTACCTTTA
ACTCTACAAAGCCAACGGTCTTAGGCCCCAAAAATCCCCAGTTTGATTGT
TGTTTTGTGGTGAGTGAATGCTAAGCCAAGTCAAATCAATACCTCTAAA
CAATGAATTGACGCTTATTTGTCAAGGCTTTTCATCCCGATTCCAATATTA
CATTAGAAGTTTAAGTACAGAGCCAACTTATCAATTTTATACCGGTGAT
TTCCTTGTCTGCTGGTTACGAAGCAAGACAAGGTTTTCGAATTGAGCCTGG
TAGATACATTTGATGCTATCAATCAAGAGAACTGGAAAGATTGTGTAACCT
TGAAAAACGGTGAAACTTACGGGTCCAAGATTGTCTACAGATTTTCCCTGA

YBR019C, 699 aa (SEQ ID NO 40)

MTAQLQSESTSKIVLVTGGAGYIGSHTVVELIENGYDCVVADNLSNSTYD
SVARLEVLTKHHIPFYEVDLCDRKGLEKVFKEYKIDSVIHFAGLKAVGES
TQIPLRYHHNNILGTVVLELMQQYNVSKFVSSSATVYGDATRFNMIIP
IPEECPLGPINPNYPGHTKYAIENILNDLYNSDKKSWKFAILRYFNPIGHP
SGLIGEDPLGIPNNLLPYMAQVAVGRREKLYIFGDDYDSRDGTPIRDYIH
VVDLAKGHIAALQYLEAYNENEGLCREWNLGSGKGSTVFEVYHAFCKASG
IDLPHYKVTGRRAGDVLNLAKPDRAKRELKWQTELQVEDSCKDLWKWTE
NPFQYQLRGVEARFSAEDMRYPDARFVTIGAGTRFQATFANLGASIVDLKV
NGQSVVLGYENEEGYLNPDSAYIGATIGRYANRISKGKFSLCNKDYQLTV
NNGVNAHSSIGSFHRKRLGPIIQNP SKDVFTA EYMLIDNEKDETFPGD
LLVTIQYTVNVAQKSLEMYKGLTAGEATPINLTNHSYFNLNPKPYGDTI
EGTEIMVRSSKSVVDKNMIP TGNIVDREIATFNSTKPTVLGPKNPQFDC
CFVVDENAKPGINTLNNELTLIVKAFHPDSNITLEVLSSTEPTYQFYTG
FLSAGYEARQGF AIEPGRYIDAINQENWKDCVTLKNGETYGSKIVYRFS

YDR345C, 2204 bp, CDS: 501-2204 (SEQ ID NO 123)

TCCTAGCTATATCTTCCAGCTTCGCCTGCTGCCCGGTCATCGTTCCCTGT
CACGTAGTTTTTCCGGATTTCGTCCGGCTCATATAATACCGCAATAAACAC
GGAATATCTCGTTCCGCGGATTTCGGTTAAACTCTCGGTCCGCGATTATCA
CAGAGAAAGCTTCGTGGAGAATTTTTCCAGATTTTCCGCTTTCCCCGATG
TTGGTATTTCCGGAGGTCATTATACTGACCGCCATTATAATGACTGTACA
ACGACCTTCCTGGAGAAAGAAACAACCTCAATAACGATGTGGGACATTGGGG
GCCCACTCAAAAAATCTGGGGACTATATCCCCAGAGAATTTCTCCAGAAG
AGAAGAAAAGTCAAAGTTTTTTTTTCGCTTGGGGGTGTCATATAAATACAG
GCGCTGTTTTATCTTCAGCATGAATATTCATAATTTTACTTAATAGCTT
TTCATAAATAATAGAATCACAAACAAAATTTACATCTGAGTTAAACAATC
ATGAATTCAACTCCAGATTTAATATCTCCACAAAAGTCAAGTGAGAATTC
GAATGCTGACCTGCCCTTCAATAGCTCTCAGGTAATGAACATGCCCTGAAG
AAAAAGGTGTTCAAGATGATTTCCAAGCTGAGGCCGACCAAGTACTTACC
AACCCAAATACAGGTAAAGGTGCATATGTCACTGTGTCTATCTGTTGTGT

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TATGGTTGCCCTTCGGTGGTTCGTTTCGGTTGGGATACGGTACCATTTC
CTGGTTTCGTCGCCCCAACTGATTTCTTGAGAAGATTTCGGTATGAAGCAT
AAAGATGGTAGTTATTATTGTCTAAGGTTAGAAGTGGTTTAATTGTCTC
CATTTTCAACATTGGTTGTGCCATTGGTGGTATTATTTTGGCTAAATTGG
GTGATATGTACGGTCGTAAAAATGGGTTTGATTGTCTGTTGTTATCTAC
ATCATCGGTATTATTATTCAAATTGCATCCATCAACAAATGGTACCAATA
TTTCATCGGTAGAATTATTTCGGGTTTGGGTGTTGGTGGTATTGCCGTTT
TATCTCCTATGTTGATTTCTGAAGTCGCTCCTAAGGAAATGAGAGGTACT
TTAGTCTCCTGTTACCAACTGATGATTACCTTGGGTATTTTCTTGGGTTA
CTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGCAATGGAGAG
TTCCATTAGGTTTGTGTTTTCGCTGGGCTTTGTTTATGATCGGTGGTATG
ACTTTCGTTCCAGAATCCCCACGTTATTGGTTGAAGCTGGTCAAATGA
CGAAGCAAGAGCATCTCTTCCAAAGTTAACAAGGTTGCCCCAGACCATC
CATTCATTCAACAAGAGTTGGAAGTTATTGAAGCTAGTGTGGAAGAAGCT
AGAGCTGCTGGTTCAGCATCATGGGGTGAGTTGTTCACTGGTAAGCCGGC
CATGTTTAAAGCGTACTATGATGGGTATCATGATCCAATCTCTACAACAAT
TGACTGGTGATAACTATTTCTTCTACTATGGTACTACCGTTTTTAACGCT
GTTGGTATGAGTGATTTCTTCGAACTTCTATTGTTTTTCGGTGTCTGTCAA
CTTCTTCTCTACTTGTGTTCTTTGTACACTGTGATCGTTTGGACGTC
GTAACGTGTTGTTATATGGTGCCATTGGTATGGTCTGCTGTTATGTAGTT
TACGCTTCTGTTGGTGTACACAGACTATGGCCAAATGGTGAAGGTAATGG
TTCATCCAAAGGTTGCTGGTAACGTATGATGTTGCTTTTGCTGTTTCTATA
TTTTCTGTTTTGCTACCACCTGGGCTCCAATTGCTTATGTTGTTATTTCT
GAAACTTTCCCATTTGAGAGTCAAGTCTAAGGCTATGTTCTATTGCTACAGC
TGCTAATTGGTTGTGGGGTTTTCTTGATTGGTTTTCTTCACTCCATTTATTA
CTGGTGCTATTAACTTCTACTACGGTTACGTTTTTCATGGGCTGTATGGTT
TTCGCCCTACTTCTACGTTTTCTTTCTTTGTGCCAGAACTAAGGGTTTGAC
TTTGGAAGAAGTCAATGATATGTACGCTGAAGGTGTTCTACCATGGAAGT
CTGCTTCATGGGTTCCAACATCTCAAAGAGGTGCTAACTACGATGCTGAT
GCATTGATGCATGATGACCAGCCATTCTACAAGAAAATGTTCCGCAAGAA
ATAA

YDR345C, 567 aa (SEQ ID NO 124)

MNSTPDLISPOKSSSENSNADLPSNSSQVMNMPEEKGVQDDFQAEADQVLT
NPNTGKGAYVTVSICCVMAFGGFVFGWDTGTISGFVAQTDPLRRFGMKH
KDGSYYLKVSRITLIVSIFNIGCAIGGIIILAKLGDYGRKMGLIVVVVIY
IIGIIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVAPKEMRGT
LVSCYQLMITLGLIFLYCTNFGTKNYSNSVQWRVPLGLCFAWALFMIGGM
TFVPESPRYLVEAGQIDEARASLSKVNKVAPDHPFIQQELEVIEASVEEA
RAAGSASWGELEFTGKPAMFKRTMMGIMIQLQLTGDNYFFYYGTTVFNA
VGMDSDFETSIVFGVNNFFSTCCSLYTVDRFGRNCLLYGAIGMVCCYVV
YASVGVTURLWPNGEGNGSSKGAGNCMIVFACFYIFCFATTWAPIAYVVIS
ETFPLRVKSKAMSIATAANWLWGFLIGFPTPFITGAINFYGYVFMGCMV
FAYFYVFFFVPETKGLTLEEVNDMYAEGVLPWKSASWVPTSQRGANYDAD
ALMHDDQPFYKMF GK

YKR097W, 2150 bp, CDS: 501-2150 (SEQ ID NO 263)

ATAGGAAAAAACCGAGCTTCCTTTTCATCCGGCGCGGCTGTGTTCTACATA
TCACTGAAGCTCCGGGTATTTTAAGTTATACAAGGGAAGATGCCGGCTA
GACTAGCAAGTTTATAGGCTGCTTAACATTATGGATAGGCGGATAAAGGGC
CCAAACAGGATTGTAAAGCTTAGACGCTTCTGGTTGGACAATGGTACGTT
TGTGTATTAAGTAAGGCTTGGCTGGGGATAGCAACATTGGGCAGAGTATA
GAAGACCACAAAAAAGGTATATAAGGGCAGAGAAGTCTTTGTAATGTG
TGTAACCTCTCTTCCATGTGTAATCAGTATTCTACTTACTTCTTAAATA
TACAGAAGTAAGACAGATAACCAACAGCCTTCCAGATATACATATATA
TCTTTATTTTACGCTTAAACAATAATTATATTTGTTTAACTCAAAAATAAA

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AAAAAAAAACCAAACACGCAACTAATTATTCCATAATAAAATAACAAC
ATGTCCCCTTCTAAAATGAATGCTACAGTAGGATCTACTTCCGAAGTTGA
ACAAAAAATCAGACAAGAATTGGCTCTTAGTGACGAAGTCACCACCATCA
GACGCAATGCTCCAGCTGCCGTTTTGTATGAAGATGGTCTAAAAGAAAAT
AAAACGTGTCATTTTCATCAAGCGGTGCATTGATCGCTTATTCCGGTGTTAA
AACCAGGAAGATCTCCAAAGGACAAACGTATTGTTGAAGAACCTACCTCGA
AAGACGAAATTTGGTGGGGTCCGGTCAATAAACCATGTTCTGAAAGAACA
TGGTCTATCAACCGTGAAAGAGCTGCAGATTACTTGAGAACAAGAGACCA
CATTTATATTGTGATGCATTTGCAGGATGGGATCCAAAATACAGAATCA
AAGTCCGCGTTGTTTGTGCCAGGGCTTACCACGCTTATTTCATGACAAAT
ATGCTTATTAGACCTACAGAAGAAGAATTAGCCCATTTTGGAGAACCTGA
TTTTACTGTCTGGAACGCTGGTCAGTTCCAGCCAATTTACACACCCAGG
ATATGTCTTCAAAGAGTACTATAGAAAATTAACCTCAAAGCAATGGAAATG
ATCATTTTAGGTACCGAATACGCCGGTGAAATGAAAAAGGTATTTTCAC
AGTTATGTTTACTTGATGCCTGTGCACCATAACGTTTAACTTTGCACT
CTCCGCCAACCAGGGTATTCAAACGGTGACGTTACTTTATTCTTTGGC
CTAAGTGGTACCGGGAAACCACTTTATCCGCAGACCCACATAGATTGTT
GATCGGCGATGATGAACATTGTTGGTCCGACCATGGTGTCTTCAATATCG
AAGGTGGTTGTTACGCCAAGTGTATTAATTTATCTGCCGAAAAGGAGCCT
GAAATTTTCGACGCTATCAAGTTTGGTTCTGTATTAGAAAACGTTATCTA
TGACGAGAAGTCGCATGTAGTCGACTATGACGACTCTTCTATTACTGAAA
ATACTAGATGTGCCTACCCAATTGACTACATTCCAAGTGCCAAGATTCCA
TGTTTGGCGGACTCTCATCCAAAGAACATTATCCTGCTAACTTGTGATGC
TTCGGGTGTTTACCACCAGTATCTAAATTGACTCCTGAACAAGTCATGT
ACCATTTTCATCTCTGGTTACACTTCTAAAATGGCTGGTACTGAGCAAGGT
GTCACGTAACCTGAACCAACATTTTCATCTTGTTCGGACAACCTTCCT
AGCCTTGCACCCTATTAGATACGCAACCATGTTAGCTACAAAGATGTCCTC
AACATAAAGCTAATGCGTACTTAATCAACACCGGCTGGACTGGTTCCTCC
TACGTATCTGGTGGTAAACGTTGCCCATTTGAAGTACACAAGGGCCATTCT
GGATTCTATTTCATGATGGTTCGTTAGCCAATGAAACGTACGAAACCTTAC
CGATTTTCAATCTTCAAGTACCTACCAAGGTTAACGGTGTTCAGCTGAG
CTTTTGAATCCTGCTAAAAACTGGTCTCAAGGTGAATCCAAATACAGAGG
TGCAGTTACCAACTTGGCCAACTTGTTCGTTTCAAAATTTCAAGATTTATC
AAGACAGAGCCACACCAGATGTATTAGCCGCTGGTCTCTCAATTCGAGTAA

YKR097W, 549 aa (SEQ ID NO 264)

MSPSKMNATVGSTSEVEQKIRQELALSDEVTTIRRNAPAAVLYEDGLKEN
KTVISSSGALIAYSVKVTKRSPKDKRIVEEPTSKDEIWWGPVKNPCSERT
WSINRERAADYLRTDHIYIVDAFAGWDPKYRIKVRVVCARAYHALFMTN
MLIRPTEEEELAHFGEPDFTVWNAGQFPANLHTQDMSSKSTIEINFKAMEM
IILGTEYAGEMKKGIFTVMFYLMPVHNVLTLLHSSANQGIQNGDVTLLFFG
LSGTGKTTLSADPHRLIGDDEHCWSDHGVFNIEGGCYAKCINLSAEKEP
EIFDAIKFGSVLENVYIDKSHVVDYDDSSITENTRCAYPIDYIPSAKIP
CLADSHPKNIILLTCDASGVLPPVSKLTPEQVMYHFISGYTSKMAGTEQG
VTEPEPTFSSCFGQPFLALHPYATMLATKMSQHKANAYLINTGWTGSS
YVSGGKRCPLKYTRAILDSIHGSLANETYETLPIFNLQVPTKVNGVPAE
LLNPAKNWSQGESKYRGAVTNLANLFVQNFKIYQDRATPDVLAAGPQFE

YMR173W, 1793 bp, CDS: 501-1793 (SEQ ID NO 313)

AAACAAGTGTAACATAAATACATTCTGTAAATCTACAAAAATCGTTAGTG
CTGTTTTCTTTTTGAGATTGAAAAGTACGAATCATACACATCTCTTATTC
TGAGAAGGGTGCATATGACGTAAATCAATGCGTACAAAGCGGTTTCCGGT
GCTGGCCTGGCCCAACACAGTTTGGCGTGGTTGATTTTAAAAACCTTCG
GGAAGGTGAAAAAACCACTCCGAAGGTTGAGGATGACAAATCGCCCCTT
AGCTGTGGCCATACAAGCTTGGCACCGACGAAAAAGGGAAAAAGGAAAAAG
AATGTCGTACAAGAACTCTTACAACCACGTTGAGATTTTCATTTAACAACG

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CCCCCCTTTCCATTATATAAGAAGGCATTAATTTTATGTAATAAAAAA
GAATTTCTCGAAAATGCTTACAATTAATTTTCTTTTGTAAGTAGAGTAGGG
CTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCA
ATGGGTTTATTTGATAAAGTGAAGCAATTTGCTAACAGCAATAATAACAA
CAATGATTCTGGCAATAACAATCAAGGCGATTATGTTACCAAAGCTGAGA
ATATGATCGGCGAAGATAGAGTCAATCAATTCAAAAGCAAAATCGGAGAG
GACAGATTTGATAAGATGGAGTCCAAGGTTCTGCAACAATTTTCTAATAC
CTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTTCTAATA
ACAACGATTTCATATGGTTCTAACAACAATGATTTCATATGGCTCTAACAAC
AATGATTTCATATGGCTCCAACAACAATGATTTCATATGGCTCTAACAACGA
TGATTTCCTACGGTTCTTCCAACAAGAAGAAGAGCTCTTATGGTTCTAACA
ATGACGATTTCGTACGGCTCCAGCAACAACAATGACTCTTACGGTTCCAAC
AACAATGACTCTTACGGTTCCAACAACAATGACTCTTACGGTTCCAACAA
TGACGACTCTTACGGTTCTGCAACAAGAATAAGAGCTCTTACGGTTCCA
ACAATGACGATTCTTATGGCTCTAACAATGATGATTTCATATGGTTCTTCC
AACAAGAAGAAGAGTTCTTATGGTTCCAGCAACAACGATTTCGTATGGTTC
TAACAACGATGATTTCATATGGTTCTAACAACAATGATTTCATATGGCTCTA
ACAACGATGATTCTTACGGTTCTTCCAACAAGAAGAAGAGCTCTTATGGT
TCTAACAATGACGATTTCGTACGGCTCCAGCAACAACAATGACTCTTACGG
TTCCAACAATGACGACTCTTACGGTTCTGCAACAAGAATAAGAGCTCTT
ACGGTTCTTCTAGCAACGATGATTCTTACGGATCTTCCAATAACGACGAC
TCTTACGGTTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCCAACAATGA
CGATTCTTATGGCTCTAACAATGATGATTTCATATGGTTCTTCCAACAAGA
AGAAGAGTTCTTATGGTTCCAGCAACAACGATTTCGTATGGTTCTAACAAC
GATGATTTCCTACGGTTCTTCTAACAACAAGAAGAGTTCTTATGGTTCCA
CAACGATGATTTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTCCA
ACAATGACGACTCTTACGGTTCTCTAATAGAAACAAGAACTCTATGGG
TCTTCCAACACTACGGTTTCATCCAACAATGATGACTCTTATGGTTTCATCTAA
TAGAGGCGGTTCGTAATCAATACGGTGGTGACGACGATTACTAA

YMR173W, 430 aa (SEQ ID NO 314)

MGLFDKVKQFANSNNNNNSGNNNQGDYVTKAENMIGEDRVNQFKSKIGE
DRFDKMESKVRQQFSNTSINDNDSNNNDSYGSNNNDSYGSNNNDSYGSNN
NDSYGSNNNDSYGSNNDDSYGSSNKKKSSYGSNNDDSYGSSNNNDSYGSN
NNDSYGSNNNDSYGSNNDDSYGSSNKNKSSYGSNNDDSYGSSNNDDSYGSS
NKKKSSYGSNNNDSYGSNNDDSYGSSNNNDSYGSNNDDSYGSSNKKKSSYG
SNDDSYGSSNNNDSYGSNNDDSYGSSNKNKSSYGSNNDDSYGSSNNDD
SYGSSNKKKSSYGSNNDDSYGSSNNDDSYGSSNKKKSSYGSNNNDSYGSNN
DDSYGSSNKKKSSYGSNNDDSYGSSNNNDSYGSNNDDSYGSSNRNKNSYG
SSNYGSSNNDDSYGSSNRGGRNQYGGDDDY

YIL057C, 995 bp, CDS: 501-995 (SEQ ID NO 217)

CCCAACAGATTTCAAGTCTGTCGCCTTAACCACTCGGCATAGTGCCTAA
AACAATGTAGGTTATTTAAGCAAGTATTGTAGATACTTTTCGTAATAAAC
TACAATGCACCCACGACTCGCGGTGAATGATGGCATGAAATCATTGAAC
GAAGTTTTGCGGCTATACGGCTGAAGGACGAGACTAAAGGGACAGGAATT
ATTAATGCGGGGTATAATTTGAATAGTATTAACGGGCACTGCCGTTTAGC
CATCAAATGCTATTGTTGGGGTATTCTCTCTACTTTTGTTCCTTGGCTTG
AACCTTTTCGGCGGTGGCAATCGTCCGTATATAAGCATCGGCTGTCCCA
ATCCTCTATTGCCCTTTTCCCTTGCACTCCTTCTCAATTCTTCGTATCT
TTCGCGTAAAGGTAGATCTTGATTCACCTATCTGTCGAAACACGATTAAG
TGCAACGAAACAACGTACAGTATATAACAAAGTATTTTAAATAATAAGA
ATGACGAAAAAGGATAAGAAAGCAAAGGGTCCTAAGATGTCCACCATCAC
TACAAAAAGTGGTGAGTCCTTAAAGGTTTTTGAGGATTTGCATGATTTTG
AAACATATTTAAAGGGTGAGACGGAAGATCAAGAGTTTCGACCATGTCCAT
TGCCAACCTGAAGTACTATCCACCTTTGTCTTCATGATGCGCATGATGA

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TCCGGAAAAGATCAAAGAGACTGCCAATTCGCACTCTAAGAAGTTTGTTTC
GCCATTTACACCAGCATGTTGAGAAGCACCTGCTAAAGGACATCAAAACC
GCTATCAACAAGCCAGAATTGAAATTCCACGATAAGAAAAAGCAGGAATC
CTTTGACCGGATTGTTTGAATTATGGCGAAGAAACGGAGTTGAACGCCA
AGAAATTCAAGGTGTCTGTCTGAAGTTGTATGTAAACACGATGGCGCAATG
GTAGATGTTGATTACAAGACAGAACCCTTGCAGCCACTCATCTAA

YIL057C, 164 aa (SEQ ID NO 218)

MTKKDKKAKGPKMSTITTKSGESLKVPEDLHDFEYFLKGETEDQEFDHVH
CQLKYYPFVLHDAHDDPEKIKETANSHSKKFVRHLHQHVEKHLKDIKT
AINKPELKFHDKKKQESFDRIWVNYGEETELNAKKFKVSVEVVCKHDGAM
VDVDYKTEPLQPLI

YDR544C, 929 bp, CDS: 501-929 (SEQ ID NO 135)

TAAAGTAGTCGGTACGTACTTTTCGTTTTCAATTTCCATGGTGCACAGTAT
CTTAACATATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGTTGCTCAG
CCGCTTCGTGGATATTCCTTTGGATACTTTAAATATGGACCTACGCTTAG
CCTGCGCTTAGCCTACAACCTTCCTCGCTCTCGAAAAGACCAATATAATA
GAAAGTTATAAATTACATTTCCCTTATTAGGTATACGACCTCGCGCTTCGA
AGTAGAGGAGCCCTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AAC'TCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCAT'T
CACCCACGACGTATCAAGTTACTTCCTTGGTGCAATGTCCCACTATAAAA
AAATTCCTTGACGCTAGATCGTTGGACTAAAATCTGCGTCACAATCGCCT
AAACAGGAAATATTGCCATTTTTCGTACAAGGTTACTTCCTAGATGCTAT
ATGTCCTTACGGCTTGTCTAACACCATCCAGCATGCAATACAGTGACAT
ATATATACACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA
CCACACACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA
CCAGAGAGAAGCCTAAGCCTAAGACTAAGACAAGCCAAGCCTGACCAACC
TGCTCTCTCAAATTACCCTCCATTACCCTACCTCCCCACTCGTTACCCTGA
CTCATTTCAACTATACCACCCCAACCACCATCCATCTCCCTGTGTACTACC
ACCAACCGACCGTCCACCATAACCGTTACCCTCCAATTACCCATATCCAA
CTCCACTACCACTTACCCTACCATCTCCCATCTACTACTACCATACTAT
TGTTCTACCCACCACTATTGAAACGCTAA

YDR544C, 142 aa (SEQ ID NO 136)

MSLRPCLTPSSMQYSIDIYIHTTPHPHTPHHTHHHTHTTPTPTPHPHHTHTPT
PERSLSRLRLRQAKPDQPVQSITLHYPTSPLVTLTHSTIPPQPPSISLCTT
TNRPSTITVTLLQLPISNSTTTYPTISHLLLLTILLFYPPLLKR

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 255)

GGGCTTTTCCAGTGCCGCGGCCTCGAGATCCAGGCACCAGGAAGTACGGCA
CGCTGTGTATTCTAACACATTGAAGGGCCTAGGCCGCTGACGTGGGGTC
TAGTTCCACTTTTTTATTACCTTTTCTCGGTCTTTTCTTGCTCCACAGG
CCGTTAATGGCCTGAAACAGTTTGTGACTTTGGACTTATGATAACGATG
TTTGTCCGGGTGCCACCGGATTCTATCGCGCGAATCAAGTCTAGTCTGT
TTGCATCCATCAAGGCACTGCTCATTTGTGTAATAATTGTTCTACGCTTTTG
TCATCAATCATATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAG
TGGTAAGGTAGCCGGCTCGTCTTTGGTCATGCGCCAATACTGTGCAACGG
CCCGCGCGTAGCGTTCTTCGGCTTCAACCTTAGAGCTGATACCTTTTGCC
TGGTCAAAGGCGAAAACGTCTACCTCGCTTTCACTGCTGCTTTTCGCTTTT
ATGACTTCGTTTCAAGCGGTCTCTTCGCTCTCGGTGTGAACACACTTGT
AGCCTGCTATGCTTTACCGTACTCGAAAAGCGTAGCCTCATGACTAGTT
GTACCAACGCCCTTTCTTTTCTTTTCTTCTTCTTGACACTTCGGCGTATT
CATCGCCACTGGTACAAGCCGTATGGTGCTTTTTTGCTCATTTTCGTTTTT
GACGTTGCGATGGTTTCGCGGACCAATCGCATGGGTGGTGGTGGATGTTG
TCTTTGCTAGTTGCAACGTAGTCTTCTTCTCTCTGCGCTTTCTGACGAA

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AATTGGCCTTACGTATCTTTTTTCGGCGTCGTTGTCGTCATCGCTGTTCA
TATAATCGTCGTCATCATATCGGCGCTTTTACTGCATGCTGTCTTTTGA
AGAGAGTTTCATTGAAAAGTAGTGAAGAAAAAAAAAAAAAAAAAAAAA
AAAAAGGAAAAAAGCTTACATACGGAAGAGAAAAAAAAAAAAAAGAAATT
TTAA

YKR040C, 167 aa (SEQ ID NO 256)

MTSFQAVSFALGCNTLVACYAFTVLEKRSMLTSCTNALSFLFFLLTLRRI
HRHWYKPYGAFLLIFVLTLRWFRGPIAWVVVDVVFASCNVVFSPALSDE
NWPYVSFFGVVVVIAVHIIVVTHIGAFTACCLLKRVSLKSSEKKKKKKK
KKEKSLHTEREKKKKKF

YNL338W, 659 bp, CDS: 501-659 (SEQ ID NO 337)

TAAAGTAGTCGGTACGTACGTTCGTTTTCAATTTCCATGGTGCACAGTAT
CTTAAGTATCTGCTTAGTCGAGGAGAACCAGGATTCGTTTCGTTGCTCAG
CCGCTTCGTGGATATTCCTTGGATACTTTAAATATGGACCTACGCTTAG
CCTGCGCTTAGCCTACAACCTCTTCCGCTCTCGAAAAGACCAATATAATA
GAAAGTTATAAATTACATTTCCCTATTAGGTATACGACCTCGCGCTTCGA
AGTAGAGGAGCCCCTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTTACCCCGCCGAATAAGAAAACAGACCCATT
CACCACGACGTATCAAGTTACTTCTTGGTGCAATGTCCCACTATAAAA
AAATTCCTTGACGCTAGATCGTTGGACTAAAATCTGCGTCACAATCGCCT
AAACAGGAAATATTGCCATTTTTCTGTACAAGGTTACTTCTTAGATGCTAT
ATGTCCCTACGGCCTTGCTTAACACCATCCAGCATGCAATACAGTGACAT
ATATATACCCACACCCACACCCACACCCACACCCACACCCACACCCAC
ACCCACACCCACACCCACACCCACACCCATCACAACCCCTAACCCCTACC
CTATTCTAA

YNL338W, 52 aa (SEQ ID NO 338)

MSLRPLTPSSMQYSDIYIPTPTPHHTHTPTPHPHPTHHTHTHNPNT
LF

YJR115W, 1010 bp, CDS: 501-1010 (SEQ ID NO 235)

GCCAGTATCCCTTTCTGAAATAAGCTAAACCCTTGCAACCACCAGGGTG
CCGCCGTCCTAACTTTCCAGCCTGGCAGCGCGTCGAGTCGCCGAATGTTG
CGGGCGCTGCCCCGCCCCGAACACCGCGCCCCGCGCTGCTCAGCTTAACC
GAAACCACACGGGTCCTGCCATCTTCCATATACCCCTGGCTCTTCTTTCACA
ATGCCCGCTCACAACGCCAACTGCAAAAGAAGCCCGCCCTTAGTCGGTTT
TCCCCACTTTGATATAACCCCCCCCCCCCCCCCCCGCATCAACTGGTAA
TTTAACCCCAAACACCACGGGGTCATAATTTAAAAGCGAAAAACCTTAAAG
CGTTC'TCGAAGAAATCTTCCCTGTAGATGATGTCGTAGCAAAC'TTATCTTT
TAGAGTGT'TTGTC'TTACTGCA'TTGTGATCAAAATTTACGTAGCCGCC
CTTTTCAACCCCTGTGCAAGAGTAGCATAACAGCAGCGTAGTGAACGTGC
ATGTTTCAAAATACACGTACAATATTAATATACAATAGTAAGGTGATGAA
CACACACACACACACACACACACACACACACACATATATATATATA
CAGGAGATCAAGTTAGTGTGAGGGGACGACTACTGAGTTTGAAGTTC'TTT
AAAGTGT'TAAAGTTATTTTCCCTCTCCACCTCGTTGGCAACCTCTCA
CCCACCGCTTAGCAGCATGTCTCCGTACATGACCATACCTCAGCAATACT
TATACATAAGCAAGATACGTTCCAAGCTGTCTCAGTGCGCCCTTACTCGA
CACCACCACAGAGAACTTGATCTACGAAAAATGGTGGGCCACGCCAATAT
GCTGGACAGGATCCTCGACGAAATAGACGAAATCGACAGCGAGGTAGTAC
TGTGTGACGCTGCCGATGGTTCTTCTACTGCAGAAGCTCATTCCGCTTCC
CCAGCATCCAGCGACTCTTCTCCTCTCACTAATAACATCCGGCCCATTAG
CATATATGTGA

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YJR115W, 169 aa (SEQ ID NO 236)

MFTNTRTILIYNSKVMNTHTHTHTHTHTHIYITGDQVSVRGRLLSLKFF
KVLKLFPPSPTSLATSHPLSSMSPYMTIPQQYLYISKIRSKLSQCALTR
HHHRELDLRKVMGHANMLDRILDEIDEIDSEVVLCDAAAGSSTAEHSAS
PASSDSSPLTNNIRPISIM

YBL072C, 1103 bp, CDS: 501-1103 (SEQ ID NO 27)

GTCCCTACACACGAGCATCGCTGGGAAAGCTTTGAGGGCTTTCTCTTACGCAGTGTTTCATGGTGTACGGG
ATGGAACGTGTTTCATATACGTTATTTACAGGCCTATCTTAAAGTTATAGGAAATTACACTTGCCATTTG
CTTTTGGTACTCACAAGAAGACGTTATAAACACACCAGGACAAAAAGTATGTGCTATGGTCATATGAG
TAATGGAACCTACATATTTATTTGAATGCTACAGGACCTCTCTTTGAATGGAATAGATAGTGGAAAAAGT
AAACTTAACTAAAAGGGATGATATAAATTGTGACAGGAGCAGTGCACTAAACTGAATCCTTTGTGTACC
CCAAAAATCAAGCCTCTTATGAAACGCCGAGTTTTTCACAAGAAGAGATGAAAAGAAACCAAAGCATAT
TTCAAGATAAGAAAAAAATTCGCCAACTTTTGTACGTTCTTTATTTTACTAACAAGCGTCATTAAATTT
TCTATTACAGTTACAAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCCGCTACCGGTGCCAAGC
GTGCTCAATTCAGAAAGAAGAGAAAGTTCGAATTAGGCCGTCAACCAGCCAACACCAAGATCGGTGCTA
AGAGAATTCACCTCTGTTAGAAGTAGAGGTGGTAACAAGAAATACAGAGCTCTAAGAATTGAAACCGGTA
ACTTTTCTTGGGCTTCTGAAGGTATCTCCAAGAAGACCAGAATTGCTGGTGTGTTTACCATCCATCCA
ACAATGAATTGGTTAGAAGTAACACTTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCA
GACAATGGTTGGAAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTG
TTGCCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAATCTTCCG
TTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAGGTCAATCCGGTAGAT
GTGATGGTTACATCTTGGGAAGGTGAAGAATTAGCTTTCTACCTAAGAAGATTGACTGCTAAGAAATAG

YBL072C, 200 aa (SEQ ID NO 28)

MGISRDSRHKRSATGAKRAQFRKKRKFEELGRQPANTKIGAKRIHSVRTRGGNKKYRALRIETGNFWSWAS
EGISKKTRIAGVVYHPSNNELVRTNTLTKAAIVQIDATPFRQWFEAHYGQTLGKKKNVKEETVAKSKN
AERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCDGYILEGEELAFYLRRLTAKK

YBL092W, 893 bp, CDS: 501-893 (SEQ ID NO 33)

TACTGGAGAAGAGTGTGTTGATTCCAGCAGAAGGTAATACGCACCTTTCTCATCTATTTGCAGAATCGTT
TTATTAAATACTTTTAAAGAATTTAGATTTTGATAATTAGTTTATTCTCTTTTACAAAGATAATCACC
AAACAGGGACAAATACACTGAACGATAAAAGTATGTGACATATAGAATGCTAGAATGAATAGCCTAGACT
GCATTGTTATGAGAGCAACGTTTGATATTTGTGGCGATTGGAACAAACATAGTACATGCCAAAATGAGA
TGAAATGTCCAATTTGAACTGATTAACATACACGCGCAAGCTCGTATTTGTTTACTGGTACACCTAGAG
TTAGCCGATCAAAGAGACAGTGGCAGATATATGGGAAAATTTCTCCGGAAGATTGCATGCGAGAGTCT
CATAACCAGTCATTTCCCAAGATACAATTCTCGGAGCTGTTATACTAACAACCTTTTAATTTTCATTTT
TTTTTTTTTTTGATTAGATGGCCTCCTTACCTCACCCAAAGATTGTCAAGAAGCACACCAAGAAGTTCA
AGCGTCATCACTCTGACCGTTACCACAGAGTTGCTGAAAACCTGGAGAAAGCAAAGGGTATTGACTCTG
TTGTTAGAAGAAGATTGAGAGGTAACATCTCTCAACCAAGATCGGTTACGGTTCTAACAAGAAGACCA
AGTTTTTGTCAACATCTGGTCACAAGACTTTCTTAGTCGCTAACGTTAAGGATTTGGAAACCTTGACCA
TGACACCAAGACTTACGCCGCTGAAATTGCTCACAACATCTCCGCTAAGAACAGAGTTGTCATTTTGG
CTAGAGCTAAGGCTTTGGGTATCAAGGTCACCAACCCAAAGGGTCGTTTGGCTTTGGAAGCTTAA

YBL092W, 130 aa (SEQ ID NO 34)

MASLPHPKIVKKHTKKFKRHHSRDYHRVAENWRKQKGIDSVVRRRFRGNISQPKIGYGSNKKTKFLSPS
GHKFTLVANVKDLETMTMHTKTYAAEIAHNISAKNRVVILARAKALGIKVTNPKGRLALEA

YBR009C, 812 bp, CDS: 501-812 (SEQ ID NO 37)

GAAAAATCGCCCGGGCATTTCTGTTATCTTCCACGCTAAAAGTCAAGGAGAGATATTACGGCCAGGATCG
CAAAGGTGCAGAGCAAGGAAATGTGAGAAATTTGTGAGAACGATAATGTATGGGACAATGCCAAAATGTG
AGAACGAGAGCAAAAATCTTTTTTGTATCTCCCCGCCGAATTTGGAAACCGCGTTCTGAAAACCTTCGCA
TCTTCACATAGTAAAACCTGTTCCGAGCGCTTCTCCCCATAATGGTTAGTGGTAAAAACCGAAGTTGTTT

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ACTTTAGCAAATGCCCGCGAATACGGTGGTAAATTGCCACCCCCCTTCCCCATTTCATTGGGTAAAGAC
CAATTGATGGATAAATTGGTTGTGGAAAAGGTC TAATTCTTTTCCCTATAAATACCGAGATATTTTTT
CTATATGATGGTTTCCGTCGCATTATTGTACTCTATAGTACTAAAGCAACAAACAAAACAAGCAACAA
ATATAATATAGTAAAAATATGTCCGGTAGAGGTAAAGGTGGTAAAGGCTAGGTAAAGGTGGTGCCAAGC
GTCACAGAAAGATTCTAAGAGATAACATCCAAGGTATTACTAAGCCAGCTATCAGAAGATTAGCTAGAA
GAGGTGGTGTCAAGCGTATTCTGGTTTGTATCTACGAAGAAGTCAGAGCTGTCTTGAAATCCTTCTTGG
AATCCGTCATCAGAGACTCTGTTACCTACCCGAACACGCCAAGAGAAAGACTGTTACTTCTTTGGATG
TTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATACGGTTTCGGTGGTTAA

YBR009C, 103 aa (SEQ ID NO 38)

MSGRGKGGKGLGKGGAKRHRKILRDNIIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRD
SVTYTEHAKRKTIVTSLDVVYALKRQGRITLYGFGG

YBR189W, 1501 bp, exon1: 501-507, intron1: 508-920, exon2: 921-1501
(SEQ ID NO 59)

TGGCTTCTTCTTTGCTGTTTTGCCAGCTGGTTGATACGGGCACGTAAGTATTAATTCTTGGTCCC
TTTCTAGTGATAAATCTCGCAGAGAGGGCATACTGGTTGTAAAAAGTAGTCGCAACAAGTAAGTCGTAA
AAAAGTAGATGTAATGGAAGGCTTTGAAGGAACGGCTAGCCAGCTTTTCTGTATCATTCCTAGCCTAAT
TGACAGCATCTTGACCTTCTAGTATGGAACTTTCAATTTAGAAAAGCGGTGTTCCCGCTGCGACGAT
TTAATCCGTACATTTACACATCTGTACATTTTTCATATTGCAAAAACAAAGGTTACTTGAAAAAATCAT
AAAGTTGGCGGCTTCAGGTGGACGCGCTTCACTCATGTAGCTTAACATTCAATCCCATTAAAGCATTATG
CATAAATTTTCATGAAGTTTACTTAATAAAATTGTTTCATTTGCATAGACAAGAAAGAAAGCAACAAGACA
ACTAAGACTAAGCAACAATGCCAAGTACGTATTAGACTATATCGAAGAGGAGGGAATTTCTTCACTCTG
ACTCGTTGATTTTGAAGAGGTTCCGGTCCCTCATAAATATTTGAGAATATGAAATTTCCATAAGTATA
CCTTCATTGAGTAGCACGACAACAGCCTGAATTACTATCCATATTATGAATATCTTTATTACACTGAA
CTCCCGACACTTCAGTTAAACAGGGATACATTAGAGATCAAGGTGATCTAATAGGGAACATCTCTCTCG
TAACAATGGGACAGTATTTTATTTTCCAAGGCGGATACCTAATTATGCGTTTTTAAATCATATCTCTACA
ATATTTATGAGCACTTACTTGGGCCCTTGCAGACTTTTGTTCGGGAAAACCTTTGACTAACAAGAATC
CAATTTTACTTTTTTTTTTTTAGGAGCTCCAAGAATTTACTCTAAGACTTACTCTACACCAAAGAGACC
TTACGAATCTTCTCGTTTGGACGCAGAATTGAAGTTGGCCGGTGAATTCGGTTTGAAGAACAAGAGAGA
AATTTACAGAATTTCTTTCCAATTGTCTAAAATTCGTGCTGCTGCCAGAGACTTGTTAACTAGAGACGA
AAAGGACCCAAAGAGATTGTTTGAAGGTAATGCCTTGATCAGAAGATTGGTTAGAGTTGGTGTCTTGTC
CGAAGACAAGAAGAAGTTGGATTATGTTTTGGCTTTGAAGGTTGAAGATTTCTTGGAAAGAAGATTGCA
AACTCAAGTCTACAAGTTGGGTTTGGCCAAGTCTGTCCACCACGCCAGAGTTTAACTCACTCAAAGACA
CATTGCTGTTGGTAAGCAAAATCGTCAACATCCCATCTTTCATGGTCAGATTGGACTCTGAAAAGCACAT
TGACTTCGCTCCAACCTTCTCCATTCCGGTGGTGCTAGACCAGGTAGAGTTGCTAGAAGAAACGCTGCTAG
AAAGGCTGAAGCTTCCGGTGAAGCTGCTGAAGAAGCCGAAGACGAAGAATAA

YBR189W, 195 aa (SEQ ID NO 60)

MPRAPRTYSKTYSTPKRPYESSRLDAELKLAGEFGLKNKREIYRISFQLSKIRRAARDLLTRDEKDPKR
LFEGNALIRRLVRVGVLSDDKKLDYVLALKVEDFLERRLQTQVYKLGLAKSVHHARVLITQRHIAVGK
QIVNIPSFMVRLDSEKHIDFAPTSFPGGARPRVARRNAARKAEASGEAAEEAEDEE

YBR191W, 1371 bp, exon1: 501-511, intron1: 512-899, exon2: 900-1371
(SEQ ID NO 61)

AATCCTTATTGTCAGAAATTGAAGCCGTTAATATTTAAAGGCTAATTCTCCATGCCATCTTGCATTAC
TTTGGTATATATCTCTTGACCTCAATATATCTCGATAATATAAATCGCAATATTATACTTGTAGTCTG
ACAGTTTTACACCTGTACATCTTACCATCACCACACCCCTTTTTTACTGGAGGCAAGGATGAGTTTGAA
TATCGCCTTTTTCCAGCCGCTAGAACATGCTCAGAACCGAGGAAAAGCACCGCTGCCAAACCTCCTTT
GATGTGTTGGCCACCGCTACTAGTGGCCGTGCTGGAAGCCCAGGCAGCGGTGGGGGCCACAATACGAG
AGCTGGAAGGTAAACGGTCTCTGCGCCTCTGTGAAATTTATCACCATGGAGTGTATGTCTGGTAA
AGATAATATAGAAAGTAGTGTGCAATTTACAGGCATTACCGATTGAACCTTGGAAATAAGAGAACCAAGAC
AAAAATAACTAGCAACAATGGGTAAATCGTATGTCAATTAATCCTATGAATCTACAGCAGCAACGAATC
ATGGTATCTCAAACCGAACATATCGTCAAGAAATAAAGAGATTTAAAGACGTGTCTAGTGTGAATAAA
GCAACATATCATTAGAGCAAAATATTGGGCAGATAAGATGATGCTACACTGATTCTGAGAAAATTACG
TGACATGATAGGCTTTTAAACGGCTGTAAGTCATTAGTTTACAGTCGTTGCTTTGAAAATTAGTTCAAC

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ATTAGAAGTGTAGTAATTACAAGCCCTTTTCCAAACATTCCGGTTATGTGCTGGGACGCATCTCAGAAA
CTCGCAAAACAATAGAATACTAACATGATTTCTTATAAATCTTAATTTTGATTTATTTCCCTTATAATAC
AGACACGGTTACAGATCTCGTACTCGTTACATGTTCCAACGTGACTTCAGAAAGCATGGTGCCGTCCAT
CTTTCTACTTACTTGAAGGTCTACAAGGTGGTGACATGTGCGACATCAAAGCCAATGGTTCTATCCAA
AAGGGTATGCCACACAAGTTTACCAGGTAAAGACCGGTGTGTCTACAACGTTACTAAGTCTTCTGTT
GGTGTATCATCAACAAGATGGTCCGTAAACAGATATCTAGAAAAAAGATTAAACTTAAAGAGTTGAACAC
ATCAAGCACTCCAAGTGTAGACAAGAATTTTGGAAAAGAGTTAAGGCCAATGCTGCTAAGCGTGTGAA
GCTAAGGCTCAAGGTGTGCTGTTCAATTGAAGAGACAACCAGCTCAACCAAGAGAATCCCGTATCGTT
TCTACTGAAGGTAACGTTCCCTCAAACTTTGGCCCCAGTTCCATACGAAACTTTCATCTAA

YBR191W, 160 aa (SEQ ID NO 62)

MGKSHGYRSRTRYMFQRDRKHGAVHLSTYLVKVKVGDIVDIKANGSIQKGMPHKFYQKGTGVVYNVTK
SSVGVIIINKMVGNNRYLEKRLNLRVEHIKHSKRQEFLEVRKANAAKRAEAKAQGVAVQLKRQPAQPRES
RIVSTEGNVPQTLAPVPYETFI

YCL035C, 833 bp, CDS: 501-833 (SEQ ID NO 65)

CCGAAAGAAACCCCATGTTCTTGTGTTTGGCTGCGCTCCAAATGCTTTATCACTCTCTCACACTGTCACAAT
CGTGTGTTGCTTTCATCCTTAGAAAAGGATACCACATTGATAAAACAACATATATAAAGTTTAACTATTACCT
TGATCACTTTACACGTCAAGGTCAAACAGTTTCATAGTTATCACCTTGAAGTATGGCTCCATCATCTA
TAAACATGAACCTTCATGCACAAGTGAGCTGTCTACAGATAACGAGCAGCCGCAACGGCGTTTCCAGAT
TGCGATGCTTGTGTTTCTTTATCTACTTGCCTTACTACCCCCCTTGGCCTCCTGATTACAGTGATGT
GGGAATTTTGTCTTGAAAGGAGTAAATATATAAAATAAATGAAAAGTTTATATAATATAAAAAAGGGACT
TTAGCATAAAAAATAAGAACCTTCGTGTCAGTACTTATACGAGCATTTCGCATAATTATACAAATAGACAAAA
CCTCAGAAGGAAAAAAATGGTATCTCAAGAAACATCAAGCACGTCAAGGACCTTATTGCAGAAAAACG
AGATCTTCGTGCGCATCCAAAACGTACTGTCCATACGCCATGCAGCCCTAAACACGCTTTTGAAGT
TAAAGGTTCCAGGTCCAAAGTTCTGGTTTGTGAATTGAATGACATGAAGGAAGGCGCAGACATTCAGG
CTGCGTTATATGAGATTAATGGCCAAAGAACCGTGCCAAACATCTATATTAATGGTAAACATATTGGAG
GCAACGACGACTTGCAGGAATTGAGGGAGACTGGTGAATTGGAGGAATTGTTAGAACCTATTCTTGCAA
ATTAA

YCL035C, 110 aa (SEQ ID NO 66)

MVSQETIKHVKDIAENEIVASKTYCPYCHAALNTLFEKLKVPKSVLVLQLNDMKEGADIQAALYEI
NGQRTVPNIYINGKIHGGNDLQELRETGELEELLEPIAN

YDL004w, 983 bp, CDS: 501-983 (SEQ ID NO 81)

ATAAACATAAGATATAATAGTTTTTAAATGGTCAACGTATGCGATGCACAACATAAAAGGTACCAATTC
ATTAAATATTATAATATTTACTTCTTACTATTACACGAAAGACAAGTGTGAAATGCCTAGGAGATTGAT
GATTGACAAGCTCTGGCCTTGCAATAAAAAATACTTATACACAACCTTCAAATAATATAGAAAAGAAAGAA
GACTATAAGCTAAAAATGTAGACAACCTCATTTAAATATTATTCTTAGGACTTGGTAATAATAGCTAAT
TTGTATATTATTACCTCGGTACCGCCTGTAATCACTTTAACGAAAATAGATGCCAGCCAATCAAA
GCGCATTATGGAGTCGTCTAGGAAGGGGCCGTCCCATCATTTGTAAGTTTCATGTTAAATTAGATGGAG
GATAACAATAAAGGTATCGTACACACACTGCTAAAAGAGCCTCAATCAATTTGTGAAGGTATAACTGTA
GCCGTGAGGATAGGAAAATGTTACGTTCAATTATTGGAAAGAGTGCATCAAGATCATTGAATTTCTGTCG
CTAAGCGTTTCATATGCAGAAGCTGCTGCCGCATCATCAGGTTTGAAGTTACAATTTGCTCTACCACACG
AAACTTTTATATAGTGGCTCCGAAGTTACTCAAGTGAACCTGCCTGCTAAGTCAGGACGTATTGGTGTAT
TGGCCAACCATGTTCCACCGTTGAACAATTACTACCAGGTGTCGTTGAAGTTATGGAAGGCTCTAACT
CTAAAAAATCTTTTATATCAGGTGGATTTGCAACAGTTCAACCAGACTCGCAGTTATGTGTAAGTGC
TTGAAGCTTTTCCATTGGAATCCTTTTACAAGAAAATATAAAAAATTTGTTGGCAGAAGCTAAGAAGA
ACGTTAGTTCATCTGATGCCAGGGAAGCCGAGAGCTGCAATTCAAGTAGAAGTTTGTAGAAAACCTAC
AATCCGTATTGAAATAG

YDL004W, 160 aa (SEQ ID NO 82)

MLRSIIIGKSASRSLNFVAKRSYAEAAAASSGLKLQFALPHETLYSGSEVTQVNLPAKSGRIGVLANHVP
TVEQLLPVVEVMEGSNSKKFFISGGFATVQPDSQLCVTAIEAFPLESFSQENIKNLLAEAKKNVSSSD
AREAAEAAIQVEVLENLQSVLK

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YDL075W, 1263 bp, exon1: 501-557, intron1: 558-978, exon2: 979-1263
(SEQ ID NO 85)

ACTATATTTTGTTCCTCCCGAACCTCTCCCTTCTGGGCCCTTTTCCATTATTACAAATATTTTCATAC
CTTTACCTCCGTACACCAATCTTTATTTTACCCCATACCTTTGTATTCTGAAATTGAGAAATGATTT
GTGGTGTCTTTTTCCTGGACAATCTGCCTTCGTGGACAGTTTGAACGCTAGGCGACAGTTTGC
CGAAGGAAGTGGGAGAGCCAGAAAGGCTTTCTCTCGATGGTGGATCATTCTTGCAGGCGGAGGAT
GGGAAAGCTCCGTTCAGGTTTGGCGCTTTCTTTCTGGCATTTTCGTTCTCCCAACTGCGCAGGCAGAC
ATAGCTTGACTTTACTCATGCTCGCATTAGGCGGGTTGAATCTCATAGCTTGAAAGATAGTATTGAATT
ATATTGAAGATTTTATAACTAGTGATAATTTTCATTCAAGTTTAAAGAAAGAAATTAATAAGCAAACAGA
ACTCAATCAAAGGAAAAATGGCCGGTTTGAAGACGTTGTCACTCGTGAATACACCATTAACCTTGCACA
AAAGAGTATGTGAAAGAATAAAATATAATGCCAAGGGCTTGTCACTCTGAATGGTTAATTAAGAAGAT
ATTTCTATAGTCAAGGAATACAATATCAAGAATTTGTACCACAGAAACCTATCAACAAAGATCATTGAT
CAAGATATATTTTATAATACGGAATTTGAAGACCATAATCAATATTATAACATCCAAGAGGGGAAAGAT
ACACTTCGGCTGGACTTAAAGAGCGATGAAGACAGAAATAGTTATCTTAAATAGTGAATCCTTAGATTT
TAAGTCGACAAATATCCATATCCCAAGTTTGAATAATGAATCAGAACAAATTGGGTCCTCAATATA
CAAAACCATTCATCAAGATTACACTAATATTAAATGAACAATCGTTACTAACAAAAAATTTACCATTT
TATTTTAAATAGTTTGCACGGTGCTCCTTCAAGAAGAGAGCTCCAAGAGCTGTCAAGGAAATTAAGAAG
TTCCCAAGTTACACATGGGTACTGATGATGTCCGTCTAGCTCCAGAAATGAACCAAGCTATCTGGAAG
AGAGGTGTCAAGGGTGTGAATACAGATTGAAGTTGAGAATTTCCAGAAAGAGAAACGAAGAAGAAGAC
GCCAAGAACCCATTGTTCTCCTACGTTGAACCTGTCTTAGTTGCTTCTGCCAAGGGTCTACAACTGTT
GTTGTCTGAAGAAGATGCTTAA

YDL075W, 113 aa (SEQ ID NO 86)

MAGLKDVVVTREYTNLHKRLHGVSFKKRAPRAVKEIKKFAKLHMGTDVRLAPELNQAIWKRGVKGVEY
RLRLRISRKRNEEDAKNPLFSYVEPVLVASAKGLQTVVVEEDA

YDR064W, 1495 bp, exon1: 501-521, intron1: 522-1060, exon2: 1061-1495
(SEQ ID NO 89)

TGACGGTCGTTTCACAGGAATGGAAGATGCTTTATGCCGGCGCATTAGAAATGATCAGAGAGGAGTGCG
GTACTTTTAAATTGATAGAGGTTTCTTCAGGTTTGGAGGATGACTCAGACGTTGAAGAATTGAGGGAGC
AATTAGAAAATTGTTAGTATAGTCTATCTTAAACACTAACTACCTCCTATAATCATGTAGTGACTTT
AAACATTTTTTTATCTTCATAGCAATAATATAAGCCTTTTACCACCCATAAACCATAAAGTAGACCCAA
ACATTTTTAAAAAATTTTACGTTATAATTTTTTCTTTGTCTGTTTTCCTGAGCGCGCAAAGTAGCGGT
GAAATTTTGATACGAATGAGATTTCCTCTGTACAGATGGAATTTATGTTGGCCGACATATATCAC
AGTCGTGATTGAATTAACAATTTCTTTCTCATTAATATTTATTCTAAACGGTTAACCCTAAATCAATC
AACAAACATCAGTCAAAATGGGTCGTATGCACAGTGCCGTATGTTTATTAAACCATAGCGGAGATATTA
ATGCAAAAGTTGCATTGAATAGTTCCGCTAAATCAGATGACACTCTAATGTGGAATTCAAAAGTGGATTT
CTAATATAATTTGCTCTGTCTGGATCACAATCTATTACAAGTTCCGGTGTGTACACAGGTATAGTTTA
TACTGGAGAGTAGTTTCTACTCGCTGTACATTAGCTGGGTGATTCCAATTTCTTTTACAAATATGTTGC
ATTAGTTTAAACAGGTTATACTATCTGCCGTTTCTCAGTATAATTTACGCCGGAATAATTACTGATGGCTA
GCCGCCTTTATGAATTAGTTTTCACAAAGCTCATAACATAACACGTTAACCTATCGGAGGAGAACCAAG
ATTGAAGAATCACCCGGAATAGTTATACTTTAATGGAATTGTATGGTCTGAACGAGGAAATATGTCATG
ATACACTTTTCTTCAAGCCATATGAATCTTCATGTTACTAACATTCGATAAATTTTTTGAATATCCAA
TTCCACTAAATATTACTTTAAACAGGGTAAAGGTATTTCTTCTTCTGCTATTCCATACTCTAGAAATGC
TCCAGCTTGGTTCAAGTTGTCTCTGAATCTGTCAATTGAACAAATTTGTCAAGTACGCGAGAAAGGGTTT
GACTCCATCTCAAATTTGGTGTCTTGTGAGAGATGCTCACGGTGTTACCCAAGCTCGTGTTTACTCTGG
TAACAAGATCATGAGAATCTTGAAGTCCAATGGTTTGGCTCCAGAAATCCAGAAGATTTGTACTACTT
GATTAAAGAAGGCTGTCTCTGTGTTAGAAAGCACTTGGAAAGAAACAGAAAGGACAAAGACGCTAAGTTCAG
ATTGATTTTGATCGAATCTAGAATTCACAGATTGGCCAGATACTACAGAAGTGTGCTGTCTTACCACC
AAACTGGAAGTACGAATCCGCCACTGCCTCCGCTTTGGTCAACTAG

YDR064W, 151 aa (SEQ ID NO 90)

MGRMHSAGKGISSSAIPYSRNAPAWFKLSSESVEIQIVKYARKGLTPSQIGVLLRDAHGVTVQARVITGN
KIMRILKSNGLAPEIPEDLYYLIKAVSVRKHLERNRKDKDAKFRLLILIESRIHLARYYRTVAVLPPN
WKYESATASALVN

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YDR099W, 1322 bp, CDS: 501-1322 (SEQ ID NO 93)

TTGTTACGACCAATCCGTAATTCAGCGTGGGTATTCATATGACCAGAGATAATAATACAGCGAATACT
ATTGAAATCGTCCCTTTTTTGTAGGAAGAACGGACAAATCGGTCGCTCGCTCGAAATGATTAGTAGT
GTGTCACCCGGATCAGCAAAATGACACACACGAAATACGAGGAAAAAGTCGGTCGAAAGGGGCAAATGT
TATTATAAGTCCCTCCAGTAGTCTTTTTTTTTTCAAATATTCATCATCAAAGGTTACGAAATCTTTTGA
GCTATCTTAAACATTCGTTCTTTTTTATCAAATTTCAATTACTAACCTATTTTTTCAAAAAAATTCGCT
CTCCCGGTTTTTAATCATTATTTTTTTCGATTGATTAAAGGGGAAAAGCAAAGAACGAGAAAACTTGGA
CAGAAGGTTAATACTCTGACAATTTCAAACGAAGTAAAAAGAAAAATTATCAAATCAACAAAAAGTAC
CCGTTACAACAAAAAATGTCCCAAACCTCGTGAAGATTCTGTTTACCTAGCTAAATTAGCTGAACAAG
CCGAACGTTATGAAGAAATGGTCGAAAACATGAAGGCCGTTGCTTCATCAGGTCAAGAGTTATCTGTG
AAGAACGGAATCTATTGTGCGTTGCTTACAAGAACGTCATCGGTGCTCGCCGTGCTTCATGGAGAATAG
TTCTTTCGATCGAACAAAAAGAAGATCAAAGGAGAAATCTGAACATCAAGTTGAATTAATCCGTTCTT
ACCGTTCTAAAATTGAACTGAATTGACCAAAATCTCTGACGACATTTTATCTGTGTTAGATTCTCATT
TAATCCCTTCTGCTACTACTGGTGAGTCTAAAGTATTTTACTATAAGATGAAGGGTGACTACCACCGTT
ATTTAGCTGAATTTTCCAGCGGAGATGCAAGAGAAAAGGCAACCAACTCCTCTTTGGAGGCTTATAAAA
CCGCTTCCGAAATCGCCACAACCTGAATTGCCTCCAACCTACCCAATTTCGTTTAGGTCTAGCTTTGAATT
TCTCCGTTCTTATTACGAAATTCAAAACCTCTCTGATAAGGCTTGCCACTTGCCCAAACAAGCCTTTG
ATGATGCTATTGCTGAGTTAGATACTTTATCTGAAGAATCATACAAGGATAGCACTTTGATCATGCAAT
TATTAAGGGACAACCTTGACCTTATGGACCTCTGATATTTCTGAATCTGGTCAAGAAGATCAACAACAAC
AACAACAACAGCAACAGCAACAGCAACAACAGCAACAACAAGCTCCAGCTGAACAAACTCAAGGTGAAC
CAACCAATAA

YDR099W, 273 aa (SEQ ID NO 94)

MSQTREDSVYLAKLAEQAERYEEMVENMKAVASSQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ
KEESKEKSEHQVELIRSYRSKIETELTKISDDILSVLDShLIPsATTGESKVFYKMKGDYHRYLAEPS
SGDAREKATNSSLEAYKTASEIATTELPPTHPIRLGLALNFSVFYIEIQNSPDKACHLAKQAFDDAIAE
LDTLSEESYKDSLIMQLLRDNLTLWTSDisESGQEDQQQQQQQQQQQQQQQAPAEQTQGEPTK

YDR134C, 701 bp, CDS: 501-701 (SEQ ID NO 97)

GGAGTTTTCTTATTTTGAATTTGATGGCTGGGTTTGAGCTGCAGGACACGCTGCAGTGGGGAAGCCCTTT
TAAATCCGCGAGTCCGGTCCGTGCTCACTTTTAGACGCGTGTTCATCGGCGTTCGGATGGTTTCCAGT
GAGAAAAGGGGTACGCGTATGGTCGGTAGTCCCTTTTACGGGACCAGTGCAGAGGGTGAATCAACGGCC
CCTTCACAGAAACCGCGCAGGAATTTTTCTGGTGTGTTGTTATTTTTTTTTTCTTGTTACTTATCTCACTT
TTCTTTTTTCTAACTATTTTTTTTTGCAATTTTTTGTGTACACTTTCCACAACATATAGGATGGTTTAGT
CATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTTGTTCTTCATCGACTTCTCTCTGCTAGACTC
TCTTTTTTAAATTTTTTCATAGAATAAAAAACCAAGGATAACAAACATCTTCTTTCTGTTTCGTTTCAA
ATAACTACAAATTAATAATGCAATTTCTTACCGTCGCTTCTATCGCTGCTATTGCCGCTGTTGCCCTCCG
CCGCTTCTAACATTACCACTGCTACTGTACAGAAGAATCTACCACTTTGGTCACTATCACTTCTTGTG
AGGACCACGTTTGTCTGAAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAAATGACG
TTATCACTTAA

YDR134C, 66 aa (SEQ ID NO 98)

MQFSTVASIAIAAVASASNIITATVTEESTTLVTITSCEDHVCSETVSPALVSTATVTVNDVIT

YDR171W, 1628bp, CDS: 501-1628 (SEQ ID NO 103)

CTGGGGTTGGGTAACAAGTGAAGGAAAAAGTGAACATTTTAAGAAGAACAAATAAATAGCAAGAG
ATGGAATGGTAATGCTTGGCTCTCGAGAAGAGTAGCATAAAACGAGACTTGTPTTAAACAGGATATGAC
ATACTTCAATTCAGCTTTCCCTATCAGCCGCTCGAGCAGTTATATAGGTGTGTTGCCGGAGTAATTTGG
CGGAGGCCAACAGTGGCTAGGCGGCAACGCCGTGGAACACGCGCTTAAAAGTTCTGGAAGGTTTCGCGAAT
TGAGAACTGCTCAGGGGCGAATACAGGGGCGGCCTTGGCGGCAGGGGGAGGCCCTGTGTAAGTTAGTT
ATATAAGACTTGCTGTATCGTTTTTTTTGATCCCGGCAGGAACATATCTTTTATCTCATACATACGGTC
AAGAAGTATAATTATACATAACATAGGGACACGTTCAAGCAATTGTCCATATCCACACAAATTAAGAT
CATACCAAGCCGAAGCAATGAGTTTTTATCAACCATCCCTATCTCTTTATGACGTTTTGAACGCATTAT
CCAACCAAACTGGCCAGAGAGGGCAGCAAGGATATCTCGCCAACCACAAAGGCCACAGAGATACCATC
CCCATTATGGACAAGTGCACGTTGGCGGGCATCATCTCGTCATCATCCATTGTATAGCAGATACAATG

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GTGTTCCCTAATACCTATTACTACCAGTTCCTGGACAAGCCTATTACTATAGTCCTGAATACGGTTATG
ATGACGAGGATGGTGAAGAAGAGGACCAAGACGAAGATATGGTGGGTGACAGCGGCACTACAAGACAGG
AAGATGGTGGCGAGGACAGCAACTCGAGAAGATATCCATCATATTACCATTGTAATACTGCCAGGAATA
ATAGGACCAACCAACAGGCAAACAGTTTAAACGACTTATTAACCGCGTTAATAGGTGTTCCACCATATG
AAGGCACTGAACCAGAAATTGAAGCAAATACCGAACAGGAGGGCGAAAAGGGAGAAGAAAAGGATAAGA
AGGATAAGTCTGAAGCACCCAAAGAGGAAGCTGGCGAAACCAACAAAGAAAAACCTTTGAATCAGCTGG
AGGAATCGTCGAGACCACCATTAGCCAAAAAATCTTCATCGTTCGCTCACCTACAAGCGCCTTCCCCAA
TACCTGACCCGTTACAAGTATCCAAGCCTGAAACGAGAATGGACTTACCATTTTCACCAGAAGTGAATG
TCTATGATACCGGAGCACCTTACGTAGTTGTTCTTTCGCTTACCAGGTGCTAACTCTAGGGCTTTCCACA
TTGATTACCATTCCATCTTCTCATGAGATGCTCATCAAGGGTAAGATCGAAGACAGAGTGGGCATTGATG
AAAAATTCTTGAAGATCACGGAATAAAATATGGTTCGTTTGAGAGAACCGTTAAATTTCCCGTGCTGC
CACGCATTAAAGACGAAGAAATTAAAGCTACTTACAACAACGGTCTACTACAAATTAAGGTGCCTAAAA
TTGTCAATGACACTGAAAAGCCGAAGCCAAAAAGAGGATCGCCATTGAGGAAATACCCGACGAAGAAT
TGGAGTTTGAAGAAAATCCCAACCCTACGGTAGAAAATTGA

YDR171W, 375 aa (SEQ ID NO 104)

MSFYQPSLSLYDVLNALSNTGQRGQQGYPRQPQRPPQRYHPHYGQVHVGGHPRHHPLYSRYNGVPNTY
YYQFPQAYYYSPYEGYDDEDEEEDQDEDMVGDSGTTTQEDGGEDSNSRRYPSYYHCNTARNNRNTNQ
ANSLNDLLTALIGVPPYEGTEPEIEANTEQEKEKGEEKDKDKSEAPKEEAGETNKEKPLNQLEESSRP
PLAKKSSSFAHLQAPSPIPDPLQVSKPETRMDLPFSPEVNVYDTEITYVVVLALPGANSRAFHIDYHPS
SHEMLIKGKIEDRVGIDKFLKITELKYGAFERTVKFPVLPRIKDEEIKATYNNGLLQIKVPKIVNDE
KPKPKKRIAIEEIPDEELEFEENPNPTVEN

YDR399W, 1166 bp, CDS: 501-1166 (SEQ ID NO 129)

TCGTTTATCCTTTTTGAAGTGCATCTGGCATCGTTAACAGTAAGGCCATCTGGAACATCAAGCAAGCAC
TCCATTTTTACGTACAACCATAGTTGGTTAAGAAAAGACAGTACATATTTCCCTTCCGAGTCAC
TTATTTTTTTTTCTCTCTGAAAAAATTAATTAGATTAATTTCAATTAATATCATTTCCGCTTATCTGAC
TTCTTTTCATTTTTTTCTCTATATTTTCGCGTTTACTAGGAAAGAAAAGGAAAAAAAATTTTTCCCCCTC
CATCTGTCCCAAATCGGGTAGCGATGAGCTGCTATAGAATTTTCTATTTAAACATGTTTGATAAGCCCA
ATTTCCGTTAGATTTTGTTCCTTTCGCGAGTTTGGTTTGCGTAACCTTTTTTATTTTAGTCTCCATCT
AGCTGGAGTAATACGATGTAGTGCTTGTAACTTTTCTTATTTTTATATTACCGTTCGTGTTTATTATA
TCCATTACGTTCCCATATGTGCGCAAACGATAAGCAATACATCTCGTACAACAACGTACATCAACTAT
GTCAAGTATCCGCTGAGAGAATTAAGAATTTCAAGCCGGACTTAATCATTTGCCATTGGTGGTGGTGGTT
TCATTCTGTAGGATCCTACGTACGTTCTTAAAGGAGCCCGCGTGCCAACCATCAGAAATTTTGTGCTA
TTATTTTGTCTTTGTACGAAGATTTGAACAGTGTAGGCTCAGAAGTTGAGGAAGTTGGTGTTAAGGTTA
GCAGAACACAATGGATTGATTACGAGCAATGTAAATTAGATCTAGTCGGCAAGAACGTTCTTTATCGTTG
ACGAAGTCGATGACACCCGTACCACACTTCATTACGCTTTTGTAGTGAATTGGAAAAGGATGCAGCTGAAC
AGGCAAAGGCTAAAGGTATCGATACTGAAAAGTCTCCAGAGATGAAAACAAACTTCGGGATTTTTGTTT
TACACGATAAGCAAAAACCAAGAAAGCAGATTTGCCTGCCGAAATGTTGAATGACAAGAACCGTTATT
TTGCAGCTAAACTGTTCCAGACAAGTGGTATGCATATCCATGGGAATCTACTGACATTGTTTTCCATA
CTAGAATGGCTATTGAACAGGGCAATGACATCTTTATTCCTGAGCAGGAACACAAGCAATGA

YDR399W, 221 aa (SEQ ID NO 130)

MSANDKQYISYNNVHQLCQVSAERIKNFKPDLLIAIGGGGFIPARILRTFLKEPGVPTIRIFAILLSLY
EDLNSVGSEVEEVGVKVSRTQWIDYEQCKLDLVGKNVLIVDEVDDTRTTTLHYALSELEKDAAEQAKAKG
IDTEKSPMKTNFGIFVLHDKQKPKKADLPAEMLNDKNRYFAAKTVDPKWAYYPWESTDIVFHTRMAIE
QGNDIFIPEQEHKQ

YDR418W, 998 bp, CDS: 501-998 (SEQ ID NO 131)

TGCACTGTGGATGTTTGGGTGTGTATTTTGTCTTTCATAACATACAGATATTTTGTTTAAGGAAGTGAA
ATAAACAATATCATAAAACAGGTACTTCATAGACCATAAAGCATAACCCAGATTATCCTCTTAGATAGC
AATGCTAATGTAAACAGAGATCCGTTTTCGTGACTTTATACTAATATGATATGTCTACTTCGCTTTGTG
TTCGAGCAGCCTGGCAGTCCCCCTAGCCGCTTTTTTCCCTTTCCGAAGGTTTCGGCTAAGCCCCCTG
GCTCTAGGCCGAGAAAAATGTTAATGCTCCTTCTACGAGAAAAATGCTTGTTCGCCACACCAGGACAGGTGC
TCGACGACGCTTCCGCTAATCTTTCTCAATGTTGTATCTTCTTTGGCGGTACATTACTAGTATGAAAAT
GGAATAAAAAACAGTACCCTAAATTATTTACTTACTTCCCCGTTAAAGCAACCCCCAAGTGCCCAATAGAAGG

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ATAAATCAATAGTCAATATGCCTCCAAAGTTTGATCCAAATGAAGTTAAGTACTTGTACTTGAGAGCTG
TCGGTGGTGAAGTCCGTGCTTCCGCCGCTTGGCTCCAAAGATCGGTCCATTGGGTTTATCCCCAAAGA
AGGTTGGTGAAGATATCGCCAAGGCCACCAAGGAATTCAAAGGTATCAAAGTTACTGTCCAATTGAAAA
TCCAAAACAGACAAGCTGCTGCTTCTGTTGTTCCATCTGCTTCCTCTTTGGTCATTACTGCTTTGAAGG
AACCACCAAGAGACAGAAAGAAGGATAAGAACGTCAAGCATAGCGGTAACATCCAATTGGATGAAATTA
TTGAAATTGCCAGACAAATGAGAGACAAATCCTTCGGTAGAACTTTGGCTTCCGTTACTAAGGAAATTT
TGGGTACTGCTCAATCTGTCCGTTGTCTGTTGATTTCAGAACCCTCATGACATCATTGAAGGTATTA
ACGCTGGTGAATTTGAAATTCAGAAAACTAA

YDR418W, 165 aa (SEQ ID NO 132)

MPPKFDPNVVKYLYLRAVGGVGVGASAAALAPKIGPLGLSPKKVGEDIAKATKEFKGKIKVTVQLKIQNRQA
AASVVPSSASSLVITALKEPPRDRKKDKNVKHSNGNIQLDEIIEIARQMRDKSFGRTLASVTKEILGTAQS
VGCRVDFKNPHDIIEGINAGEIEIPEN

YDR513W, 932 bp, CDS: 501-932 (SEQ ID NO 133)

TCTCCCTCTCCTGCCATATAACCCCACTGGTATTTTCCAATGCCTTATTGTTGGAAACCTGATCTTTAT
ACCATTCCTGCACCTTTCACAGGGTCATTGCCGTGGATAATACAAAACCTGAATTTGGACACCTGCTTGT
CACATGATGTAAAATCTCCATATCTGTAATAGCTTCTAAATTGCCCTCCAATCGAATAGCAACTCGTCA
GTTGATCAAATGCCTCTCGGCAACTCATCGTTGTCGGATATTTTGTACTCATCCTTTCTCTGTTTCTTCC
TCAAGCTGCTCTCTTTTACCCTAATAGAACCATCGCCTCCCTCTTGATTTATGCTAATACCACATCCAA
TAGCAGAACTATTACTAAGATCCGATATTTTCGGCCCCCTTCGCAAGGGGGCCCGCCGCACCTTCTTTCAT
GAATTTTCATATAAAAAAGTCCCAGGACGCCAAGAAAAGGTGCCCTCTTGATTAACGGACACTCCAACCTA
CTGTTATATATTGTTTCATGGAGACCAATTTTTCCTTCGACTCGAATTTAATTGTTATTATCATTATCA
CGTTGTTTGCCACAAGAATTATTGCTAAAAGATTTTATCTACTCCAAAATGGTATCCCAGGAAACAG
TTGCTCACGTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAAGACATACTGCCCTTACT
GTAAAGCTACTTTGTCTACCTCTTCCAAGAATTGAACGTTCCCAAATCCAAGGCCCTTGTGTTGGAAT
TAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAGAAATCTCGGGCCAAAAAAGTGTAC
CTAACGTATACATCAATGGCAAGCACATTGGTGGTAACAGCGATTGGAAACTTTGAAGAAAAATGGCA
AGTTAGCTGAAATATTGAAGCCGGTATTTCAATAG

YDR513W, 143 aa (SEQ ID NO 134)

METNFSFDSNLIVIIITLFATRIIAKRFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLS
TLFQELNVPKSKALVLEDEMSNGSEIQDALEBISGQKTVPNVYINGKHIGGNSDLETLLKNGKLAEL
KPVFQ

YEL009C, 1346 bp, CDS: 501-1346 (SEQ ID NO 139)

AGTTTCACTAGCGAATTATACAACCTACCAGCCACACAGCTCACTCATCTACTTCGCAATCAAAACAAA
ATATTTTATTTTAGTTTCAGTTTATTAAAGTTATTATCAGTATCGTATTTAAAAAATTAAAGATCATTTGAAA
AATGGCTTGCTAAACCGATTATATTTGTTTTTAAAGTAGATTATTATTAGAAAATTATTAAAGAGAATT
ATGTGTTAAATTTATTGAAAGAGAAAAATTTATTTTCCCTTATTAAATTAAAGTCCCTTACTTTTTTTGAA
AACTGTCAGTTTTTTGAAGAGTTATTTGTTTTGTTACCAATTGCTATCATGTACCCGTAGAATTTTATT
CAAGATGTTTCCGTAACGGTTACCTTTCTGTCAAATTTATCCAGGTTTACTCGCCAATAAAAAATTTCCCT
ATACTATCATTAATTAATCATTATTATTACTAAAGTTTTGTTTTACCAATTTGCTCTGCTCAAGAAAATA
AATTAAATACAAATAAAATGTCCGAATATCAGCCAAGTTTATTGCTTTAAATCCAATGGGTTTTCTCAC
CATTGGATGGTTCTAAATCAACCAACGAAAAATGTATCTGCTTCCACTTCTACTGCCAAACCAATGGTTG
GCCAATTGATTTTTGATAAATTCATCAAGACTGAAGAGGATCCAATTATCAAACAGGATACCCCTTCGA
ACCTTGATTTTGATTTTGCTCTTCCACAAAACGGCAACTGCACCTGATGCCAAGACCGTTTTGCCAATTC
CGGAGCTAGATGACGCTGTAGTGGAAATCTTCTTTTTCTGCAAGCACTGATTCAACTCCAATGTTTGAGT
ATGAAAACCTAGAAGACAACCTCAAAGAATGGACATCCTTGTGTTGACAATGACATTCCAGTTACCACTG
ACGATGTTTCATTGGCTGATAAGGCAATTGAATCCACTGAAGAAGTTTCTCTGGTACCATCCAATCTGG
AAGTCTCGACAACCTTCATTCTTACCCACTCCTGTTCTAGAAGATGCTAAACTGACTCAAACAAGAAAGG
TTAAGAAACCAAAATTCAGTCGTTAAGAAGTCACATCATGTTGGAAAGGATGACGAATCGAGACTGGATC
ATCTAGGTGTTGTTGCTTACAACCGCAAACAGCGTTTCGATTCCACTTTCTCCAATTGTGCCCGAATCCA
GTGATCCTGCTGCTCTAAAACGTGCTAGAAACACTGAAGCCGCCAGGCGTTCTCGTGCGAGAAAGTTGC
AAAGAATGAAACAACCTTGAAGACAAGGTTGAAGAATTGCTTTTCGAAAAATTATCACTTGGAAAAATGAGG
TTGCCAGATTAAAGAAATTAGTTGGCGAACGCTGA

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YEL009C, 281 aa (SEQ ID NO 140)

MSEYQPSLFLALNPMGFSPLDGSKSTNENVASASTSTAKPMVGQLIFDKFIKTEEDPIIKQDTPSNLDFDF
ALPQTATAPDAKTVLPIPELDDAVVESFFSSSTDSTPMFEYENLEDNSKEWTSLFDNDIPVTTDDVSLA
DKAIESTEEVSLVPSNLEVSTTSFLPTPVLEDAKLQTRKVKPNVVKSHHVKGKDDSRDLHLGVVA
YNRKQRSIPLSPIVPESSDPAALKRARNTAAARRSRARKLQRMKQLEDKVEELLSKNYHLENEVARLKK
LVGER

YGL123W, 1264 bp, CDS: 501-1265 (SEQ ID NO 163)

TGGCTTATTCACTAAGGATTCTTAAGGTTTCTTAATAGTTTTCTACGTCGGCATGCGATTGTTTGGTT
TAGAAGACTGCTTTCTAAATATGGTTGGGTGATTTAAGCTAGACCCATACACCCGCTCTATGGGATTA
TTTACTTGTGTTGAATTTTAAGATTTGTGATAATGGAAGTGGACGCAACATTTGATGGAAAACGCATGT
CATCATTAACGAGGTAACGTAGGTATCTGTCTGCTTGTAGTATTGCACGCAGCTTCCCAGGACGCCTAG
CTATTTTTTTCATCTATTTCCCTCTGTAGTAACGTAAGAGTTTCAAGTTTAAATTCAGACTTTCTCTT
CCTTGTGTTCCAATTTCCCTTCCCTTACTGCTTGATACCTTTTCAATCCCAAAGAAACCGTGTCTTTATA
TATTGTCGATTGAAAGTTACCTACATCAACTTTCCGTGTTCCATTCCGACTATAACAAACAACCAATAA
GCTCAACTAATTAAGTAATGTCTGCTCCAGAAGCTCAACAACAAAAGAGAGGTGGTTTCGGTGGCCGTA
ACAGAGGCCGTCACAAACAGAAGAGGACCAAGAAACACTGAAGAAAAGGGATGGGTTCAGTTACCAAAC
TAGGTAGATTAGTCAAGGCTGGTAAGATTACCACCATTTGAAGAAATCTTCTTGCACTCTTTGCCAGTCA
AGGAATTCACAAATCATTTGACACTTTGTGTCAGGTTTGCAAGACGAAGTCATGAACATCAAGCCAGTTC
AAAAGCAAACAGAGCCGTCAAAGAACCAGATTTAAGGCTGTTGTCGTTGTTGGTGACTCTAACGGTC
ACGTTGGTTTGGGTATCAAGACCGCCAAGGAAGTTGCTGGTGCCATCAGAGCTGGTATCATTATTGCCA
AGTTGTCGGTTATCCCAATCAGAAGAGGTTACTGGGGTACCAACTGGGTCAACCACATTTCTTGGCCA
CCAAGACCACTGGTAAGTGTGGTTCCGTCACTGTTAGATTGATCCAGCCCCAAGAGGTTCTGGTATCG
TCGCTTCTCCAGCTGTCAAAAAGTTGTTGCAATTGGCTGGTGTGAAGATGTCCTACACCCAATCTAACG
GTAAGACTAGAACTTTGGAAAACACCTTGAAGGCTGCTTTTCGTTGCTATTGGTAACACATACGGTTTCT
TGACTCCAAACTTGTGGGCCGAACAACCATTTGCCAGTTTCTCCATTGGACATCTACTCCGATGAAGCTT
CTGCTCAAAAGAAGAGATTCTAA

YGL123W, 254 aa (SEQ ID NO 164)

MSAPEAQQQKRGFGGRNRRPNRRGPRNTEEKGWVPVTKLGRVLKAGKITTTIEEIFLHSLPVKEFQII
DTLLPGLQDEVNMIKPVQKQTRAGQRTFRKAVVVVGDSNGHVGLGIKTAKEVAGAIRAGIIIAKLSVIP
IRRGYWGNTNLGQPHSLATKTTGKCGSVTVRLIPAPRGSGIVASPAVKLLQLAGVEDVYTQSNKTRTL
ENTLKAAFVAIGNTYGFLT PNLWAEQPLPVSPLDIYSDEASAQKKRF

YGR209C, 815 bp, CDS: 501-815 (SEQ ID NO 187)

AACATCCAGACTTTTACGGGTGGCAACGGAACCAACGTATTTAGAGATTGTTTTTTGGTCAAGCGAGGA
ACCCCTGTTGGCAAAGTTGCCAGGTATATCATGGGTGGCGAGGTCACCATTGCAAGCATTTGAAACCGTT
GGCGGCGTGAGAGTCAGTGAAGAAAGTCTTGTGAGCCCGGTAAGAATGACATACTCGGCTTCAAGATC
GCTCCAAGATCAGCATAACTTGAGTGCCAGTGAATATTAAGTAATCATCAAAGTATATGTGTAATTGTT
TATACTCTTAGTAAAGGATGCTCCCTACAAGGTGGCTCTTTTCTTACTAAGCGCGTTTCAGTTTCCAGCC
AGCCGAAAGAGGGATATCAGTATATAAGAAAGCCATTCCGGGGATGAAAAGCTGACAAGAGAATAACGA
GGACCAGTTTTTATTTGTTGTCTAGCAAGAATTATACACGCACACATACACGAGAGTCTACGATATCTT
TAAATAACACATCAATAATGGTCACTCAATTAAAATCCGCTTCTGAATACGACAGTGCTTTAGCATCTG
GCGACAAGTTAGTCGTTGTTGACTTTTTTGCCACATGGTGTGGGCCATGTAAAATGATTGCACCAATGA
TTGAAAAGTTTGCAACAATATTCTGACGCTGCTTTTTACAAGTTGGATGTTGATGAAGTCTCAGATG
TTGCTCAAAAAGCTGAAGTTTCTTCCATGCCTACCCTAATCTTCTACAAGGGCGGTAAGGAGGTACCA
GAGTCGTCGGTGGCAACCCAGCTGCTATCAAGCAAGCTATTGCTTCCAACGTATAG

YGR209C, 104 aa (SEQ ID NO 188)

MVTQLKSASEYDSALASGDKLVVVDFATWCGPCKMIAPMIEKFAEQYSDAAFYKLDVDEVSDVAQKAE
VSSMPTLIFYKGGKEVTRVVGANPAAIKQAIASNV

YHR039C-B, 1007 bp, exon1: 501-503, intron1: 504-665, exon2: 666-1007
(SEQ ID NO 197)

GTACATGCACCATTCGCTTCAACTGCGTCAGATAGTTGTAGTCCCTCTGGACATAAGCATTTTCGTTTCGT
GCTTGTCTGTCGTCGCTCCGCTGTTTCAACGCCTCACTCGATATATACTCCTTAGGATCATGTGTTGACCTG

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AGCAATTGTCCCTTGTCTTGTGCTTCTTGGAACTCCAAAGAGCAAGTTTGCACCAAACATCTTGGAC
ACTTGTATTTGAACCTCTTTTATTCCGCATACACCACACAACACCGCCATACTTGCAAATTGCCACACCC
TTCCCTATTAACTGGACTCCTATTCCAGCTCATCTCATCGAATATGAACTTTGACATCCACTATTATTA
CCGCGAATTTTTTTTTTTTTTCAATTTGTTACCCCTGCCCTGGGTATCAAAAATTTTCATCTCTAAAAGGGA
GCGTGATAGATAAAGCAATCACACCTTAAACAATACATTTTTTTTTTTCCTGCAATCTCCAAAGTGTGC
AAGGTATACAAAGCAGAATGGTATGTGCCATTACATTACGTGTCAACACTTCTGTCTCTAACAAGCGTT
CTTACTAACATGAAAACTTTTTTAAACTGTGCTCTCTTGTGGACTGGTACCTCGTGACAAAGGTAT
TGGTTTTTTTCATTTGCTCAGAACTATGTAATATTCTCTTTAGTCCCAAAAAACGGAATTGCCACCC
TACTACAAGCTGAAAAGGAAGCCACGAAATAGTATCAAAGGCTAGAAAGTACAGACAAGATAAGTTGA
AGCAAGCCAAGACTGATGCAGCCAAGGAAATCGACTCATACAAATTCAAAAGACAAGGAATTGAAGG
AGTTTGAACAAAAGAATGCCGGTGGTGTGGTGAATTGGAAAAGAAAGCAGAGGCTGGTGTGCAAGGTG
AATTAGCTGAGATTAAGAAAATTGCAGAGAAGAAAAGGATGACGTTGTCAAATTTTGATCGAGACTG
TCATCAAGCCTTCTGCTGAAGTCCATATCAATGCCTTGTA

YHR039C-B, 114 aa (SEQ ID NO 198)

MSQKNGIATLLQAEKEAHEIVSKARKYRQDKLKQAKTDAAKEIDSYKIQDKELKEFEQKNAGGVGELE
KKAEGVQGELAEIKKIAEKKKDDVVKILIIETVIKPSAEVHINAL

YHR053C, 686 bp, CDS: 501-686 (SEQ ID NO 199)

AACCTCAACGATTTCTATGATGCATTTTATAATTAGTAAGCCGATCCCATTACCGACATTTGGGCGCTA
TACGTGCATATGTTTCATGTATGTATCTGTATTTAAACACTTTTGTATTATTTTCTCATATATGTGT
ATAGGTTTATACGGATGATTTAATTATTACTTCACCACCCCTTTATTTTCAGGCTGATATCTTAGCCTTGT
TACTAGTTAGAAAAGACATTTTGTCTGTCACTGTCAAGAGATTCTTTTGTGCTGGCATTTCTTCTA
GAAGCAAAAAGAGCGATGCGTCTTTTCCGCTGAACCGTTCCAGCAAAAAAGACTACCAACGCAATATGG
ATTGTCAGAATCATATAAAAGAGAAGCAATAACTCCTTGTCTTGTATCAATTGCATTATAATATCTTC
TTGTTAGTGCAATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAACTGTACAATCAATCA
ATCAATCATCACATAAAATGTTTCAGCGAATTAATTAACCTTCCAAATGAAGGTCATGAGTGCCAATGCC
AATGTGGTAGCTGCAAAAATAATGAACAATGCCAAAATCATGTAGCTGCCAACGGGGTGTAAACAGCG
ACGACAAATGCCCCTGCGGTAACAAGTCTGAAGAAACCAAGAAGTCATGCTGCTCTGGGAAATGA

YHR053C, 61 aa (SEQ ID NO 200)

MFSELINFQNEGHECQCQCGSCKNNEQCQKSCSCPTGCNSDDKCPCGNKSEETKKSCCSGK

YHR055C, 686 bp, CDS: 501-686 (SEQ ID NO 201)

AACCTCAACGATTTCTATGATGCATTTTATAATTAGTAAGCCGATCCCATTACCGACATTTGGGCGCTA
TACGTGCATATGTTTCATGTATGTATCTGTATTTAAACACTTTTGTATTATTTTCTCATATATGTGT
ATAGGTTTATACGGATGATTTAATTATTACTTCACCACCCCTTTATTTTCAGGCTGATATCTTAGCCTTGT
TACTAGTTAGAAAAGACATTTTGTCTGTCACTGTCAAGAGATTCTTTTGTGCTGGCATTTCTTCTA
GAAGCAAAAAGAGCGATGCGTCTTTTCCGCTGAACCGTTCCAGCAAAAAAGACTACCAACGCAATATGG
ATTGTCAGAATCATATAAAAGAGAAGCAATAACTCCTTGTCTTGTATCAATTGCATTATAATATCTTC
TTGTTAGTGCAATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAACTGTACAATCAATCA
ATCAATCATCACATAAAATGTTTCAGCGAATTAATTAACCTTCCAAATGAAGGTCATGAGTGCCAATGCC
AATGTGGTAGCTGCAAAAATAATGAACAATGCCAAAATCATGTAGCTGCCAACGGGGTGTAAACAGCG
ACGACAAATGCCCCTGCGGTAACAAGTCTGAAGAAACCAAGAAGTCATGCTGCTCTGGGAAATGA

YHR055C, 61 aa (SEQ ID NO 202)

MFSELINFQNEGHECQCQCGSCKNNEQCQKSCSCPTGCNSDDKCPCGNKSEETKKSCCSGK

YHR056C, 2999 bp, CDS: 501-2999 (SEQ ID NO 203)

ATGTATAGTTAAAGGTAAATTAAGTAGAGAACGTGGGAACAGTTCGCACTGTGACCACCGGAACGTAC
GTCTGGTTAGCGCAGCATTAGTCCCAGTTACATCCGATTCAAAATGCAACAGCAAGTATTAATTGGGGA
AATCATATCATTTTGAATATAACCTTGGCGTCTACTAAGGATGGTTATACATCCTAGCTCGTGTAGTG
TGATATTTTGCAGGAATGATGCAAAGAGAGGAAGAACAAGAAGAGAGTTGTTGTTTTTAATGTATCTTA
GCAATTTATGAGAGGAGCATTGTCGTTGTCTGCTGTGACTAGTGCGTAGCTTTGCCGTTGTTTTTAAT
CATGATGGACATGCAAGTGAGAAAAGTGAGGAAGCCGCCTGCTTGCACCAATGCAGGAAGAGAAAGAT
CGGGTGCAGACAGGGCCAAAACCGATATGTGGGAATTGCGTCAAGTATAACAAGCCGGACTGTTTTTATC

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CAGATGGACCTGGTAAGATGGTCGCTGTGCCCTCTGCGTCCGGGATGTCCACGCACGGCAATGGCCAAG
GTTCCAACCATTTTTAGTCAGGGAACGGGTGTAATCAGAAAAACGTAATGATTCAAACGCAGTATCCGA
TTATGCAAACGTCGATAGAGGCATTCAACTTCTCGTTCAACCCCTCTGTGGATACTGCGATGCAGTGGGA
CCAAGGCCGCTAGCTACCAGAATAATAACACCAATAATAACTGCTCCTCGTCAGAATAGTAGTACCG
TTAGTAGTAATGTTTCATGGAAACACTATTGTGAGAAGCGATAGTCCAGATGTGCCCTCCATGGATCAGA
TTAGAGAATATAACACACGATTACAAC'TGGTTAACGCTCAAAGTTT'GACTATACAGATAACCCATACT
CTTTTAATGTTGGTATCAATCAAGACTCGGCCGTTTTCGATCTAATGACTTCTCCGTTTACTCAAGAGG
AAGTATTAATCAAGGAGATAGACTTTTTAAAAAACAAATTGCTTGATTTACAAAGCTTGCAACTGAAAA
GTTTGAAAGAAAAATCGAATTTAAATGCCGACAATACCACGGCAAAACAAAATTAACAAAACAGGTGAGA
ATTCTAAGAAAGGCAAGGTTGACGGTAAAAGAGCCGGATTGATCATCAGACTTCAAGGACTTCTCAGT
CCTCACAAAATACTTTACAGCGCTCACAATAACAGATGTGCAAAGTTTAGTCCAAGTGAAACCGTTGA
AGGATACCCCCAATACCTTTTCACTAAAAACTTCATCATTTTTAGAGATCATTATCTTTTCAAGTTCT
ATAATATTTTGCACGATATCTGCCATATTAATCAGTTCAAAGTAAGTCCCTCCTAACAAATAAAAAATCACC
AACAAATTAATGGAAGTTTGCAAAGTTAACTTCCCACCAAAGCAATAATTATTGAGACACTAAACTCTG
AATCCCTTAACAACTGGAATATTGAAGAATTTTGGCCAATCTTTGACAAAACCCCTTACTAGAATTTG
TTCATAACTCTTTTCCAAATGGTGATACCTGTCTTCAATTTCAACGGTTCGATCTTCTTTTATCTCAAC
TGACCAAACTAGGCGAATTAAC'TGTGCTTCTACTGTTGTTAAACGATTCAATGACCC'TATTCATAAGC
AGGCTATTAATAACCATGTTTTCGGCATTAAATGAATAATTTGAGGTTGATTGGAAGCCAAATCACATTGA
TAAACCTGGAATATTATGACCAAGAGACAATCAAATTTATGCCATCACAAAATTTTATGAATCTCTGT
ACATGCATGATGATCATAAATCAAGTTTAGACGAAGATTTGAGCTGTCTGTTAAGCTTCCAGATAAAAG
ATTTCAAGTTATTCCATTTTTTGAaaaaaATGTATTACTCAAGACATTCGCTTCTAGGTCAGTCTTCAT
TCATGGTACCCGCTGCTGAAAACCTATCTCCGATACCTGCCTCTATTGATACGAACGACATTCTTTAA
TTGCTAACGATTTAAATTAATCTGGAACCGCAAGCAAAATTGATAAATATTCTGCAAGGTGTTCTTTCT
ACTTGCCAGTAAATTTAACCAAAATTGAAAGTCTGTTAGAAACCTTGACTATGGGCGTGAGTAATACAG
TAGACTTATATTTTTCATGACAACGAAGTCAGAAAAGAAATGGAAGACACTTTAAATTTTATCAATACCA
TTGTTTATACAAATTTTTTCTTTTTGTTCAAAACGAATCCTCTTTGTCCATGGCAGTTCAACATTCTT
CTAACAAACAATAAGACCTCGAATCTGAAAGATGTGCAAAGGATCTGATGAAAATTTATTTCTAATATGC
ACATTTTTTACTCAATAACATTTAATTTTATCTTCCCATAAAGTCGATAAAGTCATTTTCAAGCGGCA
ATAATCGCTTTCATTCTAATGGTAAAGAATTTTATTGCGCAAATCATTTTATTGAAATCTTACAGAATT
TTATAGCAATACATTTGCTATTTTCCAACGTTGTGAAGTAATATTATATGACGAATTTTACAAAAATC
TTTCAATGAGGAGATTAATGTTCAATTGCTATTGATTGATTGATGACAAGATTTTGGAATTTTAAAAA
TAGAAATTATCGTATCCTTTTTACGAGATGAAATGAATAGCAACGGAAGTTTCAAATCTATTAAAGGTT
TCAACAAGGTTTTGAATCTGATTAAATATATGCTGAGATTTAGCAAGAAAAAACAAAATTTTGCGAGAA
ACTCTGATAACAATAATGTTACAGATTATAGTCAGTCGGCGAAGAACAAAAATGTTCTCTTGAAATTC
CCGTTAGTGAACGAACAGAATCTATTTAAATTTAAGGAGATTTTCAAGATTTTAAATGGAAGAGAAG
TTGTCCAAAGGAGTATAATTATTGACAAGGATTTGGAATCTGATAATCTGGGTATTACTACGGCAAACT
TCAACGATTTCTATGATGCATTTTATAATTAG

YHR056C, 832 aa (SEQ ID NO 204)

MVAVPSASGMSTHGNGQGSNHFSGNGVNVQKNVMIQTQYPIMQTSIEAFNFSFNPSVDTAMQWTKAASY
QNNNTNNNTAPRQNSSTVSSNVHGNTIVRSDSPDVPSMDQIREYNTRLQLVNAQSFDTNPNYSFNVGI
NQDSAVFDLMTS
PFTQEEVLKEIDFLKNKLLDLQSLQLKSLKEKSNLNADNTTANKINKTGENSKKKGKVDGKRAGFDHQ
SRTSQSSQKYFTALTITDVQSLVQVKPLKDTFNYLFTKNFIIFRDHYLFKFYNILHDICHINQFKVSP
NNKNHQYMEVCKVNFPPKAIIEITLNSSESLNNLNIEEFLPIFDKTLLEFVHNSFPNGDTCPSFSTVD
LPLSQLTKLGELTVLLLLLNDSTLNFNKQAINNHVSALMNNLRILRSQITLINLEYDQETIKFIAITK
FYESLYMHDDHKSSLDLSCLLSFQIKDFKLFHFLKMYYSRHSLLGQSSFMVPAENLSPIPASIDT
NDIPLIANDLKLLETQAKLINILQGVPPFLPVNLTKIESLLETLTMGVSNVTVDLYFDNEVRKEWKDTL
NFINTIVYTNFFLVQNESSLSMAVQHSNNNKTNSERCAKDLMKIISNMHIFYSTFNFIFPIKSIK
SFSSGNRFRHSNGKEFLFANHFIETLQNFIAITFAIFQRCEVILYDEFYKNLSNEEINVQLLLIHDKIL
EILKKIEIIVSFLRDEMNSNGSFKSIKGFNKVLNLIKMYLRFSKKKQNFARNSDNNNVTDYSQSAKNKN
VLLKFPVSELNRIYLFKEISDFLMEREVVQRSIIDKDLESNDLNGITTANFNDFYDAFYN

YJL138C, 1688 bp, CDS: 501-1688 (SEQ ID NO 223)

CTGTTGAATCATGGTAAAAGAGAAAAATCAAAGCACGTTGACCTGGATATAACCTCAGTAGATCGAAAT
GCTTCGCAGAAGAGTACTGCAGAGAAACATGATATTGAGAAACCGACATCTAAGCCGCAATCTGCTTTT

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AAATTTGATTGGGAGTCTACGGATTATTTAGACCGCGTCCAAAGAGCATTCCCAAAGCCTGATACCTGA
TGCCATCCCTCTACCTCTTAGCTATCAATCATTCAACTAACTACTACATAGTATACATTAGCTGTACA
GTCGTCACATCAGACGAATACAAAAGGCCGGGTGAAAGCGTTGATTTTGCGTACCTTTTCTTTTTTTC
GAAATTTTTTTATTTTTTTTTTTCAGCATCATATATAAAGAAATCTCATCTCAAGGAGAAGGAAACAGCA
GATCCCAATACACATAGTAGGAAAAAAAAAAGGTTTCGCTAAACAAAGGACTGGTGTGTACAAGAACTAA
TAAATAGTAATTGCAATATGTCTGAAGGTATTACTGATATTGAAGAATCCCAAATTCAAACCAACTATG
ACAAGGTCGTCTACAAGTTCGATGATATGGAATTGGACGAAAACCTTGTTAAGAGGTGTTTTCGGTTACG
GTTTTCGAAGAACCATCTGCCATTCAACAACGTGCCATCATGCCTATTATTGAAGGTCACGATGTCCTTGG
CTCAAGCTCAATCTGGTACTGGTAAGACCGGTACTTTCTCCATTGCTGCTTTGCAAGAATTGACACCT
CTGTCAAGGCTCCTCAAGCTTTGATGTTGGCTCCAACTAGAGAATTGGCTTTGCAAAATCCAAAAGGTTG
TCATGGCTTTGGCTTTCCACATGGACATCAAGGTCCACGCTTGTATCGGTGGTACTTCCTTTGTTGAAG
ACGCTGAAGGTTTGAGAGATGCTCAAAATCGTCGTTGGTACTCCAGGTCGTGTTTTTGACAACATCCAAA
GACGTAGATTTCAGAACTGACAAGATCAAGATGTTTCATCTTAGATGAAGCTGATGAAATGTTGTCTTCTG
GTTTCAAGGAACAAATCTACCAAATTTTACCTTACTTCCACCAACCACTCAAGTTGTTCTATTGTCCG
CCACCATGCCAAATGACGCTTTGGAAGTTACCACCAAATTTATGAGAAACCCAGTTAGAATTTTGGTTA
AGAAGGATGAATTGACTTTGGAAGGTATCAACAATTTCTACGTTAATGTTGAAGAAGAAGATACAAAT
ACGAGTGTGTTGACCGATTATACGACTCTATCTCCGTTACTCAAGCTGTCATCTTCTGTAACACCAGAA
GAAAGGTCGAAGAATTGACCATAAGTTAAGAAACGACAAATTTACCGTTTCTGCCATCTATTCTGATT
TACCACAACAAGAAAGAGACACCATCATGAAGGAATTCAGAAGTGGTTCTTCCAGAATTTTGATCTCCA
CTGATTTGTTGGCTAGAGGTATCGATGTCCAACAAGTTTCTTTGGTTATTAACTACGACTTACCAGCTA
ACAAAAGAAAATATATTACAGAATCGGTAGAGGTGGTTCGTTTCGGTAGAAAGGGTGTGCCATCAACT
TTGTTACTAACGAAGACGTTGGCGCTATGAGAGAACTAGAAAAGTTCTACTCCACTCAAATTTGAAGAAT
TGCCATCCGACATTGCTACCTTGTTGAACATA

YJL138C, 395 aa (SEQ ID NO 224)

MSEGITDIEESQIQTNVDKVVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIIEGHDLVLAQAQSG
TGKGTGFSIAALQRIDTSVKAPQALMLAPTRELALQIQKVMALAFHMDIKVHACIGGTSFVEDAEGLR
DAQIVVGTGPRVFDNIQRRFRFTDKIKMFIIDEADEMLSSGFKEQIYQIFTLPTTQVVLVSATMPND
VLEVTTKFMRNPRVILVKDELTLLEGIKQFYVNVEEEYKYECLTDLYDSISVTQAVIFCNTRRKVEEL
TTKLRNDKFTVSAIYSDLPQQRDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYLDPANKENYI
HRIGRGGRGFRKGVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

YKL060C, 1580 bp, CDS: 501-1580 (SEQ ID NO 239)

TGGGTCATTACGTAAATAATGATAGGAATGGGATCTTCTATTTTCCCTTTTTCATTCTAGCAGCCGT
CGGGAAAACGTGGCATCCTCTCTTTTCGGGCTCAATTGGAGTCACGCTGCCGTGAGCATCCTCTCTTTCC
ATATCTAACAACGTAGCACGTAACCAATGGAAGCATGAGCTTAGCGTTGCTCCAAAAAAGTATTGGA
TGGTTAATACCATTGTCTGTTCTCTCTGACTTTGACTCCTCAAAAAAATACTACAATCAACAG
ATCGCTTCAATTACGCCCTCACAAAACTTTTTTCTTCTTCTCGCCACGTTAAATTTTATCCCTCA
TGTTGTCTAACGGATTTCTGCACTTGATTTATTATAAAGACAAAGACATAATACTTCTCTATCAATT
TCAGTTATTGTTCTTCTTTCGTTATTCTTCTGTTCTTCTTTTCTTTTGTATATATAACCATAACCA
AGTAATACATATTCAAAATGGGTGTTGAACAAATCTTAAAGAGAAAGACCGGTGTCATCGTTGGTGAAG
ATGTCCACAACCTATTCACTTACGCTAAGGAACACAAGTTTCGCTATTCCAGCTATTAACGTCACCTCTT
CTTCTACTGCCGTGCTGCTTTAGAACTGCTAGAGACAGCAAGTCCCAATCATTTTGCAAACTCTTA
ACGGTGGTGTGCTTACTTTCGCTGGTAAGGGTATCTTAACGAAGGTCAAAATGCTTCCATCAAGGGTG
CTATTGCCGCTGCCACTACATCAGATCCATTGCTCCAGCTTACGGTATCCAGTTGTCTTACACTCTG
ACCACGTGTGCAAGAAGTTGTTGCCATGGTTGCATGGTATGTTGGAAGCTGATGAAGCTTACTTCAAGG
AACACGGTGAACCATATTCTCCTCCACATGTTGGATTGTCTGAAGAAACCGATGAAGAAAACATCT
CTACTTGTGTCAAGTACTTCAAGAGAATGGCCGCTATGGACCAATGGTTAGAAATGGAAATCGGTATTA
CCGGTGGTGAAGAAGATGGTGTAAACAACGAAAACGCTGACAAGGAAGACTTGTACACCAAGCCAGAAC
AAGTTTACAACGCTTACAAGGCTTTGCACCCAATCTCTCCAACTTCTCCATTGCTGCTGCTTTTCGGTA
ACTGTACGGTTTGTACGCTGGTGACATCGCTTTGAGACCAGAAATCTTGGCTGAACACCAAAAGTACA
CCAGAGAACAAGTTGGTTGCAAGGAAGAAAGCCATTGTTCTTGGTCTTCCACGGTGGTTCCGGTTCTA
CTGTCCAAGAATTCCACACTGGTATTGACAACCGGTGTTGTCAAGGTCAACTTGGACACTGACGTCAAT
ACGCTTACTTGAATGGTATCAGAGACTACGCTTGAACAAGAAGGACTACATAATGTCCCACTGCTCGGTA
ACCCAGAAGGTCCAGAAAAGCCAAACAAGAAGTTCTTCGACCCAAGAGTCTGGGTTAGAGAAGGTGAAA
AGACCATGGGTGCTAAGATCACCAAGTCTTTGGAACTTTCCGTACCACTAACACTTTATAA

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YKL060C, 359 aa (SEQ ID NO 240)

MGVEQILKRKTGVIVGEDVHNLFTYAKEHKFAIPAINVTSSSTAVAALEAARDSKSPIILQTSNGGAAY
FAGKGISNEGQNASIKGAIAAAHYIRSIAPAYGIPVVLHSDHCAKLLPWFDMLEADEAYFKEHGEPL
FSSHMLDLSEETDEENISTCVKYFKRMAAMDQWLEMBIGITGGEEDGVNNEADKEDLYTKPEQVYINVY
KALHPISPNSFIAAAFGNCHGLYAGDIALRPEILAEHQKYTREQVGCKEEKPLFLVFHGGSGSTVQEFH
TGIDNGVVKVNLDTDCQYAYLTGIRDYVLNKKDYIMSPVGNPEGPEKPNKKFFDPRVWVREGEKTMGAK
ITKSLETFRITNTL

YKL097W-A, 779 bp, CDS: 501-779 (SEQ ID NO 245)

AGCTCCGAAGGGCAATTCCACAGGCACTCCGCGGGGGCCGCAAGGCCAAAAGGCGTGGAATATGCG
CGTTTTGGGGCCATAACACCCAGTACCACGGCCGGAACGGGCCATATAATAAGTTTTCACTCTCAAGA
ATGGTAAACGTAAATAGGAACATCCCACTACCCTAGAAATTGCGGAAATTTGCGCGTTATCATTAGAAA
ATCTGGAACCGTCTCTTTTCTCTTCTTGCAATTTCCCTTTCCGTATTATTGCCATTCTTTAACTGCAT
TTGGGGAACCGTAGACCAAAAGCCAAACAGAGAAATGTAACGTTCTAAAAAAAACAAACGAAAAAATT
GAAAAATAAGATACAATAATCGTATATAAATCAGGCTTCTTGTTTCATCATTTTTCAATTTCTTCTTGCC
ATCCCTTTTCTTATCTTTTGTTCTTTTCTTCTCATAATCAAGAATAAATAACTTCATCACATTGCTACA
CACTAACAAGAAAAAAATGCAATTTCTTACTGTGCTTCCGTTGCTTTGCTGCTTTGCTGCTTAACCTTTG
TTGCCGCTGAATCCGCTGCCGCCATTTCTCAAATCACTGACGGTCAAATCCAAGCTACTACCACTGCTA
CCACCGAAGCTACCACCACTGCTGCCCATCTTCCACCGTTGAAACTGTTTCTCCATCCAGCACCGAAA
CTATCTCTCAACAACTGAAAATGGTGCTGCTAAGGCCGCTGTCGGTATGGGTGCCGGTGCTCTAGCTG
CTGCTGCTATGTTGTTATAA

YKL097W-A, 92 aa (SEQ ID NO 246)

MQFSTVASVAFVALANFVAAESAAAIISQITDGIQATTTATTEATTTAAPSSTVETVSPSSTETISQQT
ENGAAKAAVGMGAGALAAAAMLL

YKL150W, 1409 bp, CDS: 501-1409 (SEQ ID NO 249)

CCCATCACATCGCATCACATCACATCACTCCCTATTCTGCCCTTTACAGCGCAAAGGAGTCGTGTGTGG
GTGTGTGCTCCTTTTGACGATCATAAGAGTCCATTTCTAGTATGCAAGCTGGTAACAATAGGTGAATGA
ATTAGGTTTCATTTGCGATGACCTTCAGTATCCCTCCACGCAATGCTAAACTATCCCCCTCATTATGACG
CCTATATCGTATAAGGAACCTTGTTACCCCTGACAATTCAAACCTCAAAGGTCTAAGACCAACAAGCGT
AGGAACCTATCGCTCGGAGTGTCTTCCGTTTGAAAAAAGAAGAGAAATAAGGGCCCTTGATTGGTGTCT
TGTCGAGAGAGGTACGTATATAAGAATGCAGTTTGCTCGCAATGCCCGCTTGTTGTTAAGTACTCTTACC
TTTTCCCTCAATACTAACGTTTGAAGCAGCCAACTAACAATAGTATAACGTATATAGGTTAAAAATA
TATTCCAAGTCAAAAACATGTTTCCAGATTATCCAGATCTCACTCAAAAGCATTACCGATTGCTCTAG
GTACAGTTGCTATAGCAGCTGCTACCGCATTCTATTTTGCAAACCGTAACCAACATTCCCTTTGTCTTCA
ATGAATCTAATAAAGTGTTCAAAGGTGATGACAAATGGATCGACTTGCCAATATCTAAAAATAGAGGAGG
AATCCCACGACACCAGAAGGTTTACTTTTAAGCTGCCTACCGAAGACTCAGAAATGGGGTTGGTCCTAG
CATCTGCTCTGTTTGCTAAATTTGTACACCAAAAGGGATCCAATGTGGTGAGACCATACACTCCTGTGA
GTGATCTTTCCAGAAGGGTCACTTCCAGCTGGTCTGCAAGCATTATGAAGGTGGTAAATGACCTCAC
ATTTATTTGGTCTTAAACCAATGACACCGTTTCTTTCAAGGGTCCCTATTATGAAATGGAAGTGGCAAC
CTAATCAGTTCAAGTCAATCACCTTGTTAGGTGCCGGTACCGGTATCAACCTCTGTACCAATTAGCTC
ATCATATAGTTGAAAACCCAAACGACAAGACCAAGTTAACTTGCTATATGGGAACAAGACTCCTCAGG
ACATTTTACTAAGGAAGGAACCTGGATGCGTTGAAGGAAAAGTATCCTGACAAGTTCAATGTTACTTACT
TTGTTGACGACAAGCAAGATGACCAAGACTTTGATGGTGAAATTAGTTTCATCTCCAAAGATTTTATTC
AGGAGCATGTTCCAGGTCCAAAGGAAAGCACACATTTGTTTGTCTGCGGTCCCCCACCATTTATGAACG
CTTACTCAGGTGAGAAGAAGTCACCTAAGGACCAAGGTGAATTGATCGGTATCTTGAACAATTTGGGCT
ACTCCAAGGACCAAGTTTTCAAATTTTAA

YKL150W, 302 aa (SEQ ID NO 250)

MFSRLSRSHSKALPIALGTVAIAAATAFYFANRNQHSFVFNESNKFVKGDDKWIDLPISKIEEESHDR
RFTFKLPTEDESEMGLVLASALFAKFVTPKGSNVVRPYTPVSDLSQKGHFQLVVKHVEGGKMTSHLFLK
PNDTVSFKGPIMKWKWQPNQFKSITLLGAGTGINPLYQLAHHIVENPNDKTKVNLLYGNKTPQDILLRK
ELDALKEKYPDKFNVTYFVDDKQDDQDFDGEISFISKDFIQEHVPGPKESTHLFVCGPPPPFMNAYSSEK
KSPKQDQELIGILNNLGYSKDQVFKF

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YKL156W, 1099 bp, exon1: 501-503, intron1: 504-853, exon2: 854-1099
(SEQ ID NO 251)

CGAAAGGTTTCGATCAAAGTTTGGCTCAATCAC'TGGACACTATTACTTCGAAAGCGCAGTGGGGTTAAC
AGAGACCGTGATGTCGTCAACAAGTATTTGAAGGAAAATGGTTACTATTAAGAAAAATCTCTTTTCTA
GCCATTTTGCCTTTTATATAGTCAAGTATCTATATGTGACAAATACTTCTTCTAAGCTTGGCCTTCTG
ATAGGCTTAGCTTGCAAGTGGTTGCAACATACATAAATCAACAAAAAGTACGGCTTAAAATTTTGGTA
TTCATTTATTTCAACCCGTGCACACTGGAAATAAATCTGTACATAACAGCATATTTTGTTTTGAAGAAA
ATTTCTGTGTTCCCTCCGATGTGGGAAGAATTTTAGGATCGGCTAAATTTTCGTAAAGTATCAGTAACTTG
GTATCTCTGTATAAGCGGAGTCTAATTTTCGATAACAAGCAACTTCATCGTAACACCTTCCAACAAAGCA
AAGATAGATATCCCAAATGGTATGTTAGTATCCAATAATGCAGCGCAACTGGACCAGTGAATAGAAC
AATACATATAGATAAGTCGCAAAAGAAAAGAATACATGTGGTGGAAAATTTTGCACCAAGAGAGGCAAG
AACTATGAAGAAAGACTTTTGAATATTTCAAGCGGTTGCTACATATAGTGGATAAGATTCCAGGATGGA
CGTATGAGCTTACAGTTCATTGTAGGGGAATATAAATTTCTGATGATGGCGAACTTCTCCAGCAAC
TCAAGCTATTGTTATTTTCTATTCTGCACCGAGATGAGGAGAAAAAGGAAGTTTACTAACAGTATAGA
TTTATTTCTTATTCGTCTACAACAGGTTTTAGTTCAAGATTTATTGCACCCAAGTGCAGCTTCTGAAGC
AAGAAAGCACAAATTAAGACATTAGTCCAAGGTCCAAGATCGTACTTCCTAGACGTTAAGTGCCCAAGG
TTGTTTGAACATCACTACAGTTTTCTCACACGCCCAACTGCAGTTACCTGCGAATCCTGCTCAACAAT
TTTGTGCACCCCAACTGGTGGTAAGGCAAAGCTTTCTGAGGTACATCTTTCAGAAGAAAGTAA

YKL156W, 82 aa (SEQ ID NO 252)

MVLVQDLLHPTAASEARKHKLKTLVQGPRSYFLDVKCPGCLNITTVFSHAQTAVTCECSTILCTPTGG
KAKLSEGTSFRRK

YLR029C, 1115 bp, CDS: 501-1115 (SEQ ID NO 265)

TCGACACTTACTTAATATGTTTTGCCGCCCTTCATAAGAGGGTGTCTTCTAAAATTTATTGGGCAAGAAT
GAGATGGACTCGCACCTACATGACGTTTAAATATTTAGTGTAAAGGTTTCAAGACATGCACCAGGTGCG
ACATGTGTTGCGATTATCATGACAATGTCTCTATCCGAGATGCATTTGTAGTATCAATTGATGCGTATT
ATGACATGATTTACATAGCATACATCGTCAAACATGATATTATATTCTTTTTTGTATAAATGTACGGAT
TTAAAGCTGTGCAATATATTTTCTGAAATTTCTTGGAGCTGACGCAAAATTTTCAAAGGTGCTAAAAT
TTTCAAGATTTCTCACTTTTGTCTGGTAACAAGAATGATGGCATTGCATTTTACCACCGGTACATTT
AACTGCTATTTCTCACGTTTCTTTCCCTATCCTTAAGTAATTCTTTTACAATCTAAGAAAACACGATC
AAACAAATAAATCAGCAATGGGTGCCTACAAATATTTGGAAGAATTGCAAGAAAGAAGCAATCTGATG
TTTTGAGATTCTTGCAAGAGTCAGAGTCTGGGAATACAGACAAAAGAATGTCATTACAGAGCCGCTA
GACCAACTAGACCAGACAAGGCTAGAAGATTGGGTACAAAGCTAAGCAAGGTTTTCGTTATCTACCGTG
TCAGAGTTAGACGTGGTAACAGAAAGAGACCTGTTCCAAAGGGTGCTACTTACGGTAAGCCAACCTAAC
AAGGTGTCAATGAATTGAAATACCAAAGATCCTTGAGAGCTACCGCTGAAGAAAGAGTTGGTTCGTCGTG
CCGCTAACTTGAGAGTCTTGAACCTCTACTGGGTAAACCAAGATTCTACTTACAAGTACTTGAAGTTA
TCTTGGTGCACCCTCAACACAAGGCTATCAGAAGAGATGCTCGTTACAAGTGGATCTGTGACCCAGTTC
ACAAGCACCGTGAAGCTAGAGGTTTGAAGTCCACTGGTAAGAAATCCAGAGGTATCAACAAGGGTCACA
AATTCAACAACACCAAGGCTGGTAGAAGAAAGACCTGGAAGAGACAAAACACTTTGTCTTGTGGAGAT
ACAGAAAATAA

YLR029C, 204 aa (SEQ ID NO 266)

MGAYKYLEELQRKKQSDVLRFLQVRVWVEYRQKNVIHRAARPTRPDKARRLGYKAKQGFIYRVRVRRG
NRKRPVPGKATYGKPTNQGVNELKYQSLRATABERVGRRAANLRVLNSYVWNQDSTYKYFEVILVDPQ
HKAIRRDARYNWICDPVHKHREARGLTATGKKSRIKNGHKFNNTKAGRRKTWKRQNTLSLWRYRK

YLR038C, 752 bp, CDS: 501-752 (SEQ ID NO 267)

GGAAAGCAAAGCTCTAAATGATAACTCTACAAAAAGTCAGAGAAATCTGTCACTAATTTATTTGAAGGA
TGAAGAATTAATGCTTAAAGTCTTAGAGCTTTTGGTGACAAGTGCTGCAACGCCACAGACCCAATTA
AGCTACCGATTCTGTTGGACATGTGTTTCCAATTAATACGCTTACTCAAGGAATTAGACAGAGAAAA
CACACAATTGGTTCAAAAAGCACTCGAGAGATTCAAATAAATCTATATGACACCATGTATTCTTTACCA
TATAGCTTCATAACATTGACCAATCAATTTTCAAGAAATGCGTCGCGCTAGTTTTGCCCGATATCCCCA
TCCCTTCAGGATCTTTTAAAGGTGATGAAAGATGCACCAGATAGAAAAGTTGCATTAAAATGATTAGCA
GAGATATACAAATATTTTAGTAAGAATACATAAAGTATCTTTGCTTTCACAAATAGGAACAAGCACATA
AATACAGTATAATAGACATGGCTGATCAAGAAACTCTCCACTACATACAGTTGGTTTCGATGCTAGAT

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TTCCCCAACAAACCAAACAAAGCATTGTTGGCAATCTTATGTGGATTATCACAAGTGTGTTAATATGA
AGGGCGAAGATTTTGTCTCCGTGCAAGGTCTTTTGGAAAGACCTATAACGCCCTTATGTCCCCTAGACTGGA
TCGAAAAATGGGATGATCAAAGAGAAAAAGGTATTTTCGCAGGTGATATCAACTCAGACTAA

YLR038C, 83 aa (SEQ ID NO 268)

MADQENSPLHTVGFDARFPQONQTKHCWQSYVDYHKCVNMKGEDFAPCKVFWKTYNALCPLDWIEKWDD
QREKGIFAGDINS

YLR312C, 1697 bp, CDS: 501-1697 (SEQ ID NO 285)

CATCAATTAGGGCAAACCTTGAATAGTCAGCTAGGTCATATATTTAAATCAATTAGCCCTATGACTACA
TTAGGTTTATGTTAGGTCTTTACGGCTGCATATTTGCTTTCCGCGTTCCGGCGGGTCTCTGCGACGATT
TCTGCGCGGTCTTGTATGGGTGGAGTTGACAGTTAACCCCTCCGGACCCCTACCCCGGTGTGCCCCGG
TCCATCTATCCATTTTTCGGTAACCCCTTTGCGCGACAGCTGCTTATCAAGGTACCTGGATCGAGCCAT
AAAAATTGATCTACACAGATGAGATGGGGCATTGGGATATATTATTAGTCGGAGTATCATTTATAGTTAT
TCAGTTTATGTCAGGTTACTGGCCAAACGTTTTCTTCATTTGGAATAATCGTTTTAGGAGCTACTGTTTC
CGGTATAAAGTAACAAGCACAGTAGCAGAGTAATACGCAGTGACGATAATAGAGACTAGTAAAAACAGTC
GAGTTGTGCGACCTAAAATGTCAGAAGAAGACGATCATTTGGAATTTAGTTAGATTACGTAGATTACGTA
AAGGGAGAGAAGGGGAAGAACAGTCATCGAAGTCAGAAATATCTTTGGATAGTTTGCATGAAAGCTCCT
TTGCGAGGAGAGGACGACGAGGACTTCGATGCAGATGTCTTATCGAACACTAGCAGTGAAGAGTCTGCAC
AGATGAATCGTATTTACGATTTTGAACATCTAATGAATTTAGTAATGCTGGAGTTAATATTTGATCAAA
CTGGAGTTCCCACTATTTTCAGAGTCATTTGATACTTTGTCCGGCTCAAATGTTGGCGGAACGGTATTGC
CAAGTATGGAGGGGTGAAACTGAAGGATAGTACGATAAGGAATTCTAGCACACTATCGGATCATATCA
TAGATAAAAGTGAGGGTAAATCTGCTAAATGAAGATGTGGCATGTTATCATGCTATCTTCATTGCTTTT
CCATGACCTTTTCATACCTCGCCCTCGAATATTCCTGACTGGTGATGTGTGGCAGGTTTTAAATCAC
AACAGTCATTACGTAATAATGAAAGGAAGCTGTTGTACGGCAATATCGATTTTGTGATAAAAAATCTT
ACGATTTCATCAAGTGACTCTTTAAGTCAGTGGGCTCCTTCAGGAAAAATACTACGTCGACTTCGACAATC
ATATTGCATACCCATTAAAGGATGATGACCTAATGGGCTGGAGACGATACAAAACAGACTTAGTTATTT
TATGGTATACAACAAAGCTCGAATGAAAGACGGTTGGCACAAGAGAATTAAACAAAATAAACGGAGGAA
GAATAAAGTTACACCTATTTCTCAAGAATCTTTTAAATCCGCTCAAGAAAGTTTAAGGGTATTGCATA
AAGAACAGAAACGCCGTGGAAAAGGCTCTTTGTGCTACTTCATAATAAATACAGGCAATTTTCTCCAC
ATATTTAAAGGATATTTTCGATCATTTCTGGCCAAAAGCAAAACAAATGTTGGTCCGGATCCAGATTGCAGT
TGCACAAGCTTCGTTTCAAGTCAATGAAACCATTCAGGATTTTTCAGTTTAAGGTTTCGCAAGATACCA
ACTGGTTTGTAAAGCAGCTGAAACGGTTCCGATTGAAATTACAGCATTCGAGGATGTATAAAGCGATGT
CAGAAATGCAGGAAAAAAATTTATTTTAAGTGCAAAACACTAG

YLR312C, 398 aa (SEQ ID NO 286)

MSEEDDHWNLVRLRLRKREGEEQSSKSEISLDSLHESSFAGEDDEDFDADVLSNTSSEESAQMNRIY
DFRTSNFNSNAGVNIDQTVPTISESFDTLGSGNVGGTVLPMEGSKLKDSTIRNSSTLSDHIIDKSEG
KSAKLKMWHVIMLSSLLSMTFSYLALEYSLTGDVLGAFKSQQLRNNERKLLYGNIDFVDKKSYSYSSD
SLSQWAPSGKYVDFDNHLYPLKDDDLMGWRRYKTDLVILWYTTKARMKDGWHKRINKINGGRIKLHL
FLKNSFKSAQESLRLVHKEQKRRWKRLFVLLHNKYRQFSPIHKRYFDHSCQKAKQCWSGSRLQLRKLRF
KSMKPFVRVQFKVRKDTNWFVKQLKRFGLKLQHSRMKAMSECRKKNYFKCKH

YLR414C, 1292 bp, CDS: 501-1292 (SEQ ID NO 293)

TAGTCAGCCACACATTGACGTACACTGTGAACAGCCTATTTCTTTCCATGTATCTCAGTGCCAGCTTA
TGAGAACTGTACAGCCTCCCACTTGACCCTCAGAGCCCTCTCCACTCCCCCTCTTTCAACATCGCC
AGATAGCCCGGTTGAATGGTGCAGGACACCCGGCTGGCCTGGCCAGGCAAAAAAGGACGCAGCAGC
CCTCGAGCGTTATTTCCAAATCGGGCGTACTATCAGCCAAGCCAGCTCGGTATTTTTCAGCGTTCTCG
CAGGAAATTTGGCTGAGAAGTATATACGCGAGAATGTTGCTCTTCCATGTCTCAGTAGTCAATGAGT
GTCAGATGGTGTTCATTCTGGACAGTTGTTTGGAAAGTAGAACTAAAAGAACTAGATCAAGATCATA
CAACGCTGCGCAGTAGTGAACTTGATTAAAGCAATAGAGAACTATTAAGAAAAAAACAAACACATCAT
CGAAGGACGCTATAAGCATGAGGAATTTTTTCACGTTATTTTTTGCAGCTATATTTTCGCTAGGAGCAC
TTATATTAGCCATTGTTGCATGCGCAGGATCAACGAAAAATTACAGTCCCATAAATAAAATTTACTGTG
CAGAATTGGATCTGTGCGAGATGAAGGTATCGACGGTGCTCCCTTCTTTGAGTTCTGCTACGCTATCTT
CGTTGGGCCTGCCCTCATATATAAATATAGGGCTTTGGTCTGACTGTACAGTGGACTCCTCGCATAACA
TCCAATCATGTTCTTCGCCTCACGGTATCCAGAATTTTAACCTATCGTCATTAGTGATGACAATATCA

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ACAACAATGAGGCTCTGGAGCTTATGGATTCCGTGGCCAGTGTGTTTTGCCCGAAAACTAAAAAGTA
AAATGACATACTACAACAATTTGGTCAAGTGTATGTTTCATTACCATTCTTATTGGTATTGTCTTGACCT
TTGTGAATCTAGTGTTCACCGTATTGCGCTGGATCATCCACATAAGGCCGCTAACGTGGTTTTGGTGCCCT
TTTTTTCATTTTTTCGCCCTTTGCCGCCCTATTAGTCAGTATAGGTTTCGTGTTTGGGCACCTTACTCATACA
TCAAATACATCCTAAAGCATAACTATAGTGATTACGGTATTTCAATGAGCATTGGTAGGAACACCAGG
GTTTGATGTGGGGGGCTGTCTGTTGGAGCATTACTGAATTTTCATTCTATGGTGTAGCGTGAGATCGAGGC
CCACCGTCATCTATGCGAACGCTCCAATTGAGGAAAAACCATTGATTTGA

YLR414C, 263 aa (SEQ ID NO 294)

MRNFFTLFFAAIFSLGALILAIVACAGSTKNYSPINKIYCAELDLSQMKVSTVLPSSLSSATLSSSLGLPS
YINIGLWSYCTVDSSHNIQSCSSPHGIQNFNLSSLVYDNNINNEALELMDSVASVVLPEKLKSKMTYYN
NLVKCMFITILIGIVLTFVNLVFNVLRWIHIRPLTWFGAFFSFFAFAALLVSIGSLGTYSYIKYILK
HNYSDYGISMSIGRNYQGLMWGAVVGALLNFILWCSVRSRPTVIYANAPIEEKPLI

YMR251W-A, 680 bp, CDS: 501-680 (SEQ ID NO 317)

ATCCCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTAT
CTCACAGTGGTAACGGCACCCTGGCTCGGAAACGGTTTCCTTCGTGACAATTCAGAACAGGGGCTACAG
TCTCGATAATAGAATAATAAGCGCATTTTTGTCTAGCGCCGCCCGCGGCCCGTTTCCCAATAGGGAGGC
GCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTGGGTAAGCCCCCTTCTGTTTTTCGGCCAGTGGTTG
CTGCAGGCTGCGCCGAGAACATAGTGATAAGGGATGTAACCTTTCGATGAGAGAATTAGCAAGCGGAAA
AAAATATGGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGAC
AGTTTCTGGGACGCTTAACTTTTATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAAAAA
AAGACTAATAATAAAAAATGAAGTTATCTCAAGTTGTTGTTTCCGCCGTGCGCTTCACTGGTTTAGTAA
GTGCTGCTAACAGTTCTAACAGCTCAAGCTCAAAGAATGCTGCCCAACCAATTGCCGGTTTAAACAACG
GTAAGGTTGCAGGCCCGCGCTGGTGTGTGCTCTAGCTGGTGCTTTGGCCTTTTGTGATTTAA

YMR251W-A, 59 aa (SEQ ID NO 318)

MKLSQVVVSAVAFTGLVSAANSSNSSSSKNAAQPIAGLNNKVVAGAAGVALAGALAFLLI

YNL030W, 812 bp, CDS: 501-812 (SEQ ID NO 323)

GTTTTGACACCGAGCCATAGCCGTGATTGTGCGTCACATGGGCGATAATGAACGCTAAATGACCAACT
CCCATCCGTAGGAGCCCCCTTAGGGCGTGCCAATAGTTTCACGCGCTTAATGCGAAGTGCTCGGAACGGA
CAACTGTGGTTCGTTTGGCACCGGGAAAGTGGTACTAGACCGAGAGTTTCGCATTTGTATGGCAGGACGT
TCTGGGAGCTTCGCGTCTCAAGCTTTTTCGGGCGCGAAATGCAGACCAGACCAGAACAAAACAACGTAC
AAGAAGGCGTTTAAATTAATATGTTGTTCACTCGCGCTGGGCTGTTGTTATTCGGCTAGATACATACG
TGTTTGTGCGTATGTAGTTATATCATATATAAGTATATTAGGATGAGGCGGTGAAAGAGATTTTTTTTTT
TTTCGCTTAATTTATTTCTTTCTCTATCTTTTTTCTCTACATCTTGTTCAAAAGAGTAGCAAAAACAACA
ATCAATACAATAAAATAATGTCCGGTAGAGGTAAAGGTGGTAAAGGTCTAGGAAAAGGTGGTGCCAAGC
GTCACAGAAAGATTCTAAGAGATAACATTCAAGGTATCACTAAGCCAGCTATCAGAAGATTAGCTAGAA
GAGGTGGTGTCAAGCGTATTTCTGGTTTGATCTACGAAGAAGTCAGAGCCGCTTGAAATCCTTCTTGG
AATCCGTCATCAGGGACTCTGTTACTTACACTGAACACGCCAAGAGAAAGACTGTTACTTCTTTGGATG
TTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATATGGTTTCGGTGGTTAA

YNL030W, 103 aa (SEQ ID NO 324)

MSGRGKGGKGLGKGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRD
SVTYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YOL109W, 842 bp, CDS: 501-842 (SEQ ID NO 343)

GGAGGTCTGCTTCACGAGCGCGGTGTGCGCCTAGTATTGCCCGACGGTCCGGGTGCCATCCCTAGAT
TTCGTGCTGCCCCGACCCAAATAGTTAAACGTGTGGTTTATGGGTGCACCAGGGCTTTATCGTGTTTTA
TATCGATGGCGATTGTGCTCCAGTGTATTTTGTATATCCAATTAAGGTTTCTTACCTAATTTTATT
TTTATCATCTTTAGTTAATGCTGGTTTGCTCTGTTTCTGCTGCTTTCTGTGCGGTTCTCCTCTTCTCTT
GTTTCTTCGTGTTGTCCCCCATCGCCGATGGGCTTATATGGCGTATATATATAGAGCGAGTTTTTACGT
CGAAGATCATCTCAGTTTGCTTGATAGCCTTTCTACTTTATTACTTTTCGTTTAAACCTCATTATACTT
TAGTTTTCTTTGATCGGTTTTTTTTCTCTGTATACCTTAAAAGTTCAAATCAAAGAAACATACAAAACCTAC
GTTTATATCAATTAATAATGTCTGAAATTCAAAACAAAGCTGAAACTGCCGCCCAAGATGTCCAACAAA

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AGTTGGAAGAAACCAAAGAATCTTTGCAAAACAAGGGCCAAGAAGTAAAGGAACAAGCTGAAGCTTCTA
TCGACAACCTAAAAAATGAAGCTACTCCAGAAGCTGAACAGGTGAAGAAGGAAGAACAACATTGCTG
ATGGTGTGCAACAAAAGAAGACCGAAGCTGCCAACAAGTTGAAGAACTAAGAAGCAAGCTTCCGCCG
CCGTCAGTGAGAAGAAGGAAACCAAGAAGGAAGGCGGTTTCTTGAAGAAATTGAACCGTAAAATTGCTT
CCATTTTCAACTAA

YOL109W, 113 aa (SEQ ID NO 344)

MSEIQNKAETAAQDVQKLEETKESLQNKGEVKEQAEASIDNLKNEATPEAEQVKKEEQNIADGVEQK
KTEAANKVEETKKQASAAVSEKKETKKEGGFLKLNRIASIFN

YOR285W, 920 bp, CDS: 501-920 (SEQ ID NO 365)

ACTAGCAAGATGATCGTCAGATATGGTGATTTATTTCCCTGTGCATTGTACTTCAAAGATCATACAGCA
TACTAAGCGCTTTCCAGGGACACCTTCTGTGCGCAAAATATCAGAATTTTCTTGATTAAACGCAGCATA
TTGAGTATATGAAATTAACGGGACACTGTGTGAAAAATTTGTAGTTGTACTTTTTTGTATCCCTTTG
GTAGACATATGGACGAATTACTACTAAGATTGGCTTCCATAAGGCCCAAATCCAGATATCACCTACGGT
ATGTCCTTTTCTTACTTGCAATGACAAATAATTTGTTATTTATCTTGGAACTTATATAAGTTACATCTG
ATTGCTTTTGTATTTTTTTTGGAGAAATATTATACCGCGGGGAAGGAAGTAAGGGGAGAATTTTTGAG
GTGTATAAAAGAGAGTGGAGGCTTAATCAATCAAAGAATTCTTCTCGTTTATTTTCAGGGTTTGTGAC
TAAGAAACGATATTAAATGTGGAAGGCCGTGATGAATGCTTGGAAATGGAACCGAGAGTCAAAGTAAGA
ATGTTTCAAATATTCAATCTTACAGTTTGAAGACATGAAAAGAATCGTTGGAAAGCATGATCCTAATG
TGGTTTTGGTAGATGTTAGAGAACCATCTGAGTACTCGATTGTTTCATATTCCTGCTTCCATCAATGTGC
CATATAGATCGCACCTTGACGATTTGCCCTTAGATCCTTTAGAATTTGAGAAACAGATTGGCATCCCAA
AACCTGACAGTGCCAAGGAGCTAATATTTTATTGTGCTTCTGGCAAACGCGGGGAGAAGCTCAAAAAG
TCGCCCTCTCACATGGATATTCAAACACCTCACTATATCCTGGCTCTATGAATGATTGGGTTTCTCATG
GGGGTGATAAACTTGACTTATAG

YOR285W, 139 aa (SEQ ID NO 366)

MWKAVMNAWNGTESQSKNVSNIQSYFEDMKRIVGKHDPNVVLVDVREPSEYSIVHIPASINVPYRSH
DAFALDPLEFEKIQIGIPKPSAKELIFYCASGKRGEAQKVASSHGYSNTSLYPGSMNDWVSHGGDKL
L

YOR327C, 848 bp, CDS: 501-848 (SEQ ID NO 369)

GTGTATTATTAAATACGAACAAAATAAAAATATGCCGACCAATTCTGTAGTAGTACTGTACTATATTGAA
TATTAAGGGTTTTTCTGGTCTTAGCGTATCCCTTTATCAGTCCGTGGAACAAAGCCACGGGCGGCTGTA
ACAATGACCATGGAATCATTCAGTCGCCCTAAAAGCGCATTCACGGAGCGTTTATAGTGATCTTGGTC
ACATGATATACGCGTGACTTTTTTTTTTATTTTTTCTCCCTGTCTTCCGCAAAAGTGGCTCAAAATTCTT
CGGATTTTGGCATTATAGCGGAATGGTGCAGCGCAACCAACAAACACCAGTTGTGCGACCCAAAAGA
TGCAAAAGCGGGGAGCCAGTTAGTTTTCTTCAAGTTTTGGTTGAAACAGCCTTTAATATTTTATAGAA
AGGTAAACTATCTGCTCAGTGAATAGTATCTGTAAGTCAGGCATACATTGGAACACTTCCAAATACAA
AATAAGAACGCGCAACGATGTGCTCATCAGTGCCATACGATCCATATGTGCCTCCAGAGGAGAGTAACT
CAGGCGCAAAACCAAATTTCCCAAAACAAGACTGCTGCTTTGAGACAAGAGATTGATGACACGGTGGGAA
TAATGAGAGATAATATCAACAAGGTGCTGAAACGTGGTGAAAGGCTAACATCCATTGAGGACAAAGCTG
ATAACTTGGCTATCTCCGCACAAGGATTCAGAGAGGGCGCCAACAGGGTCAGAAAGCAAATGTGGTGA
AAGATCTAAAAATGAGAATGTGTTTATTCTTAGTTGTTATTTTACTAGTGGTAATTATCGTTCTTA
TCGTCGTCCATTTTCACTAA

YOR327C, 115 aa (SEQ ID NO 370)

MSSSVPYDPYVPPEESNSGANPN SQNKTAALRQEIDTVGIMRDNINKVAERGERLTSIEDKADNLAI
A QGFKRGANRVKQMWKDLKMRMCLFLVVIILLVVIIVPIVHFS

YPL037C, 974 bp, CDS: 501-974 (SEQ ID NO 377)

TCACGGCTGCTCTTCTCTTTTTTCGCATATTCTATTTTATCATCGACTTCCCTAATTGCGACTCGTACC
AAAATGTTAAGCAGTATGGCGAAGAACGTGGCGCGCTGGAGTCGTGAATGTTTGGGTCCTTGATGATGG
ACTACGGTAGTAAGTATGTAGTAGTTGCAACTTCATATGTTTCACTTCTGATCCAAGGAAGAGCGGTTAT
GAATTAATCTCTTGGCATGAGCGGACGGGTAAGGGGACACCGCTTTTCTTCGATGGGAATCAGGGTAA

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TGGTATATGATGGATTATTTGTGGAATCATTTAGTACGGCAGATGTTGAAAAAAAAAGCAGAAAATTTTT
GAATTTTTTCGTTGACATTGGAAGATTTTCGTAGTGGAAACAGCTGCAATTGCTTGTAAAGTAGTAACC
CCTCCTTTTGTACAAAGAGAGCGAATATTTCTTAGGGAGGTTTAAAGAATAGAACATCTCACACCAGAC
GCGACTCATAATTCATAATGCCAATTGACCAAGAAAAATTAGCTAAGCTACAAAAGTTGTCTGCTAACA
ACAAAGTTGGTGGTACTAGAAGAAAGCTTAACAAGAGGCAGGCTCTTCTGCCGGTGCCAAACAAGGATG
ACACCAAGTTGCAAAGTCAATTAGCTAAGTTGCACGCTGTCACCATTGACAACGTCGCCGAAGCCAAT
TTTTCAAGGACGACGGTAAGGTCATGCACTTCAACAAGGTCGGTGCTCCAAGTTGCTGCTCAACACAACA
CTTCTGTATTCTACGGTCTACCACAGGAAAAAGAACTTGCAAGATTTGTTCCAGGTATTATCTCTCAAT
TGGGCCCCGTAAGCCATCCAAGCCTTGTCTCAATTGGCTGCCCAAATGGAAAAGCACGAAGCCAAGGCTC
CAGCTGATGCTGAAAAGAAGGATGAAGCTATTCCAGAGTTAGTTGAAGGTCAAAC'TTTTGATGCTGACG
TCGAATAA

YPL037C, 157 aa (SEQ ID NO 378)

MPIDQEKLAQLKLSANNKVGGRRLNKKAGSSAGANKDDTKLQSQLAKLHAVTIDNVAEANFFKDDG
KVMHFNKVGQVAAQHNTSVFYGLPQEKNLQDLFPGIISQLGPEAIQALSQLAAMEKHEAKAPADA EK
KDEAIPELVEGQTFDADVE

YPL079W, 1404 bp, exon1: 501-511, intron1: 512-932, exon2: 933-1404
(SEQ ID NO 381)

AAATAGGACGAAGAACTTTTTATATACGAGCATTTCCTAATTAGTAGGAAGCGGAAAAATAATAATATAA
GAAAGTAAACGCAAAAGATAGGCTGACTGCCTTCATTGACTAGGAGGTGAGGCGACATATTTGTCACC
ATTCAAGTTACCGAGATGGTAGAGAGGTGGATGGCTCGGGTGAGCTTGATTGTACACTGCAGCAACGAT
GCTTTTTCTACCCATTTTATGAAGTTTAACATCCGTACCTTTCCACCTCCAAACATTTTTTGTAACTTC
GTCCTTTGAAAAATCAAGAAGTAATAGGTGTGCAGTAGGAGGCGGCTTGAGCGCGCAATATCGGTGAGT
GAGGTAAAGATCCATCCATACCTTAGCAAAATAGGTAGTGAGGAGGCCAACTGTATTGCGTTAAAGGCAA
AAGGATTGGTATATACGAATGATTGGTAATTTGAAAAGTAGGTTTGAATCAAAAGAACTGAGACAGTC
AAGGACACTAAACAAAAATGGGTAAATCGTATGTCCATATAACTTCAAAATGAAAATATAGCAGTTGAA
ACATATCAATTAAATCATTATACATCTCCAATAAACATGTATGCAAGAGGAAAGCGTAAATATCTTCGA
TTTCGACAATACTTTGCTACTGAACTAAAAATGAAAATGAAGTTGAATTCTCAAAGGAATGTGATGCAA
GTTTCGTTAATTAAATATGGTTTGTAGTGAATTATCATAGTTTGTGATAGATACACACGAGGAGTAGTGA
GCAAAGCAAGTGCAACAGCAATGATATGTTAGCAGGAAATAATATTATAAATTGGATATTGTGTGTTTT
TTTGATATATGTTTGTGCGAAGCTAATACAGAATGATTACTAAGTGAATTTAAAAGCACAAATCATGCTC
TTGGATGATTGATCTATTAAAAAATTATAAAACAGACATGGTTACAGATCTCGTACACGTTACATGTTT
CAACGTGACTTCAGAAAGCATGGTGCCGTTACATGTCCACCTACTTGAAGATCTACAAGGTTGGTGAC
ATTGTGACATCAAAGCCAATGGTTCTATCCAAAAGGGTATGCCACACAAGTTCTACCAAGGTAAGACC
GGTGTGCTCTACAACGTTACCAAGTCTTCTGTTGGTGTATCATCAACAAGATGGTCCGTTAACAGATAC
TTGGAAGAGAGATTGAACTTGAGAGTTGAACACATCAAGCACTCTAAATGTAGACAAGAAATTTTGGA
AGAGTTAAGGCCAATGCTGCTAAGCGTGCTGAAGCCAAGGCCAAGGTGTTGCTGTCCAATTGAAGAGA
CAACCAGCTCAACCAAGAGAATCCCGTATTGTCTCTACTGAAGGTAACGTTCCCTCAAAC'TTTAGCTCCA
GTTCCATACGAAACCTTCATTTAA

YPL079W, 161 aa (SEQ ID NO 382)

MGKSHGYRSRTRYMFQRDRKHGAVHMSTYLLKIYKVGDIVDIKANGSIQKGMPhKFYQgktGVVYNVTK
SSVGVIIINKMVGNNRYLEKRLNLRVEHIKHSKRQEFLErvKANAAKRAEAKFAQGVAVQLKRQPAQPRE
SRIVSTEGNVPQTLAPVPYETFI

YBL109W 836bp CDS: 501 836 (SEQ ID NO 35)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTTCGTTTCAATTTCCATGGTG
CACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGTTGCTCAGCCGCTTCGTGG
ATATTCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTCTCGAAAAGACCAATATAATAAAAAGTT
ATAAATTACATTTTCCTTATTAGGTATACGACCTCGCGCTTCGAAGTAGAGGAGCCCTTTTTGGCGTACC
TACATATGGCGCGTCAGACAGACAAACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGAC
CCATTACCCACGACGTATCAAGTTACTTTCCTTGGTGAATGTCCCACTATAAAAAAATTCCTTGACGC
TAGATCGTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATGCTTATTTTCGTACAAGGT
TACTTCTTAGATGCTATATGTCCCTACGGCCTTGCTTAACACCATCCAGCATGCAATACAGTGACATAT
ATATATACCCTAACACTACCTTAACCTACCTTATTTCAACCTTCCAACCTGTCTCTCAACTTACCT
CACATTACCTACCTCTCCACTTGTACCTGTCCCATTCACCATACCACTCCCAACCACCATCCATC

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CCTCTACTTACTACCACCAATCAACCGTCCACCATAACCGTTACCCCTCCAATTAGCCATATTCAACTTC
ACTACCACCTTACCCTGCCATTACTCTACCATCCACCATCTGCTACTCACCATACTGTTGTTCTACCCCTC
CATATTGA

YBL109W 111aa (SEQ ID NO 36)

MSLRPCLTPSSMQYSDIYIPNTTLLPYFNPNSLSLNLPSHYPTSPLVTLSSHSTIPLPTTIHPSTYYH
QSTVHHNRYPPISHIQHLHYLPCHYSTIHHLLLTILLFYPPY

YHR094C 2213bp CDS: 501..2213 (SEQ ID NO 205)

GCATTGAGTCAAAAGTTTTTCCGAAGTGACCCAGTGCTCTTTTTTTTTTCCGTGAAGGACTGACAAAT
ATGCGCACAAGATCCAATACGTAATGGAATTCGGAAGAACTAGGAAGAAATGCTGCAGGGCATTGCCG
TGCCGATCTTTTGTCTTTTCAGATATATGAGAAAAAGAAATTCATCAAGTGCTGATAGAAGAATACCAC
TCATATGACGTGGGCAGAAGACAGCAAACGTAAACATGAGCTGCTGCGACATTTGATGGCTTTTATCCG
ACAAGCCAGGAACTCCACCATTATCTAATGTAGCAAAATATTTCTTAACACCCGAAGTTGCGTGTCCTC
CCTCACGTTTTTAATCATTTGAATTAGTATATTGAAATTATATATAAAGGCAACAATGTCCCCATAATC
AATTCCATCTGGGGTCTCATGTTCTTTCCCCACCTTAAATCTATAAAGATATCATAATCGTCAACTAG
TTGATATACGTAATAATCATGAATTCAACTCCCGATCTAATATCTCCTCAGAAATCCAATTCATCCAACT
CATATGAATTGGAATCTGGTCTGTTCAAAGGCCATGAATACTCCAGAAGGTAAAAATGAAAGTTTTACCG
ACAACCTAAGTGAAAGTCAAGTGCAACCCGCCGTTGCCCTCCAAACACCGGAAAAGGTGTCTACGTAA
CGGTTTTCTATCTGTTGTGTTATGGTTGCTTTCCGTGGTTTTCATATTTGGATGGGATACTGGTACCATT
CTGGTTTTGTTGCTCAAACCTGATTTTCTAAGAAGATTTGGTATGAAGCACCACGACGGTAGTCATTACT
TGTCCAAGGTGAGAACTGGTTTAATTGTCTCTATTTTAAACATTGGTTGTGCCATTGGTGGTATCGTCT
TAGCCAAGCTAGGTGATATGTATGGTCGTAGAACTCGTTTATTGTTGTCGTTGTAGTAATCTACACTATCG
GTATCATTATTCAAATAGCCTCGATCAACAAGTGGTACCAATATTTTCATTGGTAGAATTATCTCTGGTT
TAGGTGTCGGTGGTATCACAGTTTTATCTCCCATGCTAATATCTGAGGTGCCCCCAGTGAAATGAGAG
GCACCTTGGTTTTCATGTTACCAAGTCATGATTACTTTAGGTATTTTCTTAGGTACTGTACCAATTTTG
GTACCAAGAATTACTCAAACCTCTGTCCAATGGAGAGTTCCATTAGGTTTGTGTTTCGCCTGGGCCPTAT
TTATGATTGGTGGTATGATGTTTGTCTCTGAATCTCCACGTTATTTGGTTGAAGCTGGCAGAATCGACG
AAGCCAGGGCTCTTTAGCTAAAGTTAACAATGCCACCTGACCATCCATACTCAATATGAGTTGG
AAACTATCGAAGCCAGTGTCGAAGAAATGAGAGCCGCTGGTACTGCATCTTGGGGCGAATTATTCACTG
GTAAACCAGCCATGTTTCAACGTACTATGATGGGTATCATGATTCAATCTCTACAACAATTAACGGTG
ATAACTATTTCTTCTACTACGGTACCATTGTTTCCAGGCTGTGCGTTTAAAGTGACTCTTTTGAAACTT
CTATTGTCTTTGGTGTGCTCAACTTCTTCTCCACTTGTGTTCTCTGTACACCGTTGACCGTTTGGCC
GTCGTAACGTGTTGATGTGGGGTGCTGTGCGGTATGGTCTGCTGTTATGTTGTCTATGCCTCTGTTGGTG
TTACCAGATTATGCGCCAAACGTCGAAGATCAACCATCTCAAAGGGTGCTGGTAACGTATGATGTTT
TCGCATGTTTCTACATTTTCTGTTTTCGCTACTACCTGGGCCCCAATTGCTTACGTTGTTATTTTCA
GATTTCCCATTAAGAGTCAAAATCCAAGTGATGTCTATTGCCAGTGCTGCTAACTGGATCTGGGGTTTCT
TGATTAGTTTCTTACCCCATTTATTACTGGTGCCATCAACTTCTACTACGGTTACGTTTTCATGGGCT
GTATGGTTTTCGCTTACTTTTACGCTTTTTTCTTCTGTTCCAGAACTAAAGGTTTATCATTAGAAGAAG
TTAATGATATGTACGCCGAAGGTGTTCTACCATGGAAATCAGCTTCTGGGTTCAGTATCCAAGAGAG
GCGCTGACTACAACGCTGATGACCTAATGCATGATACCAACCATTTTACAAGAGTTTGTTTAGCAGGA
AATAA

YHR094C 570aa (SEQ ID NO 206)

MNSTPDLISFPQKSNSSNSYELESGRSKAMNTPPEGKNESEFHDNLSESQVQPAVAPPNTGKGVYVTVSICC
VMVAFGGFIFGWDGTISGFVAQTDFLRRFGMKHHDGSHYLSKVRTGLIVSIFNIGCAIGGIVLAKLGD
MYGRRIGLIVVVVIYITIGIIIIQIASINKWYQYFIGRIISGLVGGITVLSPLISEVAPSEMRGTLVSC
YQVMITLGIPLGYCTNFGTKNYSNSVQWRVPLGLCFWALFMIGGMMFVPESPRYLVEAGRIDEARASL
AKVNKCPDPHPYIQYELETIEASVEEMRAAGTASWGELFTGKPA MFQRTMMGIMIQLQLTGDNFFY
YGTIVFQAVGLSDSFETSIVFGVVNFFSTCCSLYTVDRFGRNCLMWGAUGMVCCYVVYASVGVTRLWP
NGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIAYVVISSECFPLRVKSKCMSIASAANWIWGLISFFT
PFI TGAINFYGYVFMGCMVFAYFYVFFVPETKGLSLEEVNDMYAEGVLPWKSASWVPVSKRGADYNA
DDLHDDQPFYKSLFSRK

YBL099W 2138bp CDS: 501..2138 public: 1..2138 (SEQ ID NO 693)

CCCGGGTGATGCAGTTGCGGCCGCGCCCTGGCCAATCAGATCCCTTTAAAAATGGGCCCCGGTGCGCTTCT
ACCCCTTCACGCCCTTTTACGCCCTTTTTCGAATCTTGTTATTTATTTGTAATTTATTAACATTTGGTCATATC
AAATTCACATCAGACTTCAATTTTCAATTCATTTCTGAATAAGAGCCCTTCCCTTCATACAAGTAGA
GATATTATACTGTCATAGCTCTTTCAATTGGTCTTATTAGATTGCTCCATCTTTCCCATTTGACGTTGT
TACTCCCTCTCTTTTTCGTTTTTAACTGATTTCTCATATATTTCCAAACAGGCATATATACTCGACGT
CAAGAAAGAAAAGAAAAGAAAACCCTCATAAAAAATATAATCGAGAAGTTTTTTTCTCATCGCGAACC

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ATTAGTATAACAGATTGATCGTTCAGCTCTCATAACTATCGCAAGAACAGTAACAAAATAAATAAAAA
AACACGCACATATAATAATGTTGGCTCGTACTGCTGCTATTCGTTCTCTATCGGAACTCTAATTAAC
CTACCAAGGCCGCAAGACCTGCCGCTGCTGCTTTGGCTTCCACCAGAAAGATTGGCTTCCACCAAGGCAC
AACCCACAGAAGTTTCCCTCCATCTTAGAGGAAAGAATTAAGGGTGTGTCCGACGAGGCCAATTTGAACG
AAACTGGTAGAGTTCTTGACGTCGGTGATGGTATTGCTCGTGTTTTGGTTTGAACAACATTCAGGCTG
AAGAATTGGTCGAGTTCTCTCTGGTGTTAAAGGTATGGCTTTGAACTTGGAGCCTGGTCAAGTCGGTA
TCGTTCTTTTCGGTTCCGATAGACTGGTTAAAGAAGGTGAATTGGTCAAGAGAACCGGTAATATTGTTG
ATGTCCCAGTCGGTCCAGGCCTTTTGGGTAGAGTTGTGACGCTTTAGGTAACCCATTATGATGGTAAAG
GTCCTATTGACGCTGCCGGTCTGTTCAAGAGCTCAAGTCAAAGCACCAGGTATTTTGCCAAGAAGATCTG
TCCATGAACCAGTTCAAACCGGTTTGAAGCCGTTGACGCCCTGGTCCCTATCGGTAGAGGTCAAAGAG
AGTTGATTATTGGTGATCGTCAAACAGGTAAGACTGCTGTCCCTTAGACACCATCTTGAATCAAAGA
GATGGAATAACGGTAGTGACGAATCCAAGAACTTTACTGTGTTTACGTTGCCGTTGGACAAAAGAGT
CTACCGTTGCTCAATTTGGTCCAACTTTGGAACAACATGACGCCATGAAGTACTCTATTATTGTTGCAG
CTACTGCATCTGAAGCCGCTCCTCTACAATACTTGGCTCCATTTACTGCCGCATCCATTGGTGAATGGT
TCAGAGATAATGGAAGCAGCCTTGATCGTCTATGACGATTTGTCCAAGCAAGCCGTGGCATAACCGTC
AATTATCTTTGTTGTTGAGACGTCCTCCTGGTCTGAAGCCTACCCCTGGTGATGTCTTTTACTTGCATC
CAAGATTGCTAGAAAGAGCCGCTAAGCTTTCTGAAAAGGAAGGTTCTGGTTCTTTAACTGCTTTGCCTG
TTATTGAAACCCAAGGTGGTGATGTCTCCGCTTATATTCCAACCAATGTTATTTCCATTACCGATGGTC
AAATATTCTTGAAGCTGAATTATTCTACAAGGTATCAGACCTGCCATTAAACGTTGGTTGTCCGTTT
CTCGTGTCCGTTCCGCTGCTCAAGTTAAGGCTTTGAAGCAAGTCGCTGGTTCTTGAAATTGTTTTGG
CTCAATACAGAGAAGTCGCTGCTTTTGCTCAATTCGGTTCCGATTTAGATGCCTCCACCAAGCAAACCT
TGGTTAGAGGTGAAAGATTGACTCAATTGTTGAAGCAAAACCAATATTCTCCTTTGGCTACAGAAGAAC
AGGTTCCATTGATTATGCGCGGTGTTAATGGTCATTTGGATGGTATTGAACTATCAAGAATTGGTGAAT
TTGAGTCCTCCTTTTGTCTATCTAAAATCCAATCACAATGAGCTTTTGACCGAAATTAGAGAAAAGG
GTGAATTGTCTAAAGAATTGTTGGCATCTCTAAAGAGTGCTACTGAATCATTTGTTGCCACTTTTAA

YBL099W 545aa public: 1..545 (SEQ ID NO 694)

MLARTAAIRSLSRTLINSTKAARPAALASTRRLASTKAQPTVSSILEERIKGVSDKANLNETGRVL
AVDGIARVFLNNIQAEELVEFSSGVKGMALNLEPGQVGIIVLFGSDRLVKEGELVKRTGNIVDVPVGP
GLLGRVVDALGNPIDGKGPIDAAGRSRAQVKAPGILPRRSVHEPVQTGLKAVDALVPIGRGQRELIIGD
RQTGKTAVALDITLQKRWNGSDESKKLYCVYVAVGQKRSTVAQLVQTLQHDAMKYSIIVAATASEA
APLQYLAPFTAASIGEWFRDNGKHALIVYDDLQKAVAYRQLSLLLRPPGREAYPGDVLYLHPRLLER
AAKLSEKEGSGSLTALPVIETQGGDVSAIPTNVISITDGQIFLEAELFYKGIRPAINVGLSVSRVGS
AQVKALKQVAGSLKFLAQYREVAFAQFGSDLDASTKQTLVRGERLTQLLKQNYSPATEEQVPLIY
AGVNGHLDGIELSRIGEFESSFLSYLKSNNHLLTEIREKGELSKELLASLKSATESFVATF

YDR504C 884bp CDS: 501..884 public: 1..884 (SEQ ID NO 695)

TAAAAGCCTTGCCATATGCTCAGAGTAAATTACAAGCGTTAAATGATAATTCAAAATCTCAAAATACAA
ATGACAGTTCTTCCAATAATTTACGAATGCTGCAACTTATTCAAAGCCTAAATTGAATATCAAGATTT
TAAACGCAGAATTTCAATTTGATAGAAAGGAATTAACGTTTACTACGTTTGTGAGGAGAGAAATGATT
TTAGAGACTTGATAAAAGAGCTGTTCAAATATTACAAGACAAGAATTTGGTTGTGTGCCATCCCGAATA
ATCTGTCTATTGATTCTAAGTATTATGATAAAACAAGAGCTGAAATTTATATCAAAACATAGTAA
AAAATTACAATGCTGAAGATTTAATGAATGTCAATGAGTTTTCGAGAACAGGGGGAATAACAGAGTTA
ATTTTGACCTCCGTGTAACGAAATGAACTCGACAACCTTTCAGATTGCTGTGTATGAAGAATTAGTTC
ACGAATTATTTTCAATTAATGATCTGTTATTTCCCTGTTGTAACCTATAAATTTCTAAAAGAAAAGACAA
CCATTTGCCATTATTTGTTAACATTTTTCATTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT
TTTTGTGCTACTTTTTTATGTTATTTTGTGTTTATCGTTTCTGTTGTTTACCTATTTTCTGCTGCT
ATTCAATTTGGTACTATCTTTCTATTATCAATATTTCTTTCCCTTATGTTTTTTTTCTATATGAAACT
TCACAGGGAGAAATAGAAAGAAATGTTCAATTATCTGTTTAACTTTGATAAAAATTACTTATACGTCTC
CCAATCATGGTTTCATGGTCACTGGTAAGGAAAAATTCGAAAAACTACGGGACTAA

YDR504C 127aa public: 1..127 (SEQ ID NO 696)

MICYFLVVTINFLKEKTTICHYFVNIFSLFLFVVFVVFVFFVYVILFYRFCSLFTYFPANSIWWY
LSIINIFFPLCFFLYENFTGRNRRKCSLFLTLIKITYTSPNHGFMVTGKEKFEKLRD

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YEL032W 3416bp CDS: 501..3416 public: 1..3416 (SEQ ID NO 697)

TATCTACCGGCTGCAAGCAGCCGGTCGGTGGCAAATCCGGCGCTTCCCCCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAGGGAACCTCTCAGAACGGGGGAGGTTGAAGAGCAGGCCAAGGGAATATTAGTTTTGACCTA
TGTGGGAAACAGAATTTTCAATGAGTTATGGCAACTTGGCCGAGTGGTTAAGGCGAAAGATTAGAAATC
TTTTGGGCTTTGCCCGCGCAGGTTTCGAGTCCCTGCAGTTGTCGTTATTTTTCTCTTTTTTTCAATTTCC
CTTGTTTCGTCAGATCGAGGCGGTAGAAGAAACAATTACTTTTCTAAATGGGTAAAACTCGTGTTTTA
GGAAAAAAAAAGAAAAATTTGGTCAAACTCGAAAGATAGGTTCTTAATCTCTTTCAAGTTGAAAAGGC
CTACGCTCTTTTCTTGAAGCATTTTCATCCTACTGCTCGTATTGAACCTCCACTATAAGCGCACCAAAA
AGATACAAACGTCAATTATGGAAGGCTCAACGGGATTGTATGGAGACGCTACTACTTTTTTTCGCTCCAG
ACGCTGTGTTTGGTGACAGAGTGCGCAGATTTCAGAGTTTATTAGATACTTTCACCTCATACAGAGACT
CTGTAAGGTCCATACAGTTTACAACAGCAATAACGCGCCAACTACAACGATGATCAAGATGACGCAG
ACGAACGAGATTTGCTAGGTGATGACGACGGTGATGATCTTGAAAAAGGAAAAAGAAAGCAGCATCGTCCA
CCTCATTTGAATATACTCCCTCACAGGATTATCATCTCGCTTGATGACTTGAGAGAAATTCGACAGGTCGT
TCTGGTCCGGCATTTTAGTCGAACAGCATACTTCATCCCGCTGCCGAAAAGGCGCTTACTGACCTAG
CAGATTCCATGGACGATGTTCCACATCCCAATGCCCTGTCAGTATCGTCTCGCCATCCTTGGAAGCTTT
CGTTCAAAGGCTCATTTGGTGACACGCATTGTCCTCGTACTCTAACGGCACAACATTTAAACAAAC
TGGTCTCTGTTGAGGGTATCGTAACTAAGACTTCGTTGGTCAAGGCCAAAGCTTATCAGATCTGTCCACT
ACGCGGCAAGAGACTGGTAGATTCCATTACAGAGATTATACAGATGCTACTACAACCTCACACCACCGCA
TCCCAACGCCCTGCCATCTATCCAACGGAGGACACTGAAGGTAACAAACTAACCCACGAATATGGGTATA
GTACGTTTCATAGACCATCAGCGTATCACTGTGCAAGAAATGCCGAAATGGCCCCCGCTGGCCAACTTC
CCAGGTCCATTGACGTCATTCTCGATGACGACCTTGTGGACAAGACCAAGCCAGGTGACAGAGTTAACG
TTGTCCGGGGTATTCAAGTCGCCTGGTGTGGTGGCATGAACCAAGTCCAACCTCTAATACATTGATCGGGT
TCAAAACTCTGATCCTAGGTAATACGGTGTATCCTCTCCACGCCAGATCCACGGGTGTCGCTGCGAGAC
AAATGTTGACAGATTTTCGATATAAGAAATATCAATAAACTATCCAAAAAAGGACATTTTCGATATCT
TGTCTCAATCTTTAGCGCCTTCTATTTATGGACATGACCATATAAAGAAAGCCATTTTATTGATGCTCA
TGGGAGGTGTGGAGAAAAATTTAGAAAAATGGCTCGCATTTAAGAGGTGACATCAATATCCTAATGGTGG
GTGATCCATCCACTGCCAAGTCCCAATTGCTAAGGTTTGTGTTGAATACAGCATCACTGGCAATTGCTA
CTACTGGTAGAGGTTCTTCCGGTGTGCGTTTGACCGCAGCGGTCACTACTGATAGGGAAACAGGTGAAA
GAAGACTAGAGGCTGGTGCCATGGTTCTTGCTGACCGCGGGGTGTATGTATTGATGAATTTGATAAGA
TGACAGATGTGGATAGAGTCGCCATTTCATGAAGTAATGGAACAACAAACGGTGACGATTGCCAAAGCAG
GTATTCACACAACATTAATGCTCGTTGTAGTGTATTGCTGCCGCAATCCCGTTTTTGGGCAGTACG
ATGTCAATAGAGATCCACACCAAAACATTCGCCCTACCGGACTCGCTGTTGTCGTTTTGATTTACTAT
TTGTTGTGACAGCATATCAATGAAGTACAGAGATAGATCCATTAGTGAGCATGTCTTAAGAACACACA
GATATTTGCGCTCCAGTTATTTAGAGGGTGAACCTGTGAGAGAGCGTTTGAATTTATCATTTAGCCGTTG
GGGAGGATGCAGATATAAATCCTGAAGAGCATTCCAACTCCGGGGCTGGTGTAGAAAAATGAAGGAGAAG
ATGATGAAGACCATGTCTTTCGAAAAGTTCAACCCCTTATTACAAGCAGGTGCTAAGTTAGCAAAAAACA
AAGGTAACATAACGGTACAGAAATTCCAAAGCTAGTCACCATCCCATTTCTTAAGAAAGTACGTTCAAT
ATGCCAAGGAAAGGGTTATTCCACAGTTAACACAAGAAGCCATCAATGTTATTGTGAAAAATTATACTG
ATTTAAGAAACGATGATAATACCAAAAAATCGCCATTACTGCAAGAACTTTGGAGACTTTGATCAGAT
TAGCCACAGCTCACGCCAAAGTCAGGTTATCCAAAACAGTCAACAAGGTGGATGCTAAAGTGGCTGCCA
ATCTACTAAGGTTTGCATATTGGGTGAGGATATCGGCAATGATATCGATGAAGAGGAAAGTGAATACG
AAGAAGCTTTGTGCAAGAGGTCTCCACAGAAATCACCGAAAAAAGACAAAGAGTCAGACAACCAGCAA
GCAACTCTGGATCCCCAATCAAATCTACTCCAAGAAGGTCAACGGCATCTTCCGTTAATGCCACGCCAT
CGTCAGCACGCAGAAATATTACGTTTTCAAGATGACGAACAGAACGCTGGTGAAGACGATAACGATATAA
TGTCACCGCTTCCCTGCGGATGAGGAAGCTGAATTACAAAGAAGGCTTCAACTGGGGTTGAGAGTGTCTC
CAAGACGTAGAGAACATCTTCACGCACCTGAGGAAGGTTTCGTCGGGACCTCTTACCGAGGTCCGTACTC
CAAGATTACCTAACGTATCTTCTGCAGGTGAGGATGATGAGCAACAACAGTCAGTTATTTCTTTTGACA
ATGTGGAGCCTGGTACCATTTCTACTGGTAGATTGTCTTTAATCTCAGGTATTATTGCGCGTCTGATGC
AAACAGAAATATTTGAAGAAGAATCCTATCCTGTGGCCTCTTTGTTTCGAAAGAATCAACGAAGAATACT
CGGAGGAGGAAAAATTTCCGCTCAAGAATATTTAGCAGGTTTGAAGATCATGTGCGACAGAAATAACT
TAATGGTTGCTGACGATAAAGTTTGGAGAGTCTGA

YEL032W 971aa public: 1..971 (SEQ ID NO 698)

MEGSTGFDGDATTFAPDAVFGDVRRFQEFLLDTFTSYRDSVRSIQVYNSNNAANYNDQDDADERDLL
GDDDDDDLEKEKKAASSTSLNILPHRIIISLDDLREFDRSFWSGILVEPAYFIPPAEKALTDLADSMDD
VPHPNASAVSSRHPWKLSFKGSFGAHALSPRTLTAQHLNKLVSVEGIVTKTSLVRPKLIRSVHYAAKTG

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RFHYRDYTDATTTLTTRIPTPAIYPTEDTEGNKLTTEYGYSTFIDHQRTVQEMPEMAPAGQLPRSIDV
ILDDDLVDKTKPGDRVNVVGVFKSLGAGGMNQSNSTNLIGFKTLILGNTVYPLHARSTGVAARQMLTDF
DIRNINKLSKKKIDFIDLSQSLAPSIYGHDIKKAILMLMGGVEKNLENGSHLRGDINILMVGDPSTA
KSQLLRFVLNTASLAIATTGRGSSGVGLTAAVTTDRETGERRLEAGAMVLADRGVVCIDEFDKMTDVR
VAIHEVMEQQTVTTIAKAGIHTTLNARCSVIAAANPVFGQYDVNRDPHQNIALPDSLLSRFDLLFVVTDD
INEIRDRSISEHVLRTHYRLPPGYLEGEPPVRERLNLSLAVGEDADINPEHSNSGAGVENEGEDDEDHV
FEKFNPLLQAGAKLAKNKGNYNGTEIPKLVITPFLRKVQYAKERVIPQLTQEAINVIVKNYTDLRNDD
NTKKSPIPARTLETLIRLATAHAKVRLSKTVNKVDAKVAANLLRFALLGEDIGNDIDEESEYEALSK
RSPQKSPKKRQVRVQPASNSGSPKSTPRRSTASSVNATPSSARRILRFQDDEQNAGEDDNDIMSPLPA
DEEAELQRRQLGLRVSPRRREHLHAPEEGSSGPLTEVGTPLRPNVSSAGQDDEQQQSVISFDNVEPGT
ISTGRSLSLISGIIARLMQTEIFEESYPVASLFERINEELPEEEKFSAQEYLAGLKIMSDRNNLMVADD
KVWRV

YGR146C 1136bp CDS: 501..1136 public: 1..1136 (SEQ ID NO 699)

CTTTTCAGTTGGGCATCTTTTTTTTTTTCACAATTAGGCCGCCCTTTTTTCCCAAATTGGCACTTGTTTGTA
CGATCTTTAGCTAGAACTTGGAGACCTGAAACGTGGTGATTCTTATATTTAAAGGAATACCGATCTTTT
CCGTTTTCAACACCCCAATTGTGAGAATTTTATTTCTTGCAATTCGGAAAATTTAGATACATTCACATCC
ATACTTGGACACATATATATATACAATATAATCATTGACACAGGCCATCGCCATTGAGTAAACTGTCTT
TGAACGTGTCTAAAGAACTTAGAACTATAGTGTTGTCCCAAGAAGTTAAAAATTGAACACTTGTGAGAAT
TATAAACAGAGTAAGCAAAGAAAGAATAGAGAAACAATACTCCGCTACCGATTCTCCTTTTTTTCCTT
ATAAAAAAAGCTCGAGAATAATTACTTTATTCTTATCCCTCCACTCCTTTCAGGTATTCTTTACCGATT
TGCATATCAATCATATAATGAGCACCGCATTCAACGATTACTGCACTGTTTGTGATCGTCTCATTCCAA
CATCTCCACAGAAAACGAACATTAATACCGAAGATCCAAAGGGACAATGAAACCAAGAGCAGTTTAC
AATCAAATAAGTTATATTGCTCCGAAGATTGTAAGCTGAAGGATTGCAACCTCTTAATGAGAAATPAT
TATCCCACTTGCATAAAAAATCAAAAACCTTCTCATTCGCATAATCTCACTCCACCGCTTTCATATCTTA
AAAATTTAACTGCATCAAAACCTCTTCGAGCCGACTACCTCACTATCTTCATCTCCGACATCTTCAACTA
TCCCCTTTGACGAGTTGGAGAAGCTAGAGTCTTATTAATTTACCATTGCTGCTACCTCAGGATGGTA
TAGTCAATCCTAAGCAGGAGTCTAATCCTTCTCGTGTGACGAATATGATGAAAATGAACATTATTTGA
ACTTAGCCGACTCTCTTAGACTCGATTCTAGTTACCAATTGCATTCAAAGGCACATTTGGGTTACGAAA
ACAACCTGCCACGATCAAACGATCTAATTGATGATCATTTGATCTCAGATCAGATCATTGAGAATAACT
ACAACCTATGGTTTACTATCTCCAGTTAA

YGR146C 211aa public: 1..211 (SEQ ID NO 700)

MSTAFNDYCTVCDRLIPTSPQKTNINTRKIQRDNETKSSSLQSNKLYCSEDCKLKDSNPLNEKLLSHLHK
KSKTSHSHNLTPLPSYSKNLTASNLFEPSTSLSSSPTSSTIPFDELEKLESLLISPLLLPQDGI VNPQ
ESNPSRVDEYDENEHYLNLADSLRLDSSYQLHSHKALGYENNLP RSNLDLIDHLLISDQI IENNYNLWFR
LSSS

YHR135C 2117bp CDS: 501..2117 public: 1..2117 (SEQ ID NO 701)

AGAGTATAACGAGTACATTAATGAGAAAGATTCAAGTAGAGCGCAGCGTCAAACGCTGCCGCCGTTTT
AAGCAAGCTCGCCCATGACTTTTGGGAGAACGACTGTGTCAATTGACGAAGACATATTCGAAGATTCTGTC
TGACGAAGAACAATCATGATTGCATCTCTTAATCGTTACACATACATACCTTCTACCTCTGTACTGTTA
CATATGCATTGACTTTACGATCTAATATAAATCCTTTTGATGTTACCCCGCTGTGGGCTCGTCTCCT
TTCGTTTCTTACGATTTTTTCGCCGAACAAGAAAAACAGAACAAAAAAATCAGCGATCGTATACAT
GGGTCTTTGATTTCTGCTTGCTTCTTACAAACAACAACGCAACCGTTTATTGAGTGCTCTGTGACTG
GTTTTCATGTGGATGCCATAGTAGAGAAAAGACACATACAAAAATTCGCGCATTCGCTGGCCCTTTTC
CTGCTCTCCTCTTCCCCATGTCCATGCCCATAGCAAGTACCCTCTAGCAGTTAACAACCTCACCATA
TAAACGGAAACGCAAAATPTTAACGTACAAGCAACAACAACCTCCACCACCAGGCTGTGACTCGCCCG
CAAGATCTTCGATGACCGCCACGACCGCCGCAACTCCAACAGCAACTCTTCCAGAGATGACTCTACTA
TTGTCCGCCCTACATTACAAGATCGGCAAAAAAATAGGGGAAGGTTTCTTTGGTGTGCTATTTGAAGGTA
CTAATATGATCAATGGCGTACCCGTCGCGATCAAATTCGAGCCCAGAAAAACGGAGGCCCTCAATTAA
GAGATGAATATAAAACATATAAAATTCGAATGGCACTCCCAATATCCCTACGCGTACTACTTCGGCC
AAGAAGGTTTGCACAATATCTTGGTCATTGATCTTTTGGGTCCCTCTTTGGAAGATTTATTTGATTGGT
GTGGAAGAAAATTTCTGTCAAAACGGTTGTGCAAGTTGCTGTCCAAATGATTACTTTGATTGAAGACT
TGCACGCACATGACTTGATATACCGTGATATCAAACCAGACAATTTCTTGATTGGAAGGCCCGGCCAAC
CTGACGCAACAACATCCATTTGATCGACTTCGGTATGGCCAAACAGTATCGTGATCCGAAAACCTAAAC

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AGCACATCCCATATAGAGAGAAAAATCACTCAGCGGCACTGCCAGATATATGTCCATTAATACTCACC
TTGGAAGAGAGCAGTCCAGAAGAGATGATATGGAGGCCCTTGGGTCACGTTTCTTTTATTTCTTGAGAG
GCCACTTACCCTGGCAGGGTTTAAAAGCTCCAAACAATAAGCAAAAATACGAAAAGATTGGTGAAAAGA
AAAGATCTACTAACGTTTACGATCTAGCTCAAGGCTTACCTGTGCAATTTGGCAGGTATCTAGAAATCG
TCAGAAGTC'TTTCCTTTGAAGAGTGTCCCGATTATGAAGGCTATAGAAAATATTACTATCTGTACTGG
ATGATTTAGGTGAAACCGCGGACGGCCAATATGATTGGATGAAACTGAACGATGGCCGTGGTTGGGATC
TTAACATAAACAAGAAGCCAAATCTCCACGGATACGGCCATCCAAATCCACCAAAACGAAAAATCGAGAA
AACATAGAAACAACAGCTCCAAATGCAACAGCTCCAAATGCAACAGCTCCAACAACAGCAACAGCAAC
AGCAATATGCTCAAAAAACTGAGGCAGATATGCGCAATTCTCAATATAAACCAAAAGTTAGACCCTACTT
CTTATGAAGCTTACCAGCATCAAACCCAGCAGAAATACCTGCAAGAACAACAAAAGAGACAGCAGCAAC
AAAAACTTCAGGAGCAACAACCTTCAAGAGCAACAATTGCAACAGCAGCAACAGCAACAGCAACAGCTAC
GTGCAACAGGCCAACCTCCATCTCAGCCTCAAGCGCAAACTCAATCTCAGCAGTTTGGCGCTCGTTATC
AACCACAACAACAACCTTCTGCTGCTTTAAGAACTCCTGAACAGCACCCAAATGACGATAATTCAAGTC
TAGCTGCTTCTCATAAGGGCTTTTCCAAAAATTAGGTTGTTGCTAA

YHR135C 538aa pulic: 1..538 (SEQ ID NO 702)

MSMPIASTTLAVNNLTNINGNANFNVQANKQLHHQAVDSPARSSMTATTAANSNSNSRRDDSTIVGLHY
KIGKKIGEGSFGVLFEGTNMINGVPVAIKFEPKTEAPQLRDEYKTYKILNGTPNIPYAYYFGQEGLHN
ILVIDLLGPSLEDLFDWCGRKFSVKTVVQVAVQMITLIEDLHAHDLIYRDIKPDNFLIGRPGQPDANNI
HLIDFGMAKQYRDPKTKQHIPYREKKSLSGTARYMSINTHLGREQSRDDMEALGHVFFYFLRGHLPWQ
GLKAPNNKQKYEKIGEKKRSTNVYDLAQGLPVQFGRYLEIVRSLSFEECPDYEGYRKLILLSVLDLGET
ADGQYDWMKLNDRGWDLNINKKPNLHGYGHPNPNNEKSRKHRNKQLQMQLQMQLQOQQOQQOQYQK
TEADMRNSQYKPKLDPTSYEAYQHQTQQKYLQEQKQKQKQKQEQQLQEQQLQEQQLQEQQLQEQQLQEQQLRATGQP
PSQPPAQTSQOFGARYQPQQPSAALRTPQHPNDNSSLAAASHKGFFQKLGCC

YJL060W 1835bp CDS: 501..1835 public: 1..1835 (SEQ ID NO 703)

TAGAGCAGATTGTTTTGAGTAGGATTTAGGAATCAAGACCTCCATCTTTGTGCGATTATTCCTAAATGT
AACGTAACCTCGTTTGATAAGAGAATGTCTAATCGAAGAGAGTTAATAACTTAATAAGCTCTTTAAAAGA
ACGATGGCATTATCTGCTCTCCTATGCCAAGATAATTACTGGCTCAAAATTTGTTTCAGCGTTCATAAACT
TTGATATCACTTTCTGGCGCACAAGCTAACCTTTATGTAGTTCTTACGTAGATTCTTTTACGCAAGTGC
CTGGTAGTGGTTATTACATAAATGTATCTTTTCATTTGATAACAATTTCTTTCAGTAGCATGTCGTGTCT
AGCACGTGACGTAGAACTGTGGCTTTTTTGTGTGTCATTATGACAATCAAGATACCAAAATTCAGTCATG
TTTAAAAGGGGAAGGTACGATAGAGATATATATAAAGTGTTCATTTACTATAATTGCGTATAGAATCC
ATTGTTACTTGTCTCTCAATGAAACAACGATTTCATTCGTCAATTTACGAACCTAATGTCTACTTCGAGAC
CGAAAGTTGTTGCCAACAAATATTTCACTTCTAACACTGCCAAAGATGTTTGGTTCGCTAACCAATGAAG
CCGCTGCAAAAGCTGCCAATAACTCCAAAACCAAGGCCGTGAACCTTATTAATTTAGGCCAAGGCTTTT
TTTCATATTCCCCTCCTCAATTCGCCATTAAGGAGGCTCAGAAAGCCCTAGACATTCCAATGGTCAATC
AATATTCTCCAACCTAGAGGTCGACCTTCATTAATTAATTCCTTGATTAAAGTTGTATTCCTATTTATA
ACACAGAATTGAAAGCGGAAAAATGTTACCGTAACAACAGGTGCCAATGAAGGTATAC'TTCTTGTCTTGA
TGGGGCTTTTGAACGCTGGCGACGAGGTTATGTTTGTGAACTTCTTTTGACCAATATATTTCCAAATA
TCGAAC'TTTCGGTGGTAAAAGTTGTTTACGTCCCCATAAATCCTCCAAAGGAATGGATCAAAGGAATA
CTAGAGGTGAAGAATGGACCATTTGAGCAGTTTCGAAAAAGCGATTACATCCAAGACAAAAGCTG
TCATTATCAATACCCCTCACAACCCAATTTGGTAAAGTTTTCACGCGGAGGAATTAACCAC'TTTAGGTA
ACATTTGCGTCAAGCACAACTGTTGATTATATCTGATGAAGTCTATGAACACCTTTACTTCACTGATT
CTTTCACTAGAATTGCCACACTCTCTCCAGAAATGGGCAACTAACCTTAACGGTCGGTCTGCGCGTA
AATCGTTTGTCTGCTACTGGTTGGAGAATTGGTTGGGCTTTATCCTTGAACGCAGAGTTGTTAAGTTATG
CAGCTAAGGCACATACAAGAAATTTGTTTTCATCTCCATCCCCCTTACAGGAAGCTTGTGCAAACTCTA
TTAACGACGCTTTAAAAATTTGGGTATTTTGAAAAAATGAGACAGGAATATATCAACAAATTCAAAAATTT
TCACATCGATCTTTGATGAATTGGGACTACCATATACAGCTCCAGAGGGTACATATTTTGTCTCGTTG
ATTTCTCTAAAGTGAAAAATTTCCCGAGGACTATCCCTACCCAGAGGAGATCCTGAATAAGGGAAAAGATT
TTCGCATTTCTCACTGGTTGATCAATGAATTAGGTGTGGTTGCCATTCACCAACTGAATTCATATCA
AAGAGCACGAAAAGGCTGCTGAGAATTTGTTAAGGTTTGCAGTTTGTAAAGATGATGCTTATCTAGAAA
ATGCCGTAGAGAGATTAAAACTACTCAAGGACTACTTATAA

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YJL060W 444aa public: 1..444 (SEQ ID NO 704)

MKQRFIRQFTNLMSTSRPKVVANKYFTSNTAKDVWSLTNEAAAKAANNNSKNQGRELINLGQGFYSYSP
QFAIKEAQKALDIPMVNQYSPTRGRPSLINSLIKLYSPIYNTELKAENVTVTTGANEGILSCLMGLLNA
GDEVIVFEPFFDQYIPNIELCGGKVYVYPINPPKELDQRNTRGEEWTIDFEQFEKAITSKTKAVIINTP
HNPIGKVFTRRELTTLGNICVKHNVVVISDEVYEHLYFTDSFTRIATLSPEIGQLTLTVGSAGKSFAAT
GWRIGWVLSLNAELLSYAAKAHTRICFASPSPLQEACANSINDALKIGYFEKMRQEYINKFKIFTSIFD
ELGLPYTAPEGTYFVLVDFSKVKIPEDYPYPEEILNKGKDFRISHWLINELGVVAIPPTFEFYIKEHBKA
AENLLRFAVCKDDAYLENAVERLKLLKDYL

YKL123W 881bp CDS: 501-881 public: 1..881 (SEQ ID NO 705)

AAAATTAATGGATGTAACACAAAATATTGGCATTGATCTTTTCATTGGAATTGGCGCGTTTAATGCCCGC
ATATACAAGAACATATACGAGGGATGGTCTATTGGAAGACCCGGATAATGTTAGCTTCCGTGAAGCTCT
CTCTGAAGGCAAAGATATTGAAGTCGCCAAAGATCTTCAAAGAGTTCACGATCCACATGATGAAAGTA
TGAATGACGTCAGATGAGGTGAATTACATGTTAATTTGGGCCAAGTTGGGTTTCGTTCTTTATAGAAGC
CAATGTGAAAAAATATGCGTTTGGGAGTGTTTATGGCCAAATTGGAATTCCTCCTGCGTATAATGGAAC
CGAGATCAAGAAGGATACTATTTTACAGAAAGGAGAAGAATTGCCACCAAGATATGCTGACACTGATAA
TTTCTTTGGTAGTATGAAGGTAAAAGAAGGGTCATCCTCTAGGATAACGGCGCAAACCTAGTAAGCCCCCT
GTGGTCTGTTGGGACGTATGAAAGAATCTCTTCTAATTTGACAGAGAAAATAATGTTTACCACGACAG
TCTTGAAACCGACGATAACAACACCGATAACAATGTTAATAACAACGATGAGAACGCTGGTTGCAATGA
AAATTCGCCATTATTGGAAGATGATGGCAATAAAAGACCGGAAAATTCAAATACCCCCCGTGAAGTATC
AGATGGAGCTATCAATAAGAACCCTAGAAATAAATCTACTAAAAAACGTCAAAGAAACAGAGGCAAATC
TTCTAAAAAGAAGAACAGATCGAGAAAATAAGAGACATTATGAATTTGGTTTTTTTTTACAATTTACGCA
TACACAATATATACATTCTCTACTAGCTTTTTTTTTCTTCAATTCGATAGTTTAG

YKL123W 126aa public: 1..126 (SEQ ID NO 706)

MKESLLTLTEKIMFTTTVLKPTITTPITMLITTMRTLVMKIRHYWKMAIKDRKIQIPPVKYQMELSI
RTLEINLLKNVKETEANLLKRRTDRENKRHYEFGFFYNLRHNIYIPTSFFFFNISIV

YML028W 1091bp CDS: 501..1091 public: 1..1091 (SEQ ID NO 707)

GGTAAACGATAGGGTGATAACCGCTGTGATAAAGAACTTCGTGCTCTTTTGGGTTACACTACTCCCCTA
TGTGAAGGAGAAGCTGGATGATATTGTTGCACAGAGAGCAAGGGACCGTGAGCAACCGCTCCATCTGC
CCAACAGCAGGAAAACGAAGATGAGGCCCTCATAATCCCTGACGAGGAAGAACCACCGCCACAGGTGC
GCAACCTCATCTCTACATTCTGTGTAAGACTAATTGCAATGCGATGTGGCCACGTTATATAATGCGTT
TAAGGTGTACGAAAACCCATGCTGTTCTGGCCCGTCGGGTTTTCTGACAAATTGTCCTTTAGGGATTTT
TCGGTTTTGGCTCGGGTTGGCAAAGTCGGCTGGCAACAAACCAGGACATATATAAAGGGAGGTAATTCGT
CAGATCAATGCCGAACCGTTCTCAACGGGCCTTCCCCTCGTTCAATTGCTCACAACCAACCACAACCTAC
ATACACATACATACACAATGGTCGCTCAAGTTCAAAAGCAAGCTCCAACTTTTAAGAAAACCTGCCGTCG
TCGACGGTGTCTTTGACGAAGTCTCCTTGGACAAATACAAGGGTAAGTACGTTGTCTAGCCTTTATTC
CATTGGCCTTCACTTTCTGTCTGTCCAACCGAAATCATTGCTTTCTCAGAAGCTGCTAAGAAATTCGAAG
AACAAGGCGCTCAAGTTCTTTTCGCCTCCACTGACTCCGAATACTCCCTTTTGGCATGGACCAATATCC
CAAGAAAGGAAGGTGGTTTGGGCCCAATCAACATTCCATTGTTGGCTGACACCAACCACTCTTTGTCCA
GAGACTATGGTGTCTTGATCGAAGAAGAAGGTGTCGCCTTGAGAGGTTTGTTCATCATCGACCCAAAGG
GTGTCATTAGACACATCACCATTAACGATTTGCCAGTCGGTAGAAACGTTGACGAAGCCTTGAGATTGG
TTGAAGCCTTCCAATGGACCGACAAGAACGGTACTGTCTTGCCATGTAAGTGGACTCCAGGTGCTGCTA
CCATCAAGCCAACCGTTGAAGACTCCAAGGAATACTTCAAGCTGCCAACAAATAA

YML028W 196aa public: 1..196 (SEQ ID NO 708)

MVAQVQKQAPTFFKTAUVVDGVFDEVSLDKYKGYVVLAFIPLAFTFVCPTETIIAFSEAARKFEEQGAQV
LFASTDSEYSLAWTNIIPRKEGGLGPINIPLLADTNHLSLRDYGVLIEEGBVALRGLFIIDPKGVIIRHI
TINDLPVGRNVDEALRLVEAFQWTDKNGTVLPCNWTPGAATIKPTVEDSKEYFEAANK

YOL052C-A 686bp CDS: 501..686 public: 1..686 (SEQ ID NO 709)

TGGCCACTGAAAATTCCTGGCCAGACCACCCCTGAGCTAAGGGAGTTTAGCCGCTCAAGCTTTTATTTT
CTCTGATGTAATATATCACACACCCAGACACGGTTGCCAAGGCCTCGACGGAAGGCCGCTTCAAGGGAC
GGGGCAGTGGCTATCAGAAATACCTTAATATCATCAATATTTTTTCATCAATCGCAAGGTGTCAAACATC
AATAAAGGATGATGCTCAAAGGTTTATGCCCGATGTTCTTCTAATCCCCTTTCTCTCTCTAAAATAATCC

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TTTTTTTACTCTTCTTCTTTTCCCTGTTCATTTTGTCTTTCTCACCCCTTATGGGACATCAATA
ATGCAAGTATGTTTATACATTTTATATAAATGTATATATAAATGCCATTTCTTTACACATAACCTCCAT
TCTTTGGTTAATTCTTTCTTCATTCCTTTTTTTTTTTCATTCTGAAAAGCCCTCCAAGCAAGCACGCTAAT
TTAATATCGATTTAAACATGAAAGTATCACAGTTTTCATTTCTGCCATCTCTGTCTTCGGCCTCGCTA
CTAGCGTAAATGCTCAAAACGCATCCAACACCACGAGTAACGCTGCTCCTGCTTTGCACGCTCAAAATG
GTCAACTACTAAACGCCGGAGTCGTGGTGTCTGTGTGGTGGTGTCTTTGGCCTTTTGTATTTAG

YOL052C-A 61aa public: 1..61 (SEQ ID NO 710)

MKVSQVFISAI SVFGLATSVNAQNASN TTSNAAPALHAQNGQLLNAGVVGA AVGGALAF LI

YOL099C 992bp CDS: 501..992 public: 1..992 (SEQ ID NO 711)

TGTCCAAATATGTTGATGAATTCGTTTGCAAAGGGGGAACAACTTCAATGAATTGTATTTGGAAAGGT
TGCAGAAATGTTACCAAAACAGATCTGAAAAATGCCATGCAGAAATATTTTGTCAACATGTTTGATTCCA
ATAAAAGCGTTGCCCTTTGTGAGCTGTCAATCCAGCTAAATTTGGAATCAGTTCAAGAATCTTTGAAACTC
AAGGTTTTCACGTGTCGAAAATAGAAGAGCTAGAAGATGACGATGACGAAATTGATAGTGAAGAAGACGAAA
ATGCGTGAGTACATGACCTCCATTTTCAGCTTCACTTTCAACACAGAAACAGTGCGTATTATCTGCATTC
AATAAATAGCAAAAGGAGCATTGTCTCATTCTTTTCGAATTTCTGGGATTCTGCCTTACGGCGCTCTTTC
ATTTGATTGATCGAGAATTATTATTATATTTATATGAGTACTTGAAATTCCTCATATATTTATTTTATAG
AGTATTTAAGTAGCTTGATGAAAACATTAGATAAAATTACTAATTACGACCTCTTCGATTTTGCAGATG
AGTTTTTGAATTTGTTCCTGTGTTTAGACCTAATCCCACGGTAACCTTGTCTTTTGGCAATCCGTTAA
CTAATTTACTGGTTAACGGTACTGGAGCAGCGTGTTTTTTTGAATTTTGTTCCTTGGCATTGATAAAGG
TTTCAAAAATCTGCTTGATCTGTTGCTCTTAGCGCTATTAATCGATTTCAGAAAACGAATTGTGCTTTG
AAATTGATGGAGATTGGCTATGCGTCTGGGTTTTGGCGAAGGAGACTTGGAAGTTGGAAGATCTTTAG
GTATGGCTCTTCCGGATGATGATGTTCTTCTTTCAATTACCTTTTGGTTTTCTTTGCAACAGTTCTTTCT
CTATTTTATTTGTATTTCGAATTAAGAATTTTTTTGAGAACAGTAAACAATTTGCTCGTGGTTTTTTTAT
CAGTGCTCAAAAGAAATGACTTGTA

YOL099C 163aa public: 1..163 (SEQ ID NO 712)

MKTLDKITNYDLFDFADEFLKFVPVFRPNPTVTCLFGNPLTNLLVNGTGAACFFEFCSLALIKVSKILL
DLLLLALLIDSENELCFEIDGDWLCVLGFGEGDLEVGRSLGMALPDDDVLLSITFWFLCNSSFSILFVF
ELRIFLRTVNLLLVFLSVLKRNDL

YOL100W 3746bp CDS: 501..3746 public: 1..3746 (SEQ ID NO 713)

TTAACGATCGACTCGACACATTGTTGATGGAATAATTGGTCCCTAGTTAAACAGCGGAGAAATAGCCGC
CCAGGATAATCGGAGAAAAGTCACGTGCAAAAAGAAATCATATTCGACGAAATAAACTAGAATAACTTT
TGACGTTTAGCAATAATAACCCCAATGGAAGCGAACATTTCCCGATCCTTTTAGTTTTCTTTAAGGCG
CTATTGGCATTTCATCTTCAAAGCTTCCGCAACACAGAAATTATATTTACATTTCTGAGGCAGAGAAT
AGTTTTTGACAACGAACTGTTAATATTTTTACTCCAGTTACCGCCTTTGAAGTCTGATATTGGTGACA
AAGGTACTTAGGGGTATTTAAGAACAAGAACTACATAAAATAGTTGAAAAGGGGAAAACAAAAGTAAC
ATCTTGATGAACCGAGAAGCCACTAAGTATTTTAAAAAGCAAAAGAAATTAATCTCTCTCTTTT
TTTTTCATTTCAACCAATGTATTTTGATAAGGATAATTCATGAGCCCTAGGCCGTTATTGCCAAGTG
ATGAGCAGAAGCTAAACATTAATCTTCTAACGAAAAGGAGAAATTTCTCGCATTTAGACCCCCATTATG
ACGCAAAAGCCACTCCACAAAGAGCACTTCGAATAGAAACGTTGGCGATTTACTTTTGGAAAAAGAA
CCGCTAAGCCTATGATTCAAAAGGCCCTTGACGAATACGGATAATTTCAATTGAAATGTACCATAATCAGC
AGAGAAAAATCTTGATGATGACACTATTAAAGAAGTAATGATTAATGATGAAAACGGAAAAACTGTCCG
CTAGTACCAACGACGGCAGATATGACAACGATTACGATAATAACGATATTAATGACCAAAAAACTTTGG
ATAATATAGCGGGAAGTCCCCACATGGAATAAAGTAAAGTAAAGATGAACATGACTCTTCAT
CTCAAAAACCAATAGCTAAAGAGTCATCCAAAGCCCAAAAAATATAATCAAAAAGGGAATCAAGGACT
TTAAATTTGGTAGTGTAATAGGTGATGGCGCGTATTCTACTGTAATGTTAGCGACGTCGATTGTATACCA
AAAAGAGGTACGCCGCAAAAGTACTAAACAAAGAATATTTAATACGCCAGAAAGAAAGTCAAATACGTCA
GCATAGAAAAAACCGCCCTTCAAAAGCTCAATAATTTCTCTAGTGTTGTGCGATTATTTTCCACTTTTC
AGGATGAATCAAGCCTATACTTTCTCTTAGAGTATGCCCCAATGGGGACTTTCTTTCTTTAATGAAAA
AATACGGTTTCATTAGACGAAACCTGCGCACGATATTATGCTGCGCAAATAATAGATGCCATAGACTACT
TACATTTCAACGGTATTATTTCATAGAGATATAAACAGAAAATATTCTTTTAGATGGAGAAATGAAGA
TCAAACTGACTGATTTTGGTACTGCGAAGTTACTGAATCTACAAATAATAGCGTTTCGAAACCAGAAAT
ACGATTTATCAACAAGGTCGAAATCTTTCGTTGGAAGTGCAGAAATACGTATCTCCAGAACTTTTAAATG

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ACAGTTTTACAGACTATCGTTGCGATATTTGGGCCCTTCGGATGTATACTTTTCCAGATGATTGCCGGAA
AACCACCATTCAAAGCTACCAATGAATACCTTGACTTTCCAAAAGGTAATGAAAAGTTTCAGTACGCCTTTA
CACCAGGTTTCCCACTTATTATCAGAGATTTGGTTAAGAAAATCTTAGTAAAAAACTTAGACCGAAGAT
TGACGATAAGCCAAATTAAGGAACATCATTTTTTCAAAGATTTGAATTTTAAAGACGGCTCTGTTTGGT
CAAAAACGCCCTCCAGAGATCAAACCATATAAAATCAACGCCAAATCCATGCAGGCAATGCCAAGCGGAA
GCGATAGAAAACCTGGTGAAGAAATCAGTCAACACACTTGGCAAATCGCATCTAGTGACTCAAAGGTCAG
CTTCAAGTCCCTCTGTTGAGGAAACTACTCATTCAACCCCTATACAATAACAATACTCACGCTTCTACTG
AAAGTGAATATCAATAAAGAAGAGACCCACTGATGAAAGAACAGCGCAGATACTTGAAAATGCAAGAA
AGGGTATAAACAATAGGAAAAATCAACCAGGCAAGAGAACACCAAGTGGTGACGCTTCTGCTGCCCTAG
CAGCTTCTGCTGCTTTAACCAGAAAACCATGCAAAGCTATCCAACCTTCTAGTTTGGAAAAGTAGCAGGT
CAAGCTCTCTGCGACAACATCAAGACCAGGAACCTTATAAGCGTACTTCTTCTACAGAAAGTAAACCAT
TTGCCAAATCTCCACCTTTGTTCAGCATCAGTTTTATCGTCAAAAAGTCCCAATGCCCTCCATACACACCTC
CAATGTCCGCCCTATGACACCATATGATACATATCAAAATGACACCTCCCTATACGACAAAAACAGCAGG
ATTATCTGTATACCGCAATTGCCGCACCTAAGCCTTGTTATTAGTAAGCAAAATGTTAAAAATAGCACAG
ATTCTCCCTTGATGAACAAGCAAGATATTCAATGGTCTTTTTACCTGAAAACATCAACGAACATGTAC
TAAGGACGGAAAAAC'TGGATTTTGTACCACAAATTACGATATCTTAGAGAAGAAAATGCTTAAACTAA
ATGGTTTCATGTTAGATCCTCAACTGTTTGGTAAGCCTAGACATACTTTTTTATCCCAAGTAGCTAGGA
GTGGGGGAGAGGTTACAGGTTTTCGAAATGATCCAACATGACTGCTTATTCCAAAACAGAAGATACGT
ACTATTCGAAAATATTTATCGATTTGCAGCTCTTGAAGATGATTATCGAATTGAAGGAGGTGACTTAT
CGGAGTTGCTTACTAACAGAAGCGGAGAAGGGTACAAATGCAATCAAAACAGCTCACCATGAAAGACG
ATGATAAATCCGAATCTAACAATAAAGGAAGCTCTGTTTTTCTGGCAAGATTAAAAAATTATTTTACC
CTACCTCAGCAGCTGAAACGCTCTCTTCTCTGATGAAAAACCAAGTACTATAAACGAACCATTTGTAA
TGACATCATTTGGAAGGTTTCTAGTATTTGCCAAGAGGAGGCAGCCAAATCCAGTTACAAATTTAAAGT
ATGAACTAGAATATGACATAAATTTGCGTCAACAGGGTACCAAAATAAAGAACTAATCATTTCCCTTGG
AAATGGGAACATATCATATAGTTGTGATTACAGACACCTTACAAGTCATTTCTTTTGAGCACTGATAAAA
AAACCACGAGCAAATTTGTTTACTGTTCTCAAAAAAATCTTAATTGGAATACAAATAAAATAGAGAAAG
AACTGTTGCAAAGAAACCAAAAGGTAATTGAAAGAAGAACATCATCATCCGGAAGAGCCATACCTAAAG
ATCTTCCAACCTTCCAAGTCTCTTTCGCCAAAACCCAGGACGCATAGCCAATCTCCATCAATTTCAAAGC
ACAATTCGTTTTCTGAATCGATTAAATAGCGCTAAGAGCAACAGATCAAGCAGAATTTTGAACCTTTA
TCAATGCGCAAGGAACAAAATTCAAAAAAACACGCTGCTCCAGTACCGTTAACCAGTAAATTAGTTAACG
GATTGCCAAAAGACAAGTTACCGTGGGATTAGGTCTAAACACAGGAACAAATTTCAAAAACTCATCTG
CAAAATCGAAGAGGTCTGTA

YOL100W 1081aa public: 1..1081 (SEQ ID NO 714)

MYFDKDNSMSRPLLPSEDEKLNINLLTKKEKFSHLDPHYDAKATPQRSTSNRNVGDLLEKRTAKPMI
QKALTNTDNFIEMYHNQQRKNLDDDTIKEVMINDENGKTVASTNDGRYDNDYDNDNDINDQKTLNDNIAGS
PHMEKNRNRKVKIEHDSQQKPIAKESSKAQKNLIKKGKIDFKFSGVIGDGAYSTVMLATSIDTKKRYAA
KVLNKEYLIRQKKVKYVSIKTAALQKLNNSPVVRFLSTFQDESSLYFLLEYAPNGDFLSLMKKYGS LD
ETCARYYAAQIIDAIIDYLSNGIIHRDIKPENILLDGEKIKLTDGFTAKLLNPTNNSVSKPEYDLSTR
SKSFVGTAEYVSPPELLNDSFTDYRCDIWAFCILFQMIAGKPPFKATNEYLTFFQKVMKVQYAFTPGFPL
IIRDLVKKILVKNLDRRLTISQIKEHHFFKDLNFKDGSVWSKTPPEIKPYKINAKSMQAMPSSGSDRKL
KKSVENTLGKSHLVTQRSASSPSVEETHSTLYNNNTHASTESEISIKKRPTDERTAQILENARKGINNR
KNQPGKRTPSGAASAALAASALTKKTMQSYPTSSSKSSRSSSPATTSRPGTYKRTSSSTESKPFKSP
LSASVLSSKVPMPYPYTPMSPMPYDTPYQMTTPPYTTKQQDYSDTAIAAPKPCISKQNVKNSTDSPLMN
QQDIQWSFYLNINEHVLRTKLDVFTTNYDILEKKMLKLNGSLLDLPQLFGKPRHTFLSQVARSGGEVT
GFRNDPTMTAYSKTEDTYYSKNIIDLQLEDDYRIEGGDLSELLTNRSGEGYKCNQNSSPMKDDDKSES
NNKGSSVFGKIKKLFHPTSAEELSSSDEKTKYKRTIVMTSFGRLVFAKRRQPNPVTNLKYELEYD
INLRQQGTKIKELIIPLEMGTNHIVVIQTPYKSFLSTDKKTTSKLFTVLKKILNSNTNKIEKELLQRN
QKVIERRTSSSGRAIPKDLPTSKSPSPKPRTHSQSPSISKHNSFSESINSAKSNRSSRIFETFINAKEQ
NSKKHAAPVPLTSKLVNGLPKRQVTVGLGLNTGTNFKNSSAKSKRS

YOR302W 578bp CDS:501..578 public:1..578 (SEQ ID NO 715)

GTGTATGATGTAATCCATCACCCCCCTATAAAAACACCTGTGCACCGCATATTTCCATAGCGCGTGACC
CTAAGTACAAGAAACAGCGAGGGGCCGTTAAGTGCAGGCTTTACCGAGGGCGCCGGCTGGCGCTTCCCG
TGGAAGGGTGTGTTGACTCATCATCGCATCGCATTACCTCATGATGAGTAAATAGTTGCGATTTCACTTA
TCACCTCTCGCGGAAAAAAAAGCGATGACATGATATATAAGGCTCTCTCGTAAGACACTTAACATATCC

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AACGTTCAATTAGATTATTCGGTCAATTTCTTTTTTCATGCCCTCCTTTTTCTTTTCTTTCTTGACTC
GTCGTTTCTTTTTCTTTTTTTTTTTTTTTTTTTTTCTTCAGAACTATAACACATAGATACACTCGAACAT
CTAATTGTTTAAATACTGCAAAGAATACAAGGTAATCGACTCTTCTACATACCCTTTTTGCAGATTTGA
AATAAAAAAACATTATATGTTTAGCTTATCGAACTCTCAATACACCTGCCAAGACTACATATCTGACC
ACATCTGGAAACTAGCTCCCACTAA

YOR302W 25aa public: 1..25 (SEQ ID NO 716)

MFSLSNSQYTCQDYISDHIWKTSSH

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Figure 2**Candida spp. homologues**

YBL002W_homolog 393bp public: 1..393 (SEQ ID NO 397)

ATGGCCCCAAAGCAGAAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAA
ACCGCTTCCACCGATGGTGCTAAAAAGAGAACCAGCTAGAAAAGAACTTATTCCTCATATATATAT
AAAGTTTTGAAACAAACACATCCAGACACTGGTATCTCCAAAAGGCCATGTCAATTATGAATTCGTTT
GTAAACGATATTTTCGAAAGAATTGCCACCGAAGCCTCCAAATTAGCTGCTTACAATAAAAAATCCACA
ATTTCCGCTAGAGAAATCCAACTGCTGTTAGATTAATTTTGCCAGGTGAATTGGCCAAACATGCCGTT
TCCGAAGGTACCAGAGCCGTCACAAAATACTCATCTGCTTCTAGTTAG

YBL002W_homolog 130aa (SEQ ID NO 398)

MAPKAEKKPASKAPAEKKPAAKKTASTDGAKKRTKARKETYSSYIYKVLKQTHPDTGISQKAMSIMNSF
VNDIFERATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTRAVTKYSSASS

YBL064C_homolog 732bp public: 1..732 (SEQ ID NO 399)

ATGAGAGACAAAAACAAACAAAAAATCTTTTTTTTCGCCACGCACACTACCATGTGCGCAA
CAACCAGATTTACGTCTCGGATCTACCGCACCTGATTTCAAAGCTGATACAACTAACGGGCCATTCTG
TTTCACGAATACATTTGGTGATAGCTGGGCTATCTTGTTCTCACATCCCGCTGCCCACACCAGTGTGTGT
AGCACCGAGCTTTCTGCGTTTCGCACGACTCGAACCGAGTTCACGAAGAGAGGGGTGAAATTGCTTGCA
ATTTACGCCGACCCCTGTTGAAGCAAATTCGACTGGATTGATGATATGGAAGATTTTAGCGGATCCAGG
GTCAAATTTCCAATTATCGCAGACCCGTGAGAGAAAAAGTTGCTACCTTGTTACGACATGATCGATACCAA
GATGCCACCAATCTCGATGACAAAGGGCTTCAATTGACAATTCGTGCAGTGTTTATCATTGATCCAAGT
AAGAAAATCAGATTGATCATGACCTACCTGCGCTCGACCGGTAGAAACACCGCTGAAGTATTGAGAGTA
CTCGACTCATTTACAGCTTGTTGATAAAACAAAAGGTTATCACTCCAATCAATTGGGTTCCAGGTGACGAT
GTTCTTGTTCCATATGGGTGTTCCAGATGATGAGGCAAGAGTTTTGTTTCTTAAATATAGGGCTATAAAG
CCATATATTAGATTGACTCCGTTGGAAAAGGAAGACAAGTAA

YBL064C_homolog 243aa (SEQ ID NO 400)

MRDKKQTKKKKSFFFATHTTMSQQPHLRLGSTAPDFKADTTNGPISFHEYIGDSWAILFSPAAHTSVC
STELSAFARLEPEFTKRGVKLLAISADPVEANSWDWIDMEDFSGSRVKFPPIADPERKVATLYDMIDHQ
DATNLDDKGLQLTIRAVFIIDPSKKIRLIMTYPASTGRNTAEVLRVLDLQLVDKQKVITPINWVPGDD
VLVHMGVPDDEARVLPKYRAIKPYIRLTPLEKEDK

YBR149W_homolog 981bp public: 1..981 (SEQ ID NO 401)

ATGAAATTAGCCACTGAAATTGATTTCAAACCTCAACAATGGTAAAACCAATTCCTGCCTTAGGACTAGGT
ACTGTTGCCTCAAAAGATCCCTAAAGATGTTAAGGATCAAGTAATCACTGCTGTTAAAGCAGGATATCGT
CATATTGATACTGCTTGGTTTTATGGTACTGAAAAATATATTGGTGAAGCATTACAAGAATTATTTGCT
GAAGGAATTATTAAGAGAGAAAGATTTATTTATCACGACAAAATTTTGGCCATCATATTGGGCTAATCCA
GAAAAATCTTTAGATGAATCTTTAAAGATTGCAACTTGATTATGTTGATTTATTTTACAACATTGG
CCAATTTGTTTACATGGTGATGAAAATGGATTACCGAAAATACCTAAGGATGAGAATGGTGAATTGATT
TATGATGATGATCCCAACCCCAATGGTACTAAATATATACGACGTTTATCATAAATTAGAGGATATTTTA
GAAACAACCACCAAGTTAGATCAATTGGTGTCTTAATTATTCAAATTCAAAACCTTCGTCAATTATTA
CCTAAAGTTAAAAACATATTCCTGTTTGTAATCAAAATTGAATATCATCCACAATTACCTCAACAAGAT
TTAGTTGATTATTGTACTAAAAATAATATATTGATTTCTTGTATTACACAGTTGGTAGTTATGGAGCT
CCAGTATTGAAAATCCCATTAGTTAAGCAATTGGCAGAAAAATATCAAGTCACAGAGAATGAAATTGCT
GATGCTTATAATATTTGAATGGTAGAGTTACATTACCAAGATCTTCTAATCTTGAAAGAATTAAACC
ATTATTAGATTACCACATTTGACTAAAGAAGAATTGGATGAATTGTATCAAGTTGGAGTTAAAGATCCA
CAAAGATATATTTGTGATCCTTGGGGGTATGGTATAGGATTCCGTTGGTGAAAGGCGATACTTTAAGT
AAAGAATTTGATTAA

YBR149W_homolog 326aa (SEQ ID NO 402)

MKLATEIDFKLNGKTIPALGLGTVASKDPKVDKQVITAVKAGYRHIDTAWFYGTEKYIGEALQELFA
EGIIKREDLFITTKFWPSYWANPEKSLDES LKDLQLDYVDLFLQHWPICLHGDENGLPKIPKDENGELI
YDDDPPTNGTKYIDVYHKLEDILETTTKVRSIGVSNYSIPKLRQLLPKVKKHIPVCNQIEYHPQLPQQD
LVDYCTKNILISCYSPVGSYGAPVLKIPLVKQLAEKYQVTENEIADAYNILNGRVTLPRSSNLERIKT
IIRLPHLTKEELDELYQGVKDPQRYICDPWGYGIGFRWWKGDLSKEFD

YBR289W_homolog 1389bp public: 1..1389 (SEQ ID NO 403)

ATGAAACCAATGCAAAACGTTAAGGAGTGGTCAGAAAAATTGAAACAGGAAGGTAAAGATGTACCTCTT
GATTTGAAAGTGATGAAGATTTGATTAGAAAGGATAAGGAATTTGTGGGTAAATTGAATAAACAGTTG
CATGACAACAAATTTATTATGGAATAATTAACAGAGATATCAAGTCTTATAATCAAATCAAACAATTG

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AGGATGAATTCTATTGCGTTGTCCAACAAAGGACAGTATAATAACAGTATTTGGGGGGAAAGGATATCAA
GGTTATGGCAATGGAATAACAAACTCCAGTACAAAGTTATTTATTTCCCAACAGGGATTTAACTGATAGA
ATCATCAATGAAAGAGTGATGAAAAACAAAAATAAACCAAAACATTATGTACCCATTTCGATTAGAGTTT
GACCAAGAAAGGGATCAATTTAAATTTGAGAGACACATTTCTTTGGGATTTGAATGAAGAGATTATAAAA
GTGGAAGATTTCACTGCTCAATTTGTTAGAGGATTATAAATTTATCTCCAAAGTTTCATTATGAAACAATT
TTGTCATCTATTAAAGAGCAGATTGCTGACTATCTGCAGAAACCTAGCAAAACAATGGGTGAATTGAGA
ATTCCAATTAAGATCGATATCACCATTAACAATACACAATTAACCTGACCAATTTGAATGGGATATATTG
AATAGCCAGGAAGGCGATGCAGAAGATTTTCATCTTACATGTGCGACGAATTTGTGCTTACCGGGAGAG
TTTTGCACTGCCATCGCGCATAGCATAAGAGAACAATCGCAGATGTACTATAAAGCATTGAATATGGTA
GGGTACGGTTTCGACGGTTCCACAGTACACGAAGATTAGATTAGAAATCATTATTGCCACCTTTAAGA
TTAGTATCATCGGACTCTGGAAATCGTGGATGATTTTTCCTCAATTTTAAGAAACCCATCAAGTTTGCCA
GACTTTTTCACCTACGTTAGGTAAATTTGCCCAATTGGAAGTTGAAAGATTGGACAAGGAAATGGAGAGA
GAAAGTAGAAGGAAAAGAACACACAATTACAATGAAGATCAGCAACAGGGTTCTGGTCGAGGCTTCACT
TCGAGAAGAATTGCAGCTCATGCTGGTAGGGGAAACACCATTTCCCGACTTGTTCAGACATACCCAAGACA
TTTAGGACGCTGCCCCCTCATCCATATTGCCAGGTGCTGTTGATATGGGTGTACCTGAGGTGTATGAA
TATAATGAAGTTTAAATCAATAGAACTCAAGTTAGGAATCCAGATTATAGACCGCCAACACCTATTTCGT
CTTGAATAAGTGAACCTAGTGGATTATAACCATGATCCAAATTGAAGGTACTTTTATGGTTACAATCAAATTA
CCCGTATAA

YBR289W_homolog 462aa (SEQ ID NO 404)

MKPMQNVKEWSEKLKQEGKDVPLDLKVYEDLIRKDKFEVVGKLNKQLHDNKFIMENINRDIKSYNQIKQL
RMNSIALSNKGQYNNNSIWGEYQGYNGITNSSTKLFIPNRDLTDRIINERVMKNKNPKHYVPIRLEF
DQERDQFKLRDTPFLWDLNEEI KVEDFTAQLLEDYKFIKVIHYETILSSIKEQIADYSQKPSKTMGELR
IPIKIDITINNTQLTQDQFEWDILNSQEGDAEEFSSYMCDLCLPGEFCTAIAHSIREQSOMYKALNMV
GYGFDGSPVHEDEIRNHLLPPLRLVSSDSGIVDDFFSILRNPSSLPDPSPTLGKLSQLEVERLDKEMER
ESRRKRHRHYNEDQQQSGRGRFTSRRIAHAHAGRGNTIPDLSDIPKTFRTAPSSILPGAVIDMGVPEVYE
YNEVLINRTQVRNPDPYRPPTPIRVENELVDYNHDPLEGTFMVTIKLPV

YCR004C_homolog 597bp public: 1..597 (SEQ ID NO 405)

ATGGCACAAGGAAAAGTAGCAATTATCATTTATTCATTATATCATCATGTTTATGATTTAGCCTTAGCT
GAAAAAGCTGGAATTGAAGCTGCTGGAGGTGTTGCTGATATTTATCAAGTTGCCGAAACATTATCTGAT
GATGTTTTAGCTAAAATGCATGCACCAGCAAAACCAGATATTTCAATTGCAACTCATGAACTTTAACT
CAATATGATGCATTTTTATTTGGTATTTCCAACCAGATTTGGTAATTTCCCTGCTCAAATTAAGAGCTTTT
TGGGATAGAACCGGTGGTTTTATGGCTAAAAATGCTTTAAGAGGGAAATATGCTGGTGGTTTTCTCT
ACTGGTACTCCAGGTGGTGGTCAAGAACTACCATTATTAATAGTTTGAGTACTTTGGCTCATCATGGG
ATTATTTATGTTCCATTTGGGTATGGATATCCTGGTATGACTGATTTAGAAGAAGTTTCATGGTGGATCT
CCTTGGGGGGCTGGTACTTTTGCTTCAGGTAATGGGTCAAGAAAAGTTACTGATTTAGAAAAGCTATT
GCTAAACAACAAGGTGAAGATTTCTTTAAAACTGTCTTCAATGA

YCR004C_homolog 198aa (SEQ ID NO 406)

MAQGKVAIIIIYSLYHHVYDLALAEKAGIEAAGGVADIYQVAETLSDDVLAKMHAPAKPDIPIATHETILT
QYDAFLFGIPTFRGNFPAQIKAFWDRGTGGLWAKNALRGKYAGVFVSTGTPGGGQETTIINSLSTLAHHG
IIYVPFGYGYPGMTDLEEVHGGSPWGAGTFASNGSRKVTDLEKALAKQQGEDFFKTVFK

YCR013C_homolog 450bp public: 1..450 (SEQ ID NO 407)

ATGATAACAATGTTACCATTTTCAGCAGATTTGACAGCAGCATCCAATAAGGATTTAGTACCGTTGGCG
AATTTTTCAAATTCGAAAACACCTGGTGGACCGTTCCAACAATGGTCTTAGCTTTGGCAACAGCTTGT
TGGAAACAATTCGACAGATTTTGGACCACAGTCCAAACCCATCCAGTTGTCTGGAATACCTTCAGCATCA
GTAGCAGAAGAAGTTTTGGCATCTTTGTGCAATTTATCAGCAGTGACAAAATCAACTGGCAAGATCAAT
TCAACATTTGTTTTCTTAGCTTTTTCAACCAAGTGTTCAACGTTTTTAGCACCGGCTTCATCGAAAAGA
GAATCACCATTTGGCATTTTGTTCAGATTTTCTTGAAAGTGAAGGCCATACCACCACCAACAATCAAC
ATATCAACCTTGTCCAACAAGTTGTCAATCAATTGA

YCR013C_homolog 149aa (SEQ ID NO 408)

MITMLPFSADLTAASNKDLVPLANFNSNKTGGPFQTMVLALATACWNNSTDFGPQSKPIQLSGIPAS
VAEEVLASLSNLSAVTKSTGKINSTLFFLAFSTKCTFLAPASSKRESPIGILFKIFLKVKAIPPTIN
ISTLSNKLIN

YDL147W_homolog 840bp public: 1..840 (SEQ ID NO 409)

ATGGATAGGAGTTGGGTAGTAGGTTGTGCCATAAAGGGTGGTTGTTTAGTTAGTTATGGCACATGTTGT
GGTAGTTTTGATTTTTTTTTTGTGGTCCACACGACTGGCCAAACATTTATCAAAAATCGAGTTCAACTTT
TTTTTTTTTTCCAGTTGCCACCACCAACTACTTTTACCACCACTAACAACATGTCAAGAGAAGATCCA
ATTAAGGCTGAAAAGACTTTTTCTGCTACTTTAGATGAACAATTTCCCATTTGATTGAAAAGATCTCTGAC

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TACAAGCAAGCATTAGATAAGTATCTTGTCTTGGAGAAACAAACTCGTCAGTCTTCCGATTGGCTTCA
TCAAAAAGAGTCTCTCAACAAGATTGTTACTGCATTCGGTTGATAATAACGATTGGGAGTATTTGAATGAC
TTGATAACTATCTTGTCAAAGAAACATGGTCAGTTAAAGTCGTCAATTCAAGCATTATCAAAAGATGTG
ATTGATAATTTGGATAAATTTGGATGAAAAACAAGCAACAATTAGAGTTGAAGATGAAATTTGATTGAA
ACTATTAGAACAGTCACAGACAAAAGATTTTGTGTAAGTTGAAAGAGCCATTGTTTCAAGACAGTTG
GCCAAAATTTATTTGAACAAAATTGAATGATTTGGATAAGGCAGTGGAAATCTTGTGTGATCTACAAGTA
GAAACGTATTTCGTTAATGCCATTTCAGTGACAAGATTGAGTATATCTTAGAACAAATTCAGTTGACTTTA
CAAAAGGGGGACTATGGCCCAAGCCAAGATTTTGTAGTCGAAAGATTTTATTAATAATCGTTGAAGAAGCTT
TGCCAAAGCTGA

YDL147W_homolog 279aa (SEQ ID NO 410)

MDRSWVVGCAIKGGCLVSYGTCCGSLIFFCGPHDWPNIYQKIEFNFFSSSPPTTFTTTNNMSREDP
IKAEKDFSATLDEQFLIEKISDYKQALDKYLVLEKQTRQSSDLASSKRVLNKIVTALVDNNDWEYLND
LITILSKKHGQLKSSIQAFIKDVIDNLDKLDENNKKQLELKMKLIETIRTVDKKIFVEVERAIVSRQL
AKIYLNKLNLDLKAIEILCDLQVETYSMPFSDKIEYILEQIQLTLQKGDYGPSQDFESKDFIKIVEEL
CQS

YDR253C_homolog 1752bp public: 1..1752 (SEQ ID NO 411)

ATGCAAAATACATAACCGTAATAATAGTAATAGTAGTAAGAATAATAGTGATAATCATCATCAACAACAA
CAACGACAACGACAACAACAAGTTGATCAATATCAATCTATTACATTACCACCATTACAATATCAATCT
AATACTCAGCAATCGATAGTATTACCTTCGCAACAACCTAAAAGAGGTCGATCTGAACATTTTAATTCA
CAATTCACAGTAATATAAATTCAGACCAGTGTTATTACCAAGTTCCTCGTGATAATAATAACACCACA
AATATACTTATACCTATAAATTTACCAAGTAGTACCAATTCACCAATCCAATTACTTCTAGTAGCAAT
TCAAGAATGTTTTTACCTTAATCCTGTGAGTCCATTATATCCCGTGGTCACCACACCATCATCAGATTA
TCACCACCAACACAACACCATCAACAACAACAGCAACAATTACATAAAAAATTCAAAACATCAAATTCA
GGTTCCAATACTCCGATTACTGGTGGTGGAAATTGGATCTCCTAGTACTACTAGTTATTTAGCTAATTCT
GCTAATATCAGTTATACTAGAAGTCAACCATTAAAAGATAACAACCAACATCTTCCACAACATAAGGAT
AATAATAACACGATAATTGAAAATGAAGACCAGAAGTTTTTCCGATTAGCAAAAGAAGCATTAGTAGCT
ACTGCCAAGGGAGTTAAGACGAATCATTCCAATAATAATGGTAAATTTGGTAATAATACTTCTAAGATT
GATATTAAATAATCATAATAAGAACAACAACAACAAGTGATGGTAATGAAACCATACCTTGATTCTACA
ATTGCAGATTTATTAAGAAGATTACAATATGCTAGTGTCTCCTCATGGTAATCCCATTGGCCAAATAAGT
GGACTTCAAACATAATTCTAAAGGATTACTTGAAGTACAAGATGAATACTCTAATTTCCCTGATTACAA
AACAATAATTTTTTCAAAGTTAATAATGGTGATAATAATAATAC TAGTAATAGCAAGTTTAGTAATAAT
TATCATCATCCATCAGGTAATGAACCAGGATGGAATTTTTTACTTGATGAAGCATCAACGAAAAACAACA
TCAAAACAATACAGATCAACAGGAACAACAGGAACAGGAATAGGAGCAACAACCAATATAATATCAGAA
TCAGAATCGGAATTAAAAGTGAAACGAGAATCAAGTATTGCCAATATAATCAATCCCTCAACAACAACA
ACTTCCACAACAATAATAAGAATAACAATAACACTTCATCATCTACTAAAAC TAGAAAATATTCTCAA
GATCCAACAAGAAAATTTCTTGTGATAAATGTCCCATGTCTATTTTCGTGATCATCAGATTTAAACGT
CATGAAAAACAACATTTAACTATCCCACCTAATATTTGTCAATTTTGTGGTAAAGGTTTGTCTAGAAAA
GATGCTTTTAAAAGACATATTGGGACTTTAACATGTAAGAAGAAATGCTGATAAGAAATATATATTGAA
AATTTAAATTATTTAAATAAATTCAGTCAAGATGATGATGATGAAGAGGAGGAGGATGAAGAAGAAGAA
GAAGGATTGGAACAGGATAGATTGTATAAGAAGAGGAGGAAGAGTAATAATAATAATCAAATAATTA
GAAGAAGGATTTGAACATAATGATGACGATGATGATGATGATGAAGAGGATGAAGTGAACGAGAATTT
CCAACCTTATGGATATCAACAGAATTGA

YDR253C_homolog 583aa (SEQ ID NO 412)

MQNTNRNNSNSKNNSDNHHQQQQRQRQQQVDQYQSITLPLQYQSNTHESIVLPSQQPKRGRSEHFNS
QFQRNINSRPVLLPSSRDNNNTNIPIPIILPSSTNSNNPITSSNSRMFSPNPVSPLYPVVTPSSAL
SPPTQHHQQQQQLHKKFKTSNSGSNTPITGGGIGSPSTTSYLSANSANISYTRSQPLKDNNTQTSSTTKD
NNNTIIENEDQKFFRLAKEALVATAKGVKTNHNNNGKFGNNTSKIDINNHNKNNNNKSDGNETILDST
IADLLRRLQYASAPHGNPIGQISGLQTNKGLLEVQDEYSNFPDLQNNNFFKVNNGDNNNTSNSKFSNN
YHHPSGNEPGWNFLLEASTKTTSMNTRSTGCTGTGIGATTNIISESESELKVKRESSIANIINPSTTT
TSTTTNNNNNTSSSTKTRKYSQDPTRKFPDCKCPMSFRRSSDLKRHEKQHLTIIPNICQFCGKGFPARK
DALKRHIGTLTKRNADKKLYIENLNYLNSSQDDDDDEEEDEEEEGLEQDRLYKKRRKSNNNNQIIK
EEGFHNDDDDDDDEDEVKREFPTYGYQQN

YDR276C_homolog 516bp public: 1..516 (SEQ ID NO 413)

ATGTGTTTATGTCTTTCCGATTATTTCTTATTATTCTTTTCAGTATTATTTCCACCATTACCTGTTTGG
ATTAGAAGAGGATGTTGTTTCATGTGATTTCATTAATTAATTTAGCTTATGTATGTTAGGATATTTCCCA
GGGTTAATTCATTTCATGGTATATAATAGCTAAATATTCTTCTTATTATTATCAACAACAACAACA
CGTAAAGATACCATTTATTATGTTTATCGAAGTGATTTAGAAAATCAAACACCAAGAAGAGATGGCAGA
GATGGGAGAGATGAATGTCATCATGACCACCACCACCACCATCATCATCATCACAACCAGGCAGAAATCA
CAAAGTGCGGGATTAAATAGTTTCTAATAATCATAATAATAATAATAATAACTATGGATCTGTGGTTGAA

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GGTTCATCATCATCGAATTGACTCCTGTGGCTCCTATTCTGTGAAAATGGAGCTCCACCACCAGCT
TATACTGAGATTGATAATAAAACACAACATTAA

YDR276C_homolog 171aa(SEQ ID NO 414)
MCLCLSDLFLIILSVLPVWIRRGCCSCDSLINALCMLGYFPGLIHSWYIIAKYSSYYYQQQQQQ
RKDTIYYVYRSDLENQTPRRDGRDGRDECHDHHHHHHHHHQAESQSAGLIVSNNHHNNNNNNYGSVVE
GSSSSNLTPVAPIPVENGAPPPAYTEIDNKTQH

YEL039C_homolog 333bp public: 1..333(SEQ ID NO 415)
ATGCCAGCTCCATTGAAAAAGGTTTCAGAAAAAGAAAGTGCCACTTTATTTAAAACTAGATGTTTACAA
TGTCACACCGTTGAAAAAGGTGGTCCACACAAAGTTGGTCCAAATTTGCATGGTGTTCGGTAGAAAA
TCCGGTTTGTAGTGAAGGTTATTCCTTATACTGATGCTAACAGAAGAAAGGTGTTGAATGGACTGAACAA
ACCATGAGTGATTTTGGAAAAATCCAAAGAAATATATTCAGGTACTAAAAATGGCTTTTGGTGGTTTA
AAGAAACCAAGGACAGAAACGATTAGTTACTTTTGAAGAAAGCTACTTCTTAA

YEL039C_homolog 110aa(SEQ ID NO 416)
MPAPFEKGSEKKGATLFKTRCLQCHTVEKGGPHKVGPNLHGVFGRKSGLAEGYSYTDANKKKGVWTEQ
TMSDYLENPKYIPGTKMAFGGLKKPKDRNDLVLYLKKATS

YER112W_homolog 321bp public: 1..321(SEQ ID NO 417)
ATGTCAGCAGGTATTCCAGTAAGACTTCTAAATGAAGCACAAGGTCATATAATATCAATAGAATTGATA
AATGGAGATACATACCGTGGGAAGCTATTAGAAAAATGAAGATAATATGAATTTATCCTTATACGAGGCA
ACTATAACACAAGGCAATCGGGGAAAGTAAGTCATATGGACCAAGTGTATATAAGAGGGTCAATGATT
AGATTTATATCTGTGCCGTGATATTTTAAAGAATGCTCCTATGTTTTTTATGAAACCTGGAGATAAACCA
AAACCTCCAATAAGGGGCCCTCCACCAAAAAGAAAGAGATATGA

YER112W_homolog 106aa(SEQ ID NO 418)
MSAGIPVRLLEAQQGHIISIELINGDTYRGKLLNEDNMNLSLYEATITQKSGKVSMDQVFIRGSMI
RFISVPDILKNAPMFFMKPGDKPKPPIRGPPPKRKR

YFR010W_homolog 1239bp public: 1..1239(SEQ ID NO 419)
ATGGTTTTAGGCACTCCAGACAAGAATTTGCCTTCAAAGCCAGTTGAAAAACAAGTTTTTCTCGAAGAT
TTGAATAAAAAATCAATTGGTTAAAGTTAGTAATGAACCTAGTGGGTTGACCAATTTAGGGAACACTTGT
TACTTGAACCTCAAGTTTACAAACAATATTCCATATTGATGATGTGAATAACAGGTTGAAAGATTACACT
TTTGGTGGAGCCAATCAAGCCAATAGTGCCTTTGTGTTGTCATTGAAAAGTATGTTCCAGCAAATGTCTG
AAAAACAAGAAGTTATAACTCCTTCTACATTTCTTTCTCTTTTCAGAAGATCTTATCCTCAATTTGCT
GAACAACAAAATGGTATTTATAACAACAAGACGCCGAAGAAGCATTTCCTCAATTTGAGCTCTTTG
AGAAGCGAATTGAAAATAGATGATGTGTTCAAATTTACATTTAACACCAAGACTCAATGCTTGGCTATT
CCAGAAGATGTCACAGAAGGGTTTGAAGAAGCATATAAATTGAATTGTCATATCGGCGTCAAGACCAAT
TTTTTGAGAGATGGATTGTTGGCTGGATTAAAAGAAACGATTGAAAAACATAATTCAACTTTGAATGCT
GATACTGAGTATGAACAACCAAGACCATAACTAGATTACCAAATACTTGACAGTACATTTTATTAGA
TTTTTCTGGAACGAGACATCAATAAGAAATCCAAGTTTTGAGAAAGGTTCAATTTCCCATTTGAATTA
GATTTAGCAGAAATGTTGGATGTATCAATAAAGGCAGATAAAGTTTCCAATAGAGATACAATTAGAAAA
GTTGAAAAAGATAATTTGGATATGATAAGAGATTTCAAAAAGACCAAAAATGACACCAGTTTAACACCA
TTGGAACAACAAGAGGAGGATGAGATGAAAATAACATCAATCAAGAGTAAGTTTAAAGACGACTTGAAT
AGCGCTTTGCCCAACGTTGATTTTAACACCACCACAGAAAACCTTCTAGTGTGATGAATTAACGCA
GTCATTACTCATGCTGGATCATCTGCCGATGGTGGTCATTATAAAGCATACGTCAAGGATCCAACAGAC
TTGGATGGCGAGAGATGGTGGTTATTTAACGATGATAAGGTGAGCTCCGTAAACAAAAGAAAGATCGAA
ACTTTAGCTGGCGGTGGTGAAGCGACTCAGCTTTATTATTGATTTACAAAGGCTTAGGGCTTTAG

YFR010W_homolog 412aa(SEQ ID NO 420)
MVLGTPDKNLPSKPVEKQVFLEDLNKNQLVKVSNEPSGLTNLGNCTCYLNSSLQTIHFHIDVNNRLKDYT
FGGANQANSFVLSLKSMTQMSKKQEVITPSTFLSLFRRSYPQFAEQQNGIYKQDDAEAFSQILSSL
RSELKIDDVFKITFNTKTQCLAIPEVDTEGFEEAYKLNCHIGVKTNFLRDGLLAGLKETIEKHNSTLNA
DTEYETTKTITRLPKYLTVHFIRFWKRDINKSKILRKVQFPFELDLAEMLDVSIKADKVSNRDITRK
VEKDNLDMIRDFKKTNDTSLTPLEQQEEDMKITSIKSKFDLNSALPNVDFTNTTENPSSVYELNA
VITHAGSSADGGHYKAYVKDPTDLGGERWWLFNDKVVSVNKEKIETLAGGGESDSALLLIYKGLGL

YFR052W_homolog 834bp public: 1..834(SEQ ID NO 421)
ATGTCTTTACAAAACTCACTGCAGAAATATACTCACTATTTGAAAAAGGAGATTATCAAGGTTGCCAA
CAATTACTTGCTCCGATTAACTAGAATTAGTCAACATGATTTGTTGGTTCTTTACCATCCAACACC

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ACCGATAAAAACCAAATTAATGATTGAGAAATGCCCCAAGAATTTTGGAAATTGGAGCATTATCGTCA
TTATTAACCAACAACCTATCCGGTTTTGAGAATTATTTTGCCTCAGTTGAGACCATTTTACTCTAACCCC
AAATTACATAATTTACAAAAAGTCCATATCAATACCGATATAACAAAAATCATTTTATTATACCTTGTTA
TACTTGTGAGTCAGGGTTTGATTTCAAAATTCATGTTGAACTAGAAGTGATTTATAATTCATCACAA
TATGATGCCCCAACAGACAAGTATTTACAATTTCCAATAAATTTAGAAAGCAATTTAATGGAAGGTAAT
TACATAAAAATCTGGAAGTTATTAAGAAGAGAAAAACCTTACCATGTCAAGAATACACCCATTTTGTT
GATACTTTGATAAATGCTTTACGTTTTGAAATTGCCAAATCTTTGGAGAAAACCTTACGATTGATTCCA
ATTTCTAATTGCAAGAATTTATTATATTTACCACAAGAATTTGTCGATGCTAACCTTTGAGAAAACCTTA
AAGGAACTTATCAAGTTGATAATTGGAAATTCGAGGATGGAGTTATATATTTCACTAAGAATGAAAT
GAAACCAATGTTGATAACCAATCGGTTATAAAGAATTTATTAGGGTACGCTGAACAAATCGAATCCATC
GTATAA

YFR052W_homolog 277aa (SEQ ID NO 422)

MSLQKLTAEIYSLFGKGDYQGCQQLLAPIKLELVKHDLLVPLPSNTTDKNQINDLRIAQRILEIGALSS
LLTNNYSGFENYFAQLRPFYSNPKLHNLQKVHINTDITKIISLYLLYLLSQGLISKFHVELEVIYNSQ
YDAQQDKYLQFPINLESNLMEGNYIKIWKLKKEKNLPCQYTHFVDTLINALRFEIAXSLEKTYDSIP
ISNCKNLLYLPQELSDANFEKTLKETYQVDNWKFPEDGVIYFTKNENETNVDNQSVIKNLLGYAEQIESI
V

YGL080W_homolog 354bp public: 1..354 (SEQ ID NO 423)

ATGTCATCATTTAAAAAATTCAGTATTTTTATTTTCAAACAATCCCTTAGATATGTCTGTACAACT
CATTTTTGGGGTCCAGTATCAAATTTTGGGATTCCTATAGCTGCTATTTTAGATTTGAAAAAGATCCT
GATTTAATTAGTGGACCAATGACTGGTTCATTAATACCTTTTATTCTTTAGTGTATGAGGTATTCAATG
GCAGTTACTCCTCAAATTTATTATTGTTGGGTGTCAATTTGTTAATGAATTGGCACAATTGAGTCAA
GGATTTAGATGGGTTAAACATCACTATGATACTTCTTCAAATGATGGTGAAGATACCAAAAAGATAACT
CAAAATTGA

YGL080W_homolog 117aa (SEQ ID NO 424)

MSSFKKFTDFLSKQSLRYVCTTHFWGPVSNFGIPIAAILDLKDPDLISGPMTGSLILYSLVFMRYSM
AVTPQNYLLFGCHFVNELAQLSQGFRWVKHHYDTSSNDGEDTKKITQN

YGR070W_homolog 4146bp public: 1..4146 (SEQ ID NO 425)

ATGTCGAGTAATAGTTCTTGGTCTAACAACGATTCTTACCAACTGAGGAACAATCCTAATAATGGTAAT
AACCATAACCCACATTTAATGTCACAACAACACTCACAATCTGTAAATATTCCTTCTCATTTGTGCTT
CAAGCATTTTATAGAACAACAACAACCAACCAACCAACCAACAATATCCGCAAGACGGCCAA
GCTCATAACAAAAACCCACCAATCAATAATCGTTTTTCATCAATCACAACCACCACAACCTGCGCCATCAA
TACATCCCATCCAAACAAGAACAATGCAACAACCTTACCCAACCTGCCGAACAAAATAATCAACACTTT
CCTCCACCACAGGAAGATCATATAGTTTTCATCGACTATGGATCCTGGCTCACCTAGCAAAATGACG
CCACCTAATTTTTTACAAAAGGAACCAATCATTTTCTGGCTACCAACAACCACCACCACAACAACACAG
TATCCGCAGTCAACCCATAAGGCATATAACCAACAACCAACCACTCACCAGGTGGACTTCAACAGCCA
TACATTGCGCAAGACAAAACATGCCACCTGGATATATTAACCAGAATCCATATTCTCAGCAAAATGAGA
TCAGTATCATCTTTGACTCAAGATAGGACAGGAGCACCAGTACAACACCTTCTTATCCTGTCAACAAT
GATGATCCTGGATATCAACTACAACCCTGGCAATTCATACACCACCCACCACAACAACAACAACA
CAACAGCCTCCACTCCAGACACGTAGACAACCTTCGTAAGGCCCTTCGAGCAACTTGCCCCCAATTCAA
ACTGATCAAGTTTACTATAGCCCTGATGCTAGAAGAATGTTTCCACACCTACACACCAGCAGAATTTT
CCCACTCCCATACCACCAGAAGCTAGAACAATACTACTTCTCGGCATCATTAACAACACCAGAACAA
CCACTGCAACCTCTGCAACCATATTTCCAACAATCTCTGAACCTGCCAGGTAAAGACAGCAACGCTCGT
AATTCCTCCAGCAGTTCCCTTCATCATACATTTTCTTAACTCAAAATCGCGATCATTTACATCTATC
AGTAAATTGTCGTCTTTATCAACTAAGAAATTCGGTTTCTTCTCATCGTCAATACCAACAAATTAGAT
CGTTATCAATCCAGTGGAACTATTAGAAACAATCACAATCATAACCACACCAACCAAACTAGCCACAAC
ATTCAATTATGCTAAACCATCAGTATATCCCGCAATTTATCTGAAGTGGCCAAATTTGTTAAAGAGGCG
ATTATTTTGACGATCAACACCAAGGATGGTTTGAATACCATGATACTTTTACCGGGAATTTGCGAGTT
GATATATTATGTCGCATTATTCGAACAATGATCGTAACCTTGGCCTTGTTATTGGGAAGATCATATAGAC
GCTCAGAAGTTTTTCCATGATGTTACTTACAATCATAGATTAAGGGATTTCGGTACATGAAATTTATGCC
TTTAACAATGTTTATAATGATGTTGATTTTTCAACGAAGAAAATGGAGGAGCTGGTCTGGTTAGCAAT
GGGGAATAGTGCATTAAATTTCCAAACATGGGTCGTTTTCTTGATAGCAGCACACAGTTACAGAATGCT
TTGAATGGACCATATCCGATTATCATACCTCACAAGCAGTGGATCATTAATAAAATTTGCTAGTAGT
GCCACTGGATATGGTTTCACTAGGTGTTGCTGGTAAGGAGTTGAGTGAAGTCAACAAACAGGTGTTAAT
GGAGTTTTCACTATTTTGACAGAATGTTATTCGCCCATGTAGCAGAAATAGTCTTTGTTACAGTATT
GCCTGTCCAAGAAGATTAGAGCAACAAGCTAGATTAAATTTGAAACCTCAAGGTGGTTTGAACGTCGT
GTTTCAAATTTATCATTCATGATCAGGAAGAAACCGAACTTTATGGCACAAGACTGTACCTCAATCA
GTTTTAGATAAATTAGACAAGCATGAAAAGACTCGACAAGAATTGATTTATGAATTTGTTTATACGTAA
CGTGACTACGTCAAGGATTTGGAATTTATGACTGATTTCTACATTATGCCGTTACGAAATCCTGCCAAT

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AATATTATTCCTGATTACCAAAGAGAAACATTTATTCAAACGTGTTTGGGGGAGTGCCTGATTGTG
AGATTGGCCAAGAGACTCAGTGAAGCATTAACTCGAAGACAACAACAACAAAAGCCCGTTATTGAGACC
ATTGGTGATGTATTTTTAGATTATGTTGGTGATTTTGAACCTTTTGTGACATATTCTGGAAATAAAGTG
TTTGCTACTTTTGAACATGAAAGACAACAACAGTTAATATGAAATATGCTAGATTCTTAGATCCGATT
GAAAAGAAACAGAATCGAGAAGACAAGATTTATCATCTTTTTTAATTAAAGGGGTTCAAAGAGACGCA
AGATAACAGTTATTGTTATCGGGTATTTTGAACATACCAAGCCAGAGTCACCCGACTACAAGTATTTG
ACGAAAGCAAAAGAAGAGATTGAGAAATTATTGGTGAAATCAATATCCAAACTGGGGAATGTACTGAT
CGACACAAAGTCATGGTTTTGCATAGGTTATTGGGCAAAACAACTTTGGAAATAGGTTTAATTTCAAA
TTATCCTACAATAATCGTATTATCTATCAAGTGACTTTGAATAGAAAGAGGGATAACGAAAAAATTGAT
TTATACTTGTGTTGAACATGCGTTGTTATTAGTGAAACACAAGATTCAAAACAAGCGTGAAACAACATAAA
GTATTTGAAAAACCAATGTATTTACCATTGTTATTGTCATAGTGGTATGGAGATCCCCACTAATAGA
ACAATCATGCCCTCATAGATACCATGGATCCTTGGTATCTGATACCTAGTATAAGACCTCAAAGAGCAGAA
TCTAATTATATTGGTAATACTTTGAATTCCTCATCAACACCTAAATTCCAATTGAATTTTTTTGGGTTA
GGTAGTAATCAAGTTCACGCCTCATTATTTGCTGATGACTTGACTATTTCAGAACCAAGTGTGCTGCAA
ATATCGGCCCAACAGAAGAAATTAATTGATGCTAATGACATTTTTTCATTGTGTAAATTGAAACGAGA
AGATTCACTGGGAATAATAAAATCAATTGTGCTGTTCTTGTATGGTGGGAAGAAATGTTGTATGGT
ACTGATTACAGGGTATGGGTTAGTACTGTTTCGTTCAATTAGTGCCACATCTAATGAAAAAATCTGTAGT
GATCCCACTATGGTCATTTCCAAAACCTTAGTCACTCAAATTGAAGTGATTGTTGAATACTCCAAGTTG
TTAGTATTGAGTGACAAATCATTATATGAATTTGATTTATCTTGTACCGATTCTTTGGATCATGTGAAG
AATACCAAACCTGGGGAATTTGCTTTTGAGTCATGTGTCAATTTTTCAAAGTTGGTGTGTTGTATGGGAAA
TTGCTAGTGATTGGTGCTAGAACAGGTAGTCTGCATTCAATTTGTATATTTGAGCCTGTTAATCCATTT
GATAAATCGAATAAGAATAAGAACAAGAGATTAGAAATCAAGAAATTAATTTCAAGTCTGATCCAATT
TCCATCTCATTTTGAAGACTAACTTTGTATTTGGGTGCTAAAGGTTTTGAAATTTATCTTCTCAA
ACAGGAACCAAGAATCGATTTTGGATGAAGCAGACCCCTCATTAGATTTTGAACACAAAAGAGAAAGT
GTGACACCATTAGCAATTCATCGATTAGGACGTGATTTCTTATTGTGTTATTCTGAATTTGTATTTTTG
ATCAATCGAAATGGATGGAGAACAATCATGATTGGGGGATATTTTGGGAAGGTAATCCACAAAATGTT
GCGATTTTCTTCCCTTACTTGTATCATTGAACTGGATTGTTTGAATTTAGAGATTGCAATACAACT
AATTTTATAAGAGCTTTAACGGGAGAGAATATTAGATTTTGCATTGCAACGAACATGAAGCTATGTTT
GCTTGTGAAGAAATGGATATGATATTATTATTTCCATTGATTTCTTGAATTTGAAACCAAGTCTCCA
ACATAA

YGR070W_homolog 1381aa (SEQ ID NO 426)

MSSNSSWSNDSYQSRNPNNGNHNPHLMSQQHSQSVNIPSHLLPQAFIEQQQQPPQPQQYPODGO
AHNKNPPINNRFHQSQPPQSRHQYIPSKQEQMQPYPTAEQNNQHFPFPQERSYSFSSTMDPGSPSKMT
PPNFSQRNQSFSGYQPPPPQYQSPHKAQYNOQTHTHQGGGLQPYIAQRQNMPPGYINQNPYSQQR
SVSSLTQDRTGAPVQHLPPVNNDDPGYQLQPSAIQSHHPQQQQQQPPPLQTRRQLRKAPSSNLPPIQ
TDQVYVSPDARRIVSTPTHQONFPTPIPEARTKSLTSASLKHQKQPSQPSQPYFQQI SESPGKDSNAR
NSSSSSLHHTFSLTSKRSRFTSISKLSLSTKKFGSSSSVNTNKLDRYQSSGTIRNNHNNHNTNQTSHN
IHYAKPSVYPAILSEVAKLPKEAILTINTKDGLEYHDTFTGKMAVDILCRIIRTNDNRNLALLLGRSLD
AQKFHFDVYTNHRLRDSVHEIYAFNNVYNDVDFNEENGAGSVSNGENSALNSKHGSPFLDSSTQLQNA
LNDHISDYHTSQSSGSLTKIASSATGNGSVGVAGKELSASQQTGVNGVFTILTCEYSPTCRNSLCYSI
ACPRRLEQQARLNLKPQGGQLQRAVSKLSLHDQEEETLWHKTVPQSVLDKLDKHEKTRQELIYEFVYTE
RDYVKDLEFMTDFYIMPLRNPANNIIPDYQRETFIQTVFGGVPDLLRLAKRLSEALTRRQQQKPVET
IGDVFLDYVGDPEFPVYSGNKVFATFEHERQQQVMKYARFLDAIEKKPESRRQDLSSFLIKGVQRP
RYQLLSGILKHTKPESPDYKYLTKAKEEIEKLLVKINIQTGECTDRHKVMVLHRLLGKQTLNRFNFK
LSYNNRIYQVTLNRKRDNEKIDLYLFEHALLLVKHKIQNKREQHKVFEKPMYLPPLFVNSGMEIPTNR
TIMPHRYHGSLSVSDTSIRPQRAESNYIGNTLNSSSTPKFQLNFFGLGSNQVHASLFADDLTIQNVLSQ
ISAQKKLIDANDIFSLCKFETRRFTGNKNKINCAVPCYGGKKLLYGTDSGVVSTVRSISATSNEKICS
DPTMVISKTYVTQIEVIVEYSKLLVLSDKSLYEPDLSDTSLDHVKNTKSGKLLLSHVSFVKVGVCDGK
LLVIGARTGSSHSICIFEPVNPFDKSNKNKNRLEIQEINFSSDPISISFLKTKLCIGCAKGFEILSSQ
TGTKESILDEADPSLDFATQRESVTPLAIHRLGRDFLLCYSEFVFLINRNGWRTNHDWGIFWEGNPQNV
AIFFPYLLSFEPGFVEIRDHLHTNLLRALTGENIRFLHSNEHEAMFACEENGYDIIISIDFLNLKPKSP
T

YGR132C_homolog 966bp public: 1..966 (SEQ ID NO 427)

ATGCTCATTATTGACACCAAAATAATTTCTTCACCTTTTTTTCTTCTTTCTTTCTTCAAGACAAGC
ACAGTTTCTTCCCTCTGCTACTGCTAAACGTCCAATCAAACTATGTCAACGAATTGCAGATTTT
GTTTCTAAATAGCCTTGCCAGCTGGTATCACCATTGCATTGGCACAATCAGCCTTGTATGATGTTCTC
GGGGTAAGCGTCAAGTATATTTGACCGTTTAAAGGGGTCAAACAGGAGTTATTGGCGAAGGTACC
CACTTTTTTGGTGCCATGGTTACAAAAGGCAGTGATATTTGATGTTAGAGTTGAACCACGAGTAATTACT
ACCACTACAGGATCTAAGGATTTACAGAATGTTTCATTGACATTGAGGGTGTGAGTAGACCCGAAGTA
AGAAAATTGCCTACTATTTACCAAACCTTTGGGGTTGGATTACGGGGAAAGGGTGTGCTGCCATTGGT
AATGAAATTTGAAATCGATTGTGGCACAATTTGATGCTGCTGAATTGATCACCCAGAGAGAGGTTGTT

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TCTGCCAGAATAAGACAAGAGTTGTCAAGAAGAGCCGCAGAGTTCAATATAGAATTGGAAGATGTGTGCG
ATTACACATATGACATTTGGTAGAGAGTTACCAAAGCCGTGGAAAAGAAAACAAATTGCACAACAAGAT
GCAGAAAGATCAAAGTTCCTTGTGGAGAGAGCAGAACAGGAAAAGAAGGCTGCGATTATCAGAGCTGAA
GGGGAGGCCGAATCAGCAGACGTTGTTTCCAAGGCGTTGGCCAAAGCTGGGGATGGGTTATTGATGATC
AGAAGATTGGAGGCATCAAAGGACATTGCATCAACATCGGCAACTACCAAATATCACTTATTTACCT
AATGGTGGCGCTGGCGGCAGCGATAGCGACGGGTCCAAAACTCATTATTGTTGAATATTGGCCGTTAA

YGR132C_homolog 321aa (SEQ ID NO 428)

MLIIDTKIISSPFFSSFSFPKTSTVSSPSLSLNVQSNMTMSQRIADFVSKIALPAGITIALAQSALYDVP
GGKRAVIFDRLKGVKQGVIGETHFLVPWLQKAVIFDVRVEPRVITTTTGSKDLQNVSLTLRVLSRPEV
RKLPTIYQTLGLDYGERVLPALIGNEILKSIVAQFDAEELITQREVVSARIRQELSRRAAEFNIELEDVS
IHTMTFGREFTHAEKKQIAQQDAERSKFLVERAEQELKAALIRAEGEAESADVVSALAKAGDGLMI
RRLEASKDIASTLANSPNITYLPNGCAGGSDSDGSKNSLLLNIGR

YGR135W_homolog 756bp public: 1..756 (SEQ ID NO 429)

ATGTCAAGAAGATACGATTCAAGAACCCTATTTTTTACCAGAAGGTAGATTATACCAAGTGGAATAT
GCTCAAGAAGCCATATCCAATGCTGGTACAGCCATAGGGATATTATCTCCTGAAGGTGTCGTTTTAGCG
TGTGAAAAGAAAGTCACCTCCAAGTTATTTGGACGATGATGGATCAGCTGAAAAATATACATTTATCAAC
GATCAAATGATTTGCGCTGTTGCTGGTATGACTGCCGATGCATCAATTCTTGTGAATAATGCAAGAATT
CAAGCCCCAACAGTATTTGAAGTTGTACGACGAAGAGATTCTTGTGAAATGTTGATCAATCGTGTGTTGT
GATGTCAAACAAGGTTATACCCAACATGGTGGGTTGAGACCATTGGTGTAGTTTCTTTATGCCGGG
TATGATGACAGATATCAATTCCAATGTTTACATCGAATCTTCTGGTAATTACAGTGGTTGGAAGGCA
ACTAGTATTTGGTGCTAACAAATCTGCTGCTCAAACCTTTATTGAAGAAAGATTACAAGGACGATTTGACT
TTAAAGATGTCATGCGAATTTGGCTATCAAGGTTTATTCAAAACTATGGATGCTTCAACATAAATAGT
GAAAAATTAGAATTCGCTACCTTAAGTTTGGGCAAGACAACAAAGTGTTCATAAAATTTGGAACGAT
AAAGATATTGACATCCTAATTAAGGCTTCGGGGGTTTTGAACGAAAAAATAGCGATGATGAATAG

YGR135W_homolog 251aa (SEQ ID NO 430)

MSRRYDSRTTIFSPGRLYQVEYAQEASNAGTAIGILSPEGVVLACEKKVTSKLLDDGSAEKLYIIN
DQMICAAGMTADASILVNNARIQAQQYLKLYDEEIPCEMLINRVCDVKQGYTQHGGLRPFVGSFLYAG
YDDRYQFQLFTSNPSGNYSGWKATSIGANNAAQTLLKKDYKDDLTLKDACEALIKVLSKTMDSNINS
EKLEFATLSLKGDNKVLHKIWNKDIDILIKASGVLEKNSDDE

YGR155W_homolog 1491bp public: 1..1491 (SEQ ID NO 431)

ATGACATCTACAAACAAACCACAGCCTTAAAAGAAGATATTTTAGAACTTATTGGTAATACTCCATTA
GTCAAATTGAAACAAAATTCACAAATCGTTGGGAATTAAAGCCAAGGCTATGCCAAAGTTGAATTATTC
AATGCCGGAGGATCAATTAAAGATAGAATTGCCAAAAATATGGTATTGGAAGCCGAAAAACAAGGTAAA
ATCAAACCAGGCTATACCTTGATTGAACCAACCTCAGGTAATACTGGTATTGGTTTGGCTTTGGTTGGT
GCCGTTCCGTGGATACAGAACCATCATTACCTTACCAGAAAAATGTCAAACGAAAAAGTTTCTGTTTTG
AAAGCCTTAGGTGCTGAAATCATTAGAATCCAACTGAAGCTGCATGGGACTCTCCAGAATCTCATATT
GGTGTGCTAAAAAATTCGAAAAAGAAATACCAAACTCTATTATTTTGGACCAATATGGTAAACCCAGCC
AACCAGATGCTCATTATTATGGTACTGGTTATGAAATTTGGGAACAACTGAAGGTAAAATTACTCAC
TTGGTTGCTGGTGGTGGTACTGGTGGTACCATCACTGGTATTTCCAAATACTTGAAGAAAAAAATCT
AAGATTCATGTTACTGGTGCAGCCAAAAGGTTCTATTTTAGCTGAACAGAAATCTTTAAATAATTCC
ACCGAAGGTTACTTGGTTGAAGGTATTGGTTATGATTTTATTCAGATGTGTTGAACAGAAAAATATGTT
GATGATTGGATCAAAACAGATGATGCTGAATCTTTAAATTGGCTAGAAGAATTATTAGAGAAGAAGGT
ATTTTGGTTGGTGGTTCTTCTGGTTCTGCCTTACAAGCTGCTTTACAAGTAGCTAAAGACTTGACTGAA
GACGATACTGTCGTTGTTGTTTTCCAGATTCCATCAGATCTTACTTGTCTAAATTTGCCGATGACGAA
TGGTTAATCTCCAATGGATTTCGAAGTTGAAGATTACCGGGTGCATAACAAGGCTGACGAATCTTGAAT
GGTAAGACTATCAAGGATTTGGTTGCTGGCAAAGCTCCAGTTGTCACTGTCACTTTATCTGACACAGTT
GCCAAGACTTTTGATTTATTGCAATCCAATGGGTTTGATCAATTGCCAGTTTTGAATAACTCTGGAAGA
TTAGTTGGTTTGATCACCCTTATCCAAGATATTGAAATCTTTATCCACTAAAAAGATTCAAACGACCAAT
TCAATCAGTTCGATCATCATTGATTTTCAGAAAGTTGGCTGATTTTGAAAAAATCTTTCACCATCAAAA
AAATCAGGATTCACATAAGAGAAGTTATGAACCAATCAAGTTGGACACCCCATTAGCTGCTTTGAATAAAA
TTCTTTGAACCAATTCAAATGCTATAATCACAGATGATGAATTGAAACCAGTTCAAATTGTTACTAAG
GTCGATTTGCTTTCTGATTTTACTAAAAACGCTAGTTTTTAA

YGR155W_homolog 496aa (SEQ ID NO 432)

MTSTNKPALKEDILELIGNTPLVKLNKIPQSLGIAKAKVYAKVELFNAGGSIKDRIAKNMVLEAEKQKG
IKPGYTLIEPTSGNTGIGLALVGAVRGYRTIITLPEKMSNEKVSVLKALGAEIIRTPTAAWDSPESHI
GVAKKLEKEIPNSIILDQYGNPANPDHYYGTGYEIEWEQTEGKITHLVAGAGTGGTITGISKYLKEKNS
KIHVTGADPKGSILAEPESLNNSTEGYLVEGIGYDFIPDVLNRKYVDDWIKTDDAESFKLARRIIREEG
ILVGGSSGSALQAALQVAKDLTEDDTVVVVFPDSIRSLSKFADDEWLI SNGFEVEDSPGANKADEFLN

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GKTIKDLVAGKAPVVTVTLSDTVAKTFDQLQSNQFDQLPVLNNSGRLVGLITLSKILKSLSTKKIQT
TN
SISSIIIDFRKLADFESFTITKKSQFTKRSYEPKILDTPLAALNKFETNSNAIITDDELKPQIVTK
VDLLSYLTKNASF

YHR138C_homolog 384bp public: 1..384(SEQ ID NO 433)

ATGAATCAAAATAAGAAATTAACGGTTTAATATTATTAGCGATTATATCAATCATTACTTTATTCAAC
TTTAAACAATTTCCCAAATAACTGCCATCAGATCATTGTCTCCCTGCCTCTTCCACCGCTACTAAT
ACTAATACTAAATCAACAATGTCAGATTCCAAAGGTTACATTATCACTTTGAAAGATACTTGTGCTGAT
TCCGAAGCTAGTTCAATTAAATCAAAGATTACTGAATTGGGAGGTAATCACTAATGAATTTAGTTTA
ATCAAAGGATTTCTGCTCAATTGCCAACTATCCATGCTGAAGCTTTACCTAAAGATTTTGCTGGTATT
GCCAATATTGAAGAAGATGGTGAAGTTCGTACACAATAA

YHR138C_homolog 127aa(SEQ ID NO 434)

MNQNKLTGLILLAIISIITLNFNFKTISQITAIRSFVSPASSTATNTNTKSTMSDSKGYIITLKDTCAD
SEASSIKSKITELGGKITNEFSLIKGFSAQLPTIHAEALPKDFAGIANIEEDGEVRTQ

YHR179W_homolog 1212bp public: 1..1212(SEQ ID NO 435)

ATGACAATCGATAACGAAGGCATTGTCATTAAACCATTGGGTTCAACAAAATTATTCCAACCAATAAAAA
CTTGGTTTTAACACTTTATCACAAGAATAGCATTGTCACCATCCACACGTTATAGAGCAACCAAGAT
AATATCCCTACCGATTTACAATTAGAGTATTATTCTCAACGATCAGAATATCCTGGAACTTAATCATT
ACTGAAGCAACTTATACATCACGTCAAGGTGGATTAGTACCATATGTTCTGGGATTTATAATGATGCT
CAAACTAAAAGTTGGAAGAAAATTAATGATGCGATTATGCCAATGGAAGTTTCAGTTCAAGTTCAATTG
TGGTATTTAGGTAGAGTTGCTAATCCTAAAAATTTGAAAGATGCTGGATTACCATTTGTTGGAGCCTCA
TCAGTTTATTGGAATGAAGAAAGTGAAGAAATTTGGCCAAAGAAGCTGGAAATGAATTGAGGGAATTGACA
GAAGAAGAGATCGATCACATTGTTGAAGTTGAATATCCGAATGCTGCTAAACGTGCCATTGAAGCAGGA
TTTGATTATATCGAAGTGCATTACAGCTCATGGTTACTTGTAGATCAATTTTAAATCTTGCTCTAAT
AAAAGAAGTATAAATATGGTTGTGGTAGTATTGAAAATCGTGCTCGTTTATTATTAAGAATATTGAT
AAATTGATTGATATAGTTGGAGCTGAAAGATTAGCTATCCGTTTATCACCATGGGCCACGTTCCAAAAAT
GTTGACGTCGAAGGAGAAGAAATTCATAGTTATATCATTGATCAATTACAAGAAAGGGCAAATTTCTGGT
AATGAATTAGCGTATATTTCTCTTGTGTAACCAAGTGTTCAGCAAGTTGGGATATTGCTAAAGAGAAT
CAAGTTGGCTCAAATGAATTTATTTGAAACATTGGAAGGGGAAAGTAATTAGAGCAGGTACTTATGCT
CATGAATTAATAAATTAATGAAGATATTAATAATGATAGAATTTAATTGCCTTTTCAAGATTTTTC
ATTCTAATCCTGATTTAGTGAAAAAATTACATGATGGGATTTCTTTGACTCCTTATGAAAGAGCAACA
TTTTATAATCATGATAATTTTGGATATAATACTTGGATTAAATATGGAGAAAAATAAAGTTTTCATGAA
CAAGAAGAAAGGAAAAAATTTGGGTAAACCTTTAGCTTAG

YHR179W_homolog 403aa(SEQ ID NO 436)

MTIDNEGIVIKPLGSKLFPQIKLGFNTLSQRIAFAPSTRYRATKDNIPDLQLEYYSQRSEYPGLTII
TEATYTSRQGLVPYVPGIYNDAQTKSWKKINDAIHANGSFSSVQLWYLGRVANPKNLKDAGLPFVGAS
SVYWNEESEKLAKAAGNELRELTEEEIDHIVEVEYPNAAKRAIEAGFDYIEVHSAHGYYLLDQFLNLASN
KRTDKYCGSGSIENRRLRLRIIDKLIDIVGAERLAIRLSPWATFQNVDFEGEEIHSYIIDQLQERANS
NELAYISLVEPRVQASWDIAKENQVGSNEFLKHWWGKVIRAGTYAHELNKINEDINNDRTLIAFSRFF
ISNPDLVKKLHDGISLTPYERATFYNHDFNGYNTWIKYGENKVFNEQEERKKLGKPLA

YIL074C_homolog 1392bp public: 1..1392(SEQ ID NO 437)

ATGTCATCTCCTCAACAAATTTGTCAACTCATTCCAACAAGCCTTGAATTTATCAGGATCTCCAATGCT
GTTTCTACATCACCAACTCAATCATTCTTGAGTCAATATGTTCCAAGCAAGCCAGCTAAAGCTTTGAAA
CCTTTCAAACTGGTGATATCAAAATTTTATTATTGGAAAATGTTAACCAACTGCCATAAATATTTTC
AAAAACCAAGGTTACCAAGTTGAATTTTATAAATCATCATTACCCGAAGATGAATTTATAGAGAAAATC
AAAGATGTTTCATGCCATTGGTATTAGATCAAAGACTAAATTAACAGAAAAAATCCTTAAAGCTGCTAAA
AACTTGGTGGTTATTGGTTGTTTCTGTATTGGTACCAATCAAGTTGATTTGGAATTTGCTGCCAAATCA
GGTATCGCTGTTTTCAACTCTCCATTTTCAAATTTAGATCAGTTGCTGAATTAGTCATTGCTGAAATC
ATTACTTTGGCTAGACAATTGGGTGATCGTTCAATCGAATTGCACACTGGTACTTGAATAAAGTCAGT
GCCAAATGTTGGGAAATCAGAGGTAAAACCTTTGGGTATTGTAGGTTATGGTCACATTGGTTCCCAATTA
TCTGTCTTGGCTGAAGCTATGGGTATGAATGTTATCTATTATGATGTCATGACCATTATGCTTTAGGT
AACTCGAAACAAGTTGAAAGTTTGGACGAATTTGTGAAAAAAGCCGATTTTCGTTACTTTGCACGTCCCA
GCTACTCCAGAAACCAAGAACTGTTGAGTGCTCCACAATTTGCCGCTATGAAAGATGGTGCTTTACGTT
ATAAATGCTTCTAGAGGTACTGTGTGTGATATCCAGCTTTGGTTCAAGCCATGAAAGCCGGAATAAT
GCTGGTGGCGCTTTAGATGTTTACCCTCATGAACCAGCAAAGAATGGTGAAGGTTTATTTCAGTGATAGT
TTGAATGAATGGGCCAGTGAATTTGTTTCATTGAGAAATGTGATTTTGAATCCACACATTGGTGGTTCT
ACCGAAGAAGCCCAATCTGCTATTGGTATTGAAGTTGGTAAATTCATTGACCAAAATACATCAACGAAGGT
GCCTCTCAAGGTGCTGTTAACTTCCAGAAAGTTTCATTGAGACCATTAGATTTGGATCAACAAAATGTT

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GTCAGAGTATTATATATCCATCAAAACGTTCTGGTGTGTGAAAACGTGCAACAATATCTTATCCAAT
CATAACATTGAGAAACAATTCTCCGATTCTCAAGGTGATATTGCTTACTTAATGGCCGATATTTCTGAT
TTGATATCAGCGATATACAGTCATTATATGAACAATTAGAACAAACTCCATATAAAATTGCTACTCGT
TTGTTGTATTAA

YIL074C_homolog 463aa (SEQ ID NO 438)

MSSPQQIVNSFQQALNLSGSPNAVSTSPQSFSLSQYVPSKPAKALKPFKTGDIKILLLENVNQTAINIF
KNQGYQVEFYKSSLPEDELLEKIKDVHAIGIRSKTKLTEKILKAAKNLVVIGCFICIGNQVDLEFAAKS
GIAVFNSPFSNSRSVAELVIAEITLARQLGDRSIELHTGTWNKVS AKWEIRGKTLGIVGYGHIGSQL
SVLAEAMGMNVIYYDVMTIMSLGNSKQVESLDELLKKADFVTLHVPATPETKNLLSAPQFAAMKDGAYV
INASRGTVVDIPALVQAMKAGKIAGAALDVPHEPAKNGEGLFSDSLNEWASELCSLRNVILTPHIGGS
TEEAQSAIGIEVGNSLTKYINEGASQGAVNFPVSLRPLDLDQNVVRVLYIHQNVPGVLKTVNNILSN
HNIEKQFSDSQGDIAYLMADISDVIDSDIQSLYEQLEQTPYKIATRLLY

YIR037W_homolog 486bp public: 1..486 (SEQ ID NO 439)

ATGTCCTCAATTTTACGAATTAGCTCCAAAAGACGCCAAAAGGTGAACCATATCCATTTGAACAATTGAAA
GGGAAAGTTGTCCTTATCGTCAATGTTGCTTCCAAATGTGGATTCACTCCTCAATACAAGGGTTTAGAA
GAATTTGAATAAGAAATTTGCTGATCAACCAGTACAAATCTTGGGTTTCCCATGTAATCAATTTGGCCAC
CAAGAACCAAGTAGTAACGAAGAAATTTGGATCATTTCTGTTCAATTGAACTACGGTGTACATTCCCAGTC
TTGGATAAAATTTGAAGTCAATGGTGACAATACCGATCCAGTTTATAAATATTTGAAATCACAAAAGAGT
GGTGTTTTGGGATTGACCAGAAATTAATGGAAATTTTGAAAATTTCTTGATTGACCAAAATGGTAAAGTT
ATTGAAAGATTCAAGTTCATTGACTAGTCCAGAAAGTATCCGGTACCAAGATTGAAGAATTTGTTGAAGAAA
TAA

YIR037W_homolog 161aa (SEQ ID NO 440)

MSQFYELAPKDAKGEPPFEQLKGVVLIVNVASKCGFTPQYKGLEELNKKFADQPQVQILGFPCNQFGH
QEPGSNEEIGSFCSLNYGVTFPVLDKIEVNGDNTDPVVKYLSQKSGVLGLTRIKWNFEKFLIDQNGKV
IERFSSLTSPESIGTKIEELLK

YJR096W_homolog 849bp public: 1..849 (SEQ ID NO 441)

ATGTCATATCGATTAAATCAAATCAATTCGGTCATACCATTCATCAATTTGGATTAGGATGTTATGAT
ATCCCAAGAAATAAAACGGTTTCCGTAGTTTATGAAGCTTGTAAAGTTGGATATCGTCATTTTGATACT
GCAGTGTATATGGAAACGAAGAAGTCAATTTGAAGGTATAAGTAAATTCCTTACGAGAGAACCCCAAT
ATACCACGATCTGAGTTTTCACACCACAAAGCTTTGGAATAATCAATTTGGGTACTTCAAGCACTAAA
CAAGCCATTTCAACAATGATGGCTCAAGTTGGTGATAAATTAGAATATATTGATTTATTATTGATTCAT
TCTCCATTACCAGGTAAGACCAAACGTTTAGAAAGCTGGAAAGTTTGCAGGATGCTGTGGAAAAAGGA
TGGATTAAAAACATTTGGGGTTTCTAATTATGGTAAACATCATATTGAAGAATTTGTTGACCAATGCAACG
ATCCCTCCAGCTGTCAATCAAATTGAAATTAGTCCTTGGTGTATGAGACAGGATTTAGCTACTTGGTGT
TTAAGTAAAGGTATCAATGTTGAGGCATATGCACCATTAACCCATGGTAACAAATTACAAGTCAACAAT
ACTGAATTTCAAGAAATTATGCAAAAGTATAATAAATCAGCTGCTCAAATATTGATTAAATGGTCATTA
CAAAAAGGTTATATACCATTACCAAAAACAAAACCTCCATCTCGATTAAAGGAAATCTTTCTGTTGAT
GATTTTGAATTGACTAATGAAGAAATTAAGGCTATTGATCAACCTGATGCTTATGAACCAACAGATTGG
GAATGTACTGATGCTCCATAG

YJR096W_homolog 282aa (SEQ ID NO 442)

MSYRLIKLNSGHTIPSIGLGCYDIPRNKTVSVVYEACKVGYRHFDTAVLYGNEEEVIEGISKFLRENPN
IPRSEFFYTTKLWNNQLGTSSTKQAISTMMAQVGDKLEYIDLILLHSPLPGKTKRLESWKVLQDAVEKG
WIKNIGVSNYKGKHIEELLTNATIPPAVNQIEISPWCMRQDLATWCLSKGINVEAYAPLTHGNKLQVNN
TEFQEIMPQKYNKSAQILIKWSLQKGYIPLPKTKTPSRLKENLSVDDFELTNEEIKAIDQPDAYEPTDW
ECTDAP

YKL196C_homolog 603bp public: 1..603 (SEQ ID NO 443)

ATGAAGATTTATTACATTGGTATTTTAAGATCAAGTGGAGACAAGGCTTTAGAGTTAACTTCAGCCAGA
GATTTATCACAGTTTTCCTTTTCGAAAGAAATGGGGTATCCCAATTCATGACTTTTTTCGCAGAAACC
GTATCCCAAAGAACTCAACCTGGACAGAGACAAAGTGTGAAGAAGGTAATTATATTGGTCATACTTAT
ACCAGATCAGAAGGAATTTCTGGTATCATTATAACGGACAAAGATTACCTGTAAAGACCAGCATATACA
TTAATAAATAAATCTTGAAGAATATTTATCATTTGATCCCTAAATCTGATTGGGAAACATTGATAAA
GCAATGAACTTTACAATATGGACAATTAGAAGCATATTTGAAAAAATATCAAGATCCCACTCAAGCT
GATTCAATCATGAAAGTTCAACAAGAATTAGATGATACTAAGGTTGTTTTACACAAAACATTGAAGGG
GTTTTACAAAGAGGAGAGAAATTAGATTCAATTGGTTGACAAATCAGAAGCATTGTCAAGTTCTTCAAGA
ATGTTTTATAAACAAGCAAGAAAACCAATTCCTTGTGTGTGATTATGTGA

YKL196C_homolog 200aa (SEQ ID NO 444)
MKIYYIGILRSSGDKALELTSARDLSQSFERNQVSQFMFFAETVSQRTQPGQRQSVEEGNYIGHTY
TRSEGISGIIITDKDYPVRPAYTLINKILEEYLSLHPKSDWENIDKANETLQYGOLEAYLKQYDPTQA
DSIMKVOQELDDTKVVLHKTIEGVLQRGEKLSLVDKSEALSSSSRMFYKQAKKTNSSCCVIM

YKR076W_homolog_256aa(SEQ ID NO 446)
MDDKGWRFPPTKEELKTLKTEDDISLGTPDHNVDYDFSRRLRELYFKAEPYEGRFTVPVLWDKKEGTIVNNE
SAEIIIRMLNTEFNLSILPSEYAEVDLVPKDLESQIDELNSWIYDNIINNGVYKAGFASKQEVYAKECQNVF
DLHDKVEAILEKNHNSKKKGFEILLGNQLTEADIRLYTTIIRFDVPVYQHFKNIGTIRTHYPYIHNWLR
LLYWKIPGFOETTNFEHIKYHYTKINIPYGLTLPGLPVENILPLEEK

YKR092C_homolog_428aa(SEQ ID NO 448)
MGE CGW GEGIFSSQRKKRPRFVFG L I S L S L S Y S H K R R A T I K V C P N G L E K N F F N F F H L L K S Q L L Q L L P
I A K M S S N T Q D L V L A Y I N D Y V S R N E E L S K L K K A L S K F L A G K E L P K V S K Q L E S I I D E V E N Q E K K S K P R N S S
S D S E D S S S E S E S S T S D S E S S S S D S D S S S S D S E S S S S D S E S S S S D S E D S D D E E D K E D K E A E K D N K D S E D S
E N E K V E E D N K D T S S D S S S S S D S K S D S D S D S S S S S D S S S S D S D S S S S S D S D S S S S S D S D S D S D S D
S D S D D N S S E S S E D E S S S D S E S K E E Q K P E D K K R K H T D D I K E E K P V K K F K N E S E S S A S S S T S I P A T P
E P E L K P G Q R K H F S R I D R S K V N F E N S V L Q D N T Y K G A A G T W G E K A S E K L L Q V R G K D F T K N K N K M K R G S Y K G
G S I T A S G S Y K F I D

YLR043C_homolog 312bp public: 1..312(SEQ ID NO 449)
ATGGTTCACGTTGTCACCTGAAGTTAACGAATTCCAAACCCCTTTTAAAGGAAAACAACCTTAGTTATTGTT
GACTTTTTTTGCCACTTGGTGTTGGTCCATGTAAATGATTGCTCCATTATTAGAAAAATTCCAAAATGAA
TATTCTAATATTAAATTTTGTAAAATTGATGTTGATCAATTGGGTTCTTTAGCACAGAATATAATGTT
AGTTCTATTGCCAACTTTGATTTTATTTCAAAATGGTGAAGAAGTCAATCGTGTCTATTGGTGCTAACCCA
GCTGCTATTAAACAAGCTTTGGCTTCTCTTGCTTAA

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YLR043C_homolog 103aa (SEQ ID NO 450)

MVHVVTVEVNEFQTLLENLIVVDFVFATWCGPCKMIAPLLEKFQNEYSNIKFLKIDVDQLGSLAQEYNV
SSMPTLILFKNGEEVNRVIGANPAAIKQALASLA

YMR273C_homolog 4938bp public: 1..4938 (SEQ ID NO 451)

ATGTCACCTGCCTAACACGTCATTCATAGCGATTCAAATTTTGAATCAGCTGTACAAGATCTTGAACAA
GAGAAGAAAATGGTGGCAGCCTTAAAGAGACTATCTATAGGTCATATGATGCAATATGATCCCGACTTG
CCACCAGGCAGTATGGATGATATTGATCCCTTTGCAAACAATAACAACAACAGCAATACCGCTAGTAAC
AATAACCACTATAATGGTCATACCAGAGATCACACCAGCAACAACAATACACACAATCATTTCTCCC
AACTCAAAATTGAACCACCATCGTGGTCAAAGTCCTTATGATGAAGATTTAATTCACAGAATATCCAC
AGATCACACTCAACTCGATCAGATCAAAATCACATTCAACTTCTCCTTCTACTTCGCCTCAACACAAG
CAACAACAACAACAACAACCGCAACCTTTTCCACATGAACCACAGACTCCTCCATATAACAATCACCA
AGCCAGTCAAGAGACGTAGTTTTTACGACAATTCAGCGTGTGACGTCAGAAAGTCACGATATTTTT
TTCGATGCCGAGGATGAAGTTTATGATAGTTTATCCCTTTTGTGTGGGTACCAGCTAACTCTCATCCT
CAAGTGAATCCTGAATCGTTCAAGAGTTAATCAAACTCAAGTGGAAAGAGATATTGGAAAGAAAGCTA
TCTCGAAAGTCAACTATTTCAAGAAAGTCAACTTTATCAGCAGCTCCTCAACCAGTACCAAAGAGACA
TTAGCCCCAGAACCAAGAATAAGTCCAGAATGGAATGTGATGTGTACCTCCTTCTCCAGTAAGAAA
TCTTCTTTGTCTTCGTCGTCACAACAATAAATCAAAATGAAGACGTTTCTCGAAAATCGTCGTCCTCGGTT
TCTTCAACTTCTCCACAAAAGATCCAGCTAAGAGAGAATCTTGGTACTTCAACAACCTCAAAAAGATAC
CTGAATCCATCATTTGCGAGAGCTAACTTCAGAATTGGAGCAGTTGTCAAAAATGGCGGGGATGGACAAG
AATGACGCAGTAACTTTGGCAAGAATTTGTGCGGCACAATCATTTGGGGTATACAGATGTGGAAAAATTA
GCATTTGACGAATTAGATAGTTCAAAAACAACCGCTACTGCAACAACACCCAATTCAGTGGGTTCTCCA
GGAAGTTATGACTTCGAACCCACCTCGCACCACGACCTTGCATTTACAACAACGATTACAACATCAA
TTTCAACAAGCTCAAAATCAAGGCAGAAAGGGAGGCAAGATCGACAAGACATCAACAAGCGAACAA
CAGTGGCCAGTATCGAATGACGATAGTCACAAATCTCTGTACAGTTGACAGCAAGTGAGGGAGGTTCT
ACTGCTAATGCTTTTACCAGTGCTGGGAGTGGTGCTGACTTTGCCTTGAAACGAAGTAGAAGAACTGAT
TACCGGAAAAAGGAAACAGATTCGAAACAAAAGACTTCGAATAATTCGCCTCCTACAAGAAAGTACAAT
GTCCGGAATTCACAGTTGTTATTTAACTACAAGAAACAGTAGATTCTCCTTCGCTGTACCTTCACCT
TCACCATCTACATCTCAAAGCATGATGGGTACAGGGTGAAACACAAGAAATCTCAAAGCCATTTGGAA
GCAGATTGGCTAACCAATGATGGATGGTTACAGATATGTACATAACCCGTATCCCACTGCTTCAACC
ACTATTGATTTAGTTCGTATGGGTGCTAAGAAATCAGCCAGACAATCACTTAGTCCAGAGAATGCAATG
GATGGCAGATCTCGAACAAGCCCGAAAACAAGACTCATCGTGGCTATCTGCATCAAGAAAGGTCTCAT
CCTTATCATCAACAACCACAGCCTCAAGTGCAACCTCAAACCCGCCAACAACTTCCACCAGCACAAACA
GCTCATAGACAATCGACGAGACAAACCCACAATCATCCGAGCACAGGAGTTGAAAAGCATCACCGACAG
GATAACAAGCGTGTAAATGCTGTCAGTTCTTAATACAGACATAAATGATTTTATGGCTCACTCAATCAA
TTTCAGACTAATGGAACAAGAAACCATCGATATGACAACCTCCATAAAAAGGATAAGACTGCATTTTTG
CCAAATGAAGACCACCAACGTAAGTCCCATTGCAAGAATAATCAAATGTAAGAAATTTGTCTTCTCG
TCTCAACAGCATTTACATCAACCGTATCTGACAACCTTCTGTTGCGCCCAAGTCACGTCAACTACATCAA
AATTTAGACAAGTTGAGATCCGAGATCAATGAATTTAAGGAAAGCTTGAATAAATCCGAATTACCTGGT
GAGGAATCAAAAAGAGAACACAGACTGCGTCACGACCAGCACCACCAACAACGACAACGACCAGCACC
TCACAGCACCAACTTGAGCCTCGCAATTACAACCAACAATGACCGTCACCAAGACAAACAGCATGAACAT
GTACAACCCCAACAAGTCCAGCCCTTACAGTCAGATACTAGTTTTGATATCAGTTATCAAGATTTAAGC
GTTGAAGATCAATTTGGGTATTGAACAGGAAGCATTGAGAGAATTAGGCAAGGAAAAGGGGCATTCTCAT
GAGATTGATATAGATGATGATGATTTGATGAAAATTTAAAANTTCTGCCTATCAATGAACGACATGGCTCT
CAATTCACACTTGATCATGACATTTTGGACAGCTTTAATTTGGTAGATAATCAGTTGGTTGGATCTGCA
GATGAAGGAATTGATAATTTGAAGGTAAGAAATACCCGTTGGGCGACAACAACCAACAACAACA
CGTCAACAACCAAGAGCTGCTTCGCCACCATCTCACAGCAGTACTTGGGGCATGATGAATTCGACTTG
CAACAAGGTAAAGATACAAATAAAAAAGTTGGTCTCGTTTAAAGTATTGATACATTGCAGAACAAAGCCT
ATTACCCCTGAGGAACTGCAACTGGATTGGAATGAATGCGTTACCTTCCCCTACGTTGCATTTAGAT
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TTATTCAATAAGACCCTAATTTGGAGATTATAGACTCTGATAACTATAAGGAAAAAATGGGCATTGAG
ACATCTAACAATAAAAAAATTGAAAAAGAAAGAAATCTTTGGTTTGTCTTAGTACAACATCATCTGTGGGA
GCAAATGATACATCTGAAAAATGAAGGGCCCAAGAAATGAAAAAGAAAAAGTCGTGGGGCTGGTTGCGG
GAGCGTTCTGCCAGTGCCCTCGTCTGCAGATATCAACAATTTGCCGCTTTGCCCTCTTGATAAACTACCT
ACAAGATCATTTCTCAAATCCCGAAACGTCAACTGACCAACACCAGAAACATGATCTTGAGAACGGTTCA
GATCTTGAACGTGAATTTGGAACACGAACCTGAACCTTGAACCTTGAGTTGAGCTGGATCTTGAGTTTGAT
TACGAGCAACAAGAAAGCACCAGATGCTTCAATGGTAAATGATTCAAGCTTTGCAGTTGATTCTATC
TCTATGAAGATCGACAGACAAGGAAAACGTGCTTCCAAATTTTCAAGAAAAGGCAAGGTACCAGGT
TCAAGCTCACAGTCAGTATTTTCAATTTGAATCAAAAGGTTTCAAGGGCCAGCGTCGACTATGAATCGGAC
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TCGACAGCATCGAGGAGAAAGAGAATTTGCGACAAAGTAATGGCACTCGTAAGGCAGAAAGAGTTGAG

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AGTCAAGAGCAACAGGAGGAACAGTTCCCTGTAACTCGTCGCCGATACATCAATTCAACATTGAACAT
CTCAAAGACGACTTTGTCACTCTTGGGGAGAAGGACGATGTTTATAGATTCTGGTACTGATGACTTGGTT
GAAGATGTAAGATCTCGTAACATTCAGAGCACAAATAGTTATGTTGATGAGGATGAAACTCCATTCAA
AATAACAATGATAACAAAGATTTGGGGATGCTAAAAGTTGACGAATTGTCCAAAAAGAAATCAATTAGC
AGGAAAAACGGAAACAATATGCAAAAGAAGAACCTTTCTACTGAACCTTACTGATACAAAAGAGGTA
GTAGAGGAGGTTCTTGCAACTGAGCAAAGTGTCAAACCAAGCCAAGGGGAAGATCTTTTGTCTAAGAAT
GAAGATAAAGAGAAATTAGATATCCAAGAAAAGTTGAAGAAATCAATAAAACGTACATCAAGGGCCAAC
CAGCCTATTGAGTTTACTGATTACAGCCTTTGGGTTCCCTTGGCCACCACCATCTCAATCAACTTTAGTG
ATGCTTGACTACAGATTTCCAGTTTCATGTTGAGCGTGCCATTTATAGATTGTCACACTTGAACTTGCT
AACCCTAAGCGTTCACTAAGAGAGCAAGTTTGTGTCGAATTTTATGTATGCCTACCTCAACTTAGTT
GATCATACATTACATTTAGAGCAACAAAATATGAGCAGTGAGGATGGCGATCAGATGGAACGTGACGAC
GACGAAGAAGAATAAGTACACATGATGAGAAAGACATGATTTTTGGAGAGAGTAATATTGCCGAT
GACGATGATCTTATTCCTGAAGAAGCAAATGGTGAATTTCGATTGGGATTAACCTTAGATATGGATGGTTA
CATAGGAAACAGCATCATCAATCTGGAATCGAAGTATAG

YMR273C_homolog 1645aa (SEQ ID NO 452)

MSSPNTSFHSDSNFESAVQDLEQEKMMVAALKRLSIGHMMQYDPDLPPGSMDDIDPFANNNNNSNTASN
NNHYNGHTRDHTSNNNWTHNHSNPKLNHHRGQSPYGHEDLIPQNIHRSHSTRSRKSHSTSPSTSPQHK
QQQQQQPQFPPEPQTPPYNKSPSPVKRRSFYDNSSVLTSESHDIFFDAEDEVYDSSSPLLWVPANSH
QVNPESFKSLIKTQVEEILERKLSRKSTISRKSTLSRSSSTSTKETLAPEPEISPESECDVSPSPVRK
SSLSSSSQONQEDVSRKSSSSVSSTSPQKDPAKRESWYFNNSKRYSNPSLRELTSLEQLSKMAGMDK
NDAVTLARTLSAQLGYTDVEKLAFDELDSQTATATTPNSSGSPGSYDSANPPRTTTLHLQORLQHQ
FQQAQIKAEREASRTHQQSEQQWPVSNDDSHKSSSLTASEGGSTANAFTSAGSGADFAKRSRRTD
YRKETDSKQTSNNSPTRKYNVRNSQLLFNKKPVDSPSSSPSPSTQSMGHRVKHKKSQKPLE
AALANPMDGSDMSHNPYPTASTTIDFSRMGAKKSARQSLSPENAMDGRSRTKPKENKTHRGYSHQERSH
PYHQPPQVQPPQTRQQLPPAQQAHRQSTRQTHNHPSTGVEKHHRQDNKRMSSASNTDINDFMAQSNQ
FQTNQTRNHRDNLHKKDKTAFLPNEDHQRKSHSTRNSNVRNLSSSSQHLHQPYSTTSVAPKSRQLHQ
NLDKLRSEINEFKESLNKSELPGEEKREHRSRHDQHHQQRQRPAPSQHOLEPRNHNDRHQRQHEH
VQPQQVQPLQSDTSFDISYQDLSVEDQLGIEQALRELKKEKHSHEIDIDDAFDENLKKSPINERHGS
QFTLDHDIILDSFNLVDNLVGSADGIDNLKGNKNEIPVGRQPPQQRQPPRAASPPSSQQYLGHDELHL
QQGKDYNKKVGPRLSIDTLQNKPIHPEETATGFGMNALPSPTLHLDQNSTPGHSRKASNSASYDDYY
NIADKSSTAGTPKTKKETKVKTKLFNKDPNLEIIDSNDYKEKMGIEITSNNKKLKKKKSFGLLSTSSVG
ANDTSENEGPKKLKKKKSGLWLRERSASASSADINNLPLPLDKLPTRSFSPNETSTDQHQKHDLENGS
DLERELEHEPELELELESDFDYEQQRKHQDASMVNDSSFAVDSISMKSTDKENVLSKFFKKKAKVPG
SSSQSVFSFESKSGASVDYESDNDAKSIKKGNSSRLFKKKSRAKLEQENSVNKEKLRLNLVSNE
SQTIEEKENLRQSNQTRKAERVESQEQEEQFPVTSSPIHQFNIIEHLKDDFVTLGEKDDVLDSDGTDLLV
EDVRSRNIQSTIVIVDEDETPIQNNNDNKLGLMVKDELSSKKSISRKKRNNMQKKNLSTELDTNKEV
VEEVLAETEVSQKPSQGEDLLSKNEDKEKLDIQEKLKKSIRKTSRANQPIEFTDSAFGFPLPPPSQSTLV
MLDYRFVPHVERAIYRLSHLKLANKRSLREQVLLSNFMYAYLNLVDHTLHLEQQNMSSSEDGDQMERDD
DEEEEMTDTDEKDMIFGESNIADDDDLIPEEANGDSIGINLDMDGLHRKQHHQSGIEV

YNL112W_homolog 1332bp public: 1..1332 (SEQ ID NO 453)

ATGTCATACAATAACGGAGGATATAATAATAGAAACGGAGGTAGTTACGGTGGAGGCTACGGCGGTGGT
GGTAGCAGAGGTGGAAGAGATGGCTACAGTGGTGGTGCCAGAGGCGGTGGCTACGGTGGTGGTGATAGA
GATCAAGGTGGATACAGAGGTGGAAGATTAGTGGTGGTGGCCGTGGTGGTGGTAGATTTAATGATGCT
CCAAGACAAGAATTAAGTCTCCACAATGGGATTTAGAACAAATTGCCAAAATTTGAAAAAATTTCTAT
TCAGAACATTCAGATGTTGCTGCCAGATCTGATAGAGACATTGAACAATTTAGAAAAAGAAATGAAATG
ACAGTTAAAGGTCATGATATCCCTCATCCAATCACCACCTTTTGATGAAGCTGGTTTCCAGATTATGTT
TTACAAGAAGTCAAAGATCAAGGTTTCCCTAAACCAACTCCTATTAGTGTCAAGGTTGGCCATAGGCT
TTGAGTGGTAGGGATATGATTGGTATTGCCGCCACTGGTTCCGGTAAAACCTTTATCTTATTGTTTACCA
TCTATTGTCCATATTAATGCTCAACCACAATTACAATATGGTGATGGTCCAATTGTTTGGTTTATGCA
CCAACAAGAGAATTGGCAGTGCAAATTCAACTGAATGTTCAAATTTGGTAAATCATCAAGAATTAGA
AACATTGTGTTTTATGGTGGTGCAACAAAAGGTCCTCAAATTAGAGATTAGCCAGAGGGGTGAAATG
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TATTTGGTTTTAGATGAAGCTGATAGAATGTTAGATATGGGTTTTGAACCACAAATTAGAAAAATGTT
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ACTAGAGATTATTTGAACGATCCTATTCAAGTCACCATTGGTTTCATTGGAATTGGCTGCTTCTCATACT
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GCTTTAAATGAAAAAGATAACAAAATATTGGTTTTTGTCTTCTACTAAAAGAACTGTGATGAAATCACC
ACTTATTTAAGATCAGATGGTTGGCCAGCATATGCCATTGATGGTGATAAAGAGCAAAATGAAGAGAT
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ATTGGTATGTATAATTTTAA

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YNL112W_homolog 443aa (SEQ ID NO 454)

MSYNNNGGYNNRNGSGYGGGYSRGGRDGYSGGGRGGYGGGDRDQGGYRGGGRFSGGGRGGGRFNDA
PRQELTAPQWDLEQLPKFEKNFYSEHPDVAARSDRDIEQFRKENEMTVKGHDIPHPITTFDEAGFPDYV
LQEVKDQGFPKPTPIQCQGWPMALSGRDMIGIAATGSGKTL SYCLPSIVHINAQPQLQYGDGPVILVLA
PTRELAVQIQTECSKFGKSSRI RNTCVYGGAPKGPQIRDLARGVEIC IATPGRLIDMLEAGKTNLKRVT
YLVLEADRMLDMGFEPQIRKIVDQIRPDRQTL MWSATWPKEVQQLTRDYLN DPIQVTIGSLELAASHT
ITQLVEVIDEF SKRDLVKHLESALNEKNKILVFASTKRTCDEITTYLRS DGW PALAIHGDKEQNERD
WVLDEF RKGKTSIMVATDVAARGIGMYNF

YOL151W_homolog 1032bp public: 1..1032 (SEQ ID NO 455)

ATGTCAACACCAATTACTGTTATTGTTTCTGGAGCCACAGGATTTATTGCTCAACACGTTGTTAAACAA
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AAAGTATTACAAAAACATGGAGAAGCAAAAGTGTTCTTACATTTAGCTTCACCATTCCATTTAATGTG
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AATTTTGGTAAACAATATTGAAAAAGTGGTTATCACTTCATCTTATGCTGCCATTAGTACCGCTTCTAAA
GAAGCTGATAAAAAATGCAATTATTACAGAAAAGGATTGGAATGAAATCAGTTGGCAAGATGCTTTACTT
AATCCAGTTAATGGATATCGTGGATCCAAAAAATTTGCTGAAAAAGCTGCTTGGGATTTTATAAAATCT
AATGATAATGTTAAATTTTCATTGTCGACAATTAATCCATCATTTGTATTGGTCCACAATCATTTGGT
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TTTGAAATGAGGATGCCAAAAATCAAAGAATATTGTTGAATTCAGGTAGATTTACATCTCAATCACTT
GTTGATATTATTAATGATAAATTTCCAGATTTGAAAGGGAAAAATACCAGTTGATGAACCAGGTTGAGAT
AAATCTGTTATTGCTGAAAGTTGGCTACTATTGATGATACCAAATCTCGTGAATTATTAGGATTTGAA
TATTATAACCTTGAACAATCAGTTTATGATACTGTTGAACAAATTGTTAATGCTCATAAGTTGTAA

YOL151W_homolog 343aa (SEQ ID NO 456)

MSTPITVIVSGATGFIAQHVVQLLAKNYQVIGTVRSTAKGDHLLKLFNNPQNLSYEIVEDVGTGKA
KVLQKHGEAKVFLHLASPFHFNVTDVEKELLLPAVDGTKNVLQAIYNFGNNEKVVTSSYAAISTASK
EADKNAIITEKDWNEISWQDALLNPVNGYRSGSKKFAEKAAWDFIKSNDNVKFSLSSTINPSFVFGPQSF
SEIKQSLNTSSEIINSILKLPND SIPASKGWDVDRDVAKAHIIAFENEDAKNQRI LLNSGRFTSQSL
VDIINDKFPDLKGKIPVDEPGSDKSVIAESLATIDDTKSRELLGFEYNNLEQSVYDTVEQIVNAHKL

YOR286W_homolog 546bp public: 1..546 (SEQ ID NO 457)

ATGTTTGCATTTAAAAATCTACTACTTCAATTCCTCAAAACAGTGGTCGCCCCAACATCATCTCGTTAT
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GGATTAAGAATAACCAAGATTTTATAGTGTATTGACTGAATCTCCAGAGGCAAAAGTATATAAATAT
GCCGATGTTAAGGATGTGGCGGTACACCTGAAAACACCCGTGATTCTGTTTTAGTGGATGTTAGAGAA
CCAATGAATTTGGAGATGGTCATATACCAGGAGCTTTGAATATTCCATTTAAAAGTAGTCCCGGCGCA
TTGGATTTGTGAGAAGAAGATTTCCAAGAACATTTTGGATTTCTAAACCAAGTACTGATAAAGAATTG
ATTTTCTATTGTCTTGGAGGTGTTAGATCTACTGCAGCTGAAGAATTGGCCAATACTTTTGGTTATAAG
AAAAGAGGAAATTATCTTGGAAAGTTGGGAAGATTTGGGTAAACATGAAAAATAAAAGAACTAA

YOR286W_homolog 181aa (SEQ ID NO 458)

MFAFKKSTTSILKTVVAPTSSRYLSTVTLRSIPRTFHNATKVSLEFNGLRTPRFYSVLTESPEAKVYKY
ADV KDVAVHPENHPDSVLVDVREPTEFGDGHIPGALNIPFKSSPGALDLSEEDFQEHFGFPKPSTDKEL
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YPL078C_homolog 702bp public: 1..702 (SEQ ID NO 459)

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TTACCAGGTAACAACCTTATTATCTAAGACTGGTGTGTTGGCTACTTCAGCCGCTGCTGCCATCTATGGT
ATTTCCAATGGATTATTTATTATACACGATGAAACCATTTTGCTTGTCTACTTTTGCAAGTTTCACAGCT
TTGGTCGCCAAATTCGTTGCTCCTTTATACACTGAATGGGCCGATGGTGAAATCAAAAAAGTCAACGAT
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TCATTTGAATTA AAAACAAAAATGGCTGTTTCTCAGGAAGCTAAATCTGTTTGGACTCTTGGGTTAGA
TTTGAACAACAACAAAGACAATTGGAACAAGACAATTTGGCCAAAGAAGTCATTGATAAAGTTGACAAA
GAAATTGCTAATCCAAAAATCCAAGACAAAGTATTGGCTGAATCTCTTAACGAAATCGAAAAATTTGTTT
GCTAAAAACTAG

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YPL078C_homolog 233aa (SEQ ID NO 460)

MSMINRIALRSARPAMGMAFRPAPIGRLVLSAPADPKQKANSIIDALPGNNLLSKTGVLATSAAAAIYG
ISNGLFIIHDETILLVTFASFALVAKFVAPLYTEWADGEIKKVNDILNQSRNHNIEAVNKRIETVSEL
KNVVATTEDLFALSKETAQFEADSFELKQKLAVSHEAKSVLDSWVRFEQQQRQLEQEQLAKEVIDKVDK
EIANPKFQDKVLAESLNEIEKLFKN

YPL085W_homolog 2490bp public: 1..2490 (SEQ ID NO 461)

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CTTCATGAGTTTCAGAATTTGATTATGAGAATCACTGAAGTTGGATCTGGAGATGATCAAAACAACCTGG
TTTTCCGGTAAGATTAGTCGAGTCAATCTTGATAAGATCTGGGGACAAATTGATAAATTTATTGTTGGT
GGAGATGAACGTGAAAAATGGTAACAATAACGATGGTAATGGAACTGGCAATGGAAGTGGTAGTGTTC
AATAAATTTAGCCCTTCCGTGTCGAGAAATGCATCAAGTGTGAATTTACACAATTATGTACAACCTTCA
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GATCAAGTTTACATTTGAAAGAAAAACCTACAACCTGGATTCTACTCCGCAACCACCACCATTAGTTGGTCAT
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AAGTTTGA AAAATATGCCCAAGCAACAATTCATCTCATATAATCTTAGTCTTGTGAGAAAGGTCA
GCTGTTACTAGTGTGATGGTCTGAATACCCTCACCACCAACACCAACAGAGTATCAATGCGTCAACA
GTTCCCGTGCCACTTCCACCACCAACACCACCGGTAAGCATGCCACAACATGTATCTAGGTCTCCACGT
AGCCATCAACTGCACCAACCAACCAATTAACCACTGCATTACATCATGTTCAACAACCATCTAGA
GATCGGTACACCATTAGCGACACGAATCTACCCTTAGCAATAGTGTGGCGGACAAATTTCTACTACG
TCAGTGGGTTCTATTCTTAGTCAAATACCCTTGGTTCGACAGACTCATGGGAAACAACCTTCTATTTC
AGTGTAAATTTCTGGAGATAGTATTGCAGCAGTTGGTTTAGGAGAACAGAGAATGTTTTACCCCATCA
ACCGGACAAACAGGGAAAAACAGCTACAAGTGAAGTGAATAGAAATGAGGAAGGTTATGGATTGGGGGT
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TCCAGTGAAGCAGAAATTAGTAAAGACATTTCAAATGATGTAGCATTGGATAGTGCTAAGATACCAGAA
GCTTACAGGAACCCAGAAAGAAGAAACCGACGAATCAGGTAATGTGGCAGCTGCTCCACCACCTTACCT
GCTCCAGTTGCACCTCCTAGAAAAACAAATCTTCTAGATCTAATCCATATGCTCCATCTACAGATATT
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GGATCAAGAACTAACAGATATGGACCACCACAGGAGTTGGTAATAACAACCAACTATTGATGTTTCG
CCACCTTCTGCTACTAATAATACTGGTAATGAAGATTCCATTAGTATGTTTCTCTATGGTGCCTATCAA
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CAAAGTGTATTATATCAACAATATGCAATTGCTGATGATACAGTTGGTGATTATATTCCTATTATGGA
GAAGATGATGAAGATGATGAAGATGAACAAGCTAAGCAACAGAAACAAAAAGAAAAAGAGGCACAAGAA
CAAGAATTGAAGAGAAAGCAGGAACAACAACAACAAAAAGCTGCAGCAAGAATAACAACAATAGTGGC
GGTGGTGGTGGCAATTTCTTTAGCTTATTCCGTGGTGGTGGTAATAATAAGAAACAAGATAATGATGCT
AAAGTTTATAAGCTCATTTAGGACAAAAGAATACTTTTGTATTATGATGAAAAATTGAAACGTTGGATA
GATTAA

YPL085W_homolog 829aa (SEQ ID NO 462)

MLSLKLKHALTLADYGLINESQRYIDHINSSIKTLGNKSPFVTPNLLHEFQNLIMRITEVGSDDQNNW
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MIRQPSHLPPYQPPQPPQPPQQLLDQVHIERKPTTGFTPPPPPLVGHPPSTTSVNKYSPSIKSSPRQAQSN
KFEKYAPSNSSSHHNLSLVEERSAVTSADGPEYPHHQHQSSINASTVPVPLPPPTPPVSMPOHVSRSR
SHQSHQPPPTLPPSHSHHVQPPSRDRSPLATRIYPYSNSVGGQISTTSVGSIPSQIPLGRQTHGKQPSIS
SVISGDSIAAVGLGEQENVLPSTGQTGKTATSEVNNEEGYFGGHHYHDQPETITESPELRGLQQPQ
SSEAEISKDISNDVALDSAKIPEASQEPPEETDESGNVAAAPPPLPAPVAPPRKTKSSRSNPYAPSTDI
GAISNAPSAIGQTPSGKPSVRKSGSRTNRYGPPPGVGNKQPTIDVSPPSATNNTGNEDSISMFSYGAYQ
NESSPPLKQPSQFDQTAVASAPAPHLPQLAVPERVPTKNVANIDDSFDENSLAADTLTTYNNNMVNK
PYGSSPMGPTVATNGPGSVTSTPLILNQGSANMKLSNLSTISVTGTGAGTVGTGGAFDGFPIPGSPDE
TTRPNSIFGGHTRGLFSSRLSESQSVLYQQYAIADDTVGDYIPIMEEDDEDEDEQAKQKQKEKEAQE
QELKRKQEQQQQKAAAKNNNNNSCGGGGKFFSLFGGGGNKKQDNDKAVYKAHLGQKNTFVYDEKLKRWI
D

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YPL190C_homolog 396bp public: 1..396(SEQ ID NO 463)

ATGCCAAGTACAAAAAGATCATCATCTACTGAATACTCCCATAAAGACTCTAAAAAGAAAGTCAAACTA
GATTATGTAATCTCAAACCATCACAACGTTATATGTCAAAATCTAAATACCAAAATCAATAAGAAA
ATTTTATTGCATAATTTGTACCTATTATTTCTGCATTGGAGATATCATTTCTATAAATCTACAGAAT
GGTTTTGCCTTTATAATATTTAGTAATTTAAATCTGGCTACATTGGCGTTGAGAAATTTGAAAAATCAA
GATTTTTTTGACAAACCACTTGTATTAAATTATGCTGTCAAGGAATCTAAAGCTATTTCTCAGGAGAAA
CAAAACTACAAGATGAAAATGATGAAGAAGTGATGCCACTGTATGAATAA

YPL190C_homolog 131aa(SEQ ID NO 464)

MPSTKRSSSTEYSHKDSKKKVKLDYVNLKPSQTLVKNLNTKINKKILLHNLVLLFSAFGDIISINLQN
GFAFIIFSNNLSATLALRNLKNQDFDKPLVLNYAVKESKAISQEKQLQDENDEEVMPSE

YBR112C_homolog 3243bp public: 1..3243(SEQ ID NO 465)

ATGTATGCGACAGCCCATACAATTAACAACAACAACAACAACAACAACATCCACCACCACCTTTA
AACGGTGGACTACATGCAAGTGGGGCTCCTCCAAATTCCTCATGAAGCAGCAGCTATTGCTCAGCAACAA
CAACAACAGCAGCAACACCACAATGGTCTGGTATGATTGTTGCCGAGCTGCAGCTTCTGCTAACCAA
CAAGCTGTCCAAGCCAGAGCCCAACAACAACAACAGCAGCAACAACAGCGATTACCTAGTTTCACTGCT
CTTAATGAAACTACAGTATCAACTTGGTTAGCCATTGGTTTATTAGCCGAGAGTTTAGGTGACATGAA
CGTGCGACAGCTTCTTACAATTCGCTTTGAGACATTACCAAAATAACCCAGATATTTTAGTCAAAATA
GCAAATACATACCGTTCAAAGATCAGTTTCTTAAGGCTGCTGAATTGTATGAACAAGCTCTTAATTTT
CATGTTGAGAATGGTGAACTTGGGGATTATTGGGTCATTGTTACTTGATGTTGGATAATTTGCAAGA
GCTTATGCTGCTTATCAACGTGCATTGTTTACTTGGAAAACCTAACGTTCCAAAATTTGCGCACGGA
ATTGGTATTTTATATGACAGATATGGCTCATTAGAATATGCTGAAGAAGCCTTTGTGAGAGTTTGGAT
TTGGATCCAAATTTGACAAGGCTAATGAAATTTATTTCCGTTTAGGGATCATTATAAGCATCAAGGT
AAACTACAACCAGCATTAGAATGTTTCCAATACATTTTGAATAATCCACCACACCCATTAATCAACCA
GATGTTTGGTTTCAAATTTGGTTCAGTGATGAACAACAAGGATTGGAATGGTGCTAAGGATGCTTAT
GAAAAAGTGTTACAGATTAATCCTCATCACGCTAAAGTTTTGCAACAATTGGGATGTCTTATATCCCAA
GCAGATCAAATCCATCAACACCAGCTAATGGTGTGCACCACCACATAAGCCATTCCAACAAGATTTG
ACCATGTCTTTAAATATTTGAAACAATCTTTGGAAGTTGATCAAAGTGATGCTCATTATGCTACTAT
TTGGGTAGAGTAGAATGATTAGAGGTGATTTCACTGCTGCTTATGAAGCTTTCCAACAAGCTGCTAAT
CGAGATGCAAGAAACCCAACCTTCTGGTGTTCATTTGGTGTTTTGTACTATCAAATAAGCCAATATCGT
GATGCATTGGATGCTTATACCAGAGCCATTAGATTAAATCCTTATATCAGTGAAGTATGGTATGATTTG
GGGACTTTGTATGAGACTTGTAAATCAAAATTAGTGATGCATTGGATGCATATAGACAAGCAGAAAGA
TTGGATCCAAATAATCCTCATATAAAGGCAAGATTAGAACAATTGACAAAGTATCAACAAGAAGGTAAT
ACTCAACCCACCTCAACACCAGGCTTCTCAACAACCTAGATTACCTCAAGGAATGGTTTGGAAAGT
ACTCAACAACCAACAGCAACAACAACCACCACCTCCACAACAACAACAACAACAACAACCTCAACACCAA
CTGCAACTGCAACCTCAACCACAGCAACCACCTCAAACCAATCACAACCACTGTTACTTCAACACCAA
TCTTCATTGCCTCCTCAACAATCCAACCATTAATCAACAAGCTGCAAGCCTTTAGTGAATCAACAA
CAAAGTCCACCACCACCTCACTTGATGAACCTGGGACAACCGGGCAACAACCACAACAATTTGCCACCA
CATCTTCCACCACATACCCAGCAACCTTCTCAAATTCAGAAAAGCCTCCAATCAAGAACAACCACAT
TATCAACCACTCCACCTCCACAACATCAACGAATCGCAACCGCAACCTCCACACCAACCT
CAACACACTCAAAATCAACTGCCTCAATTAGCTCAATTGCCACCACACCATTTCAATCCTCCAGCTAAG
CCACATGGTGCACCTCAACAAGAACTGGTTTACCGGATTTATTACACAACCTCTGCTAATATCATATCA
GCTCCATCACAAGTACCTCAACCACAACAATATCAACAACCACATATTGCACCTGTTAGACAAGAA
CAAGTTAACCATGTTCTTCAATTTATCTGGCTCCTAGACCAACTGAGACAACACTTCTCAATCAAC
AACCCAAATGAGTCAACCACAACAAGTTCCACAACCTCAAAAAGGAGGAACCTAAACCAGAGGCTACT
GTTTCTGCTCCAGTTCTTGAGGCTATTAAAGTTCAAGATCAAGTGACAATCCAGGAGTCAGCACCAGCA
GCAGCAGCAGCAGTGTGAGCACCAGCTTCTGCTCCAGTTGGTGTATATAAAAACAGATACTGTATCTACT
ACTACACCTGCTACTTCAACCACTGCAGATGCTGTGCCAGTATCTGTGTCTCAAGTTGGTGAAGCACC
AATGTTGTTCAAGAGAAGAAAGTTCCGGACACCGAGCAGATCGTTTCAAGTTGAAAAACCCGTGGAG
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CCTACTGATAAGGACGTTGTAATGGCTCCAAGTAAAAGTGCAACACCTGTTCTCAAAGTATTGTGGAA
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AATGATGAAGAAAAATTTTAAAGAGGCCAATGTTGAAACGACTACTGAATCTGTACCACTTAAACAA
CCTGTTGAGAAAGAAAAATGAAAAAGTTGAGGTACCACCGCCACTGGAACAACCAAGTTCAAGAAAGAGA
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TCATCAAAATATCACAGCTCAAAATGAAGAGCAAAATCTGGAGAAGAACTAAAAAAGATACAACCAAG
ACAAGTCCAGCAAAAACAAGGGGAAGTTAAGGAAGTAATACCATCATCTACAGAACTGTATCAAAACCA
GATGTTGAAAAAGACAATAAAGAGAAAGACAAGATGAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
AAAAAAGATGAAAATCCAGAACCCTCAATGAGAAAGATTGAAGAAGATGAAAAATTTATGATGATGAATAG

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YBR112C_homolog 1080aa (SEQ ID NO 466)
MYATAHTIKQQQQQQQHPPPLNGGLHASGAPPNSHEAAAAIAQQQQQQQHNGPGMIVAAAAASANO
QAVQARAQQQQQQQRLPSSAALNETTVSTWLAIGSLAESLGDIERATASYNLSALRHSPNNPDILVKI
ANTYRSKDQFLKAAELYEQALNFHVENGETWGLLGHCYLMLDNLQRAYAAYQALFYLENPNVPLWHG
IGILYDRYGSLEYAEEAFVRVLDLDPNFDKANEIYFRLGITIKHQGKLPALCEFYILNNPPHPLTQP
DVWFQIGSVYEQQKDWNGAKDAYEKVLQINPHHAKVLQQLGCLYSQAESNPSTPANGAAPPHKPFQDDL
TIALKYLKQSLEVDQSDAHSWYILGRVEMIRGDFTAAYEAFQQAVERNARDARNPTFWCSIGVLYYQISQYR
DALDAYTRAIRLNPYISEVWYDLGTLTYETCNNQISDALDAYRQAEERLDNPNPHIKARLEQLTKYQQEGN
THPPQPPSSQPPRLPQGMVLESTQQQQQQPPPPQQQQQLQHQSQSQQPQQPPQTQSQPSLLQH
SSLPPQQIQPLHQAAKPLVNQQSPPPPHLMLPQGGQQPQLPPLPHTQQPSQIQEKPPTQEQPH
YQPPPPQHQQQSQQSPQPQHTQNPQSPQLAQLPPHSNPPAKPHGAPQQRGLPDLHNSANIIS
APSQVPQQQQYQPHIAPVRQEQNVHVPISIYAPRPTETTLPIINNPNESTTTQVPQLKKEPKPEAT
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NVVQEKKVPDTEQIVSQVEKPVESQPEVTPAPTPAPALATAPTEPAPTDKDVVMAPSKSATPVPQSIVE
QNRVSEATKAPESNGKHDLEDKNDEEKILKRPTVETTTESVVPVNPVEKENEKVEVPPPSEQPSSEKR
EKEVNGSIKKPLENESKVDIPQFSSNITAQNEEAKSGEETTKDITTKTSPAKQGEVKEVIPSSSTETVSKP
DVEKDNKEKDKDEDEVMADDDVKKDENEPPMRKIEEDENYDDE

YDR145W_homolog 1536bp public: 1..1536 (SEQ ID NO 467)
ATGGAAAGGTTCAATCAAATTAGACAAAACTCACTGAAGTTCAAAGGAGGGTTCAGTTGTTGGAACAA
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GCAAAGTTCCAACAGTATCAAAAAGTAGGGATTATATTAGAAATCAGTTGGTTCTTCAAGCTAAAGCA
CAACAACAGAGACAATTGCAACAGCAGCAGCAACAACAGCAACAGCAACAGCAACAGAATAACAATCTA
AAATCAGCTCAGAACCAGAACCAGAATCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAAC
CAAATACAAGGAGTGCAATCTGCTGGACAAACACCTCAGCAACAGAGCTTTTCGCCACAGTTGCAGGCT
GTACAACAACAACAATTTATGGGCAACCTGCAACAACAACAGCAGCAGCAACAACAACAACCTTAGAAAT
GCGAATAAAAGTGCACTTCAAGGTCAAGCTCCTTCACAGGCGCAACTCCTTTACCTGTTCCGGCCAACA
CCTCAGAGTCAACCTACAGCACAAGCGGGTGTGCTTCACAGGCAGCTACACCAGGATTTCAGCTTCT
CAACCCACACCATCGCAAACTTCGAGAATCGGATCAGCTCTACAACAAGGGCACCAAGTCGACAGGCA
TCTTCTACACCGCAATCTCAATTCCAACCACCATACCCTGAGAGTCGACATCCTTCTGCAACTACA
TCAGAAAAGCCACTTCCCAACAACCTGGAAGCGGAACAGCGAAGAGTCCTAGTGTTGCTGCTACTCCT
GCTCAGAATAATGGCACTGTAACCTGCCCCGTCTGCATCACCTGTTGCAACTACTACAGATAGTGCTACA
ACTGGACGCTCAGGAACCTCCCAACAACAATCAAGGTCAGGATCTGGATCATCGTTGAATTTGGCTGGC
ATTACAGTCAACCTCATGCTCCCATCATTTGCCAATTTTCAGTTCTATTAATGTAAAACAGCCCAATCACC
ACATTTAATAGTATCAATGATACGAGACCCAGTTTGACGGGAGGAGCTGCCAATCCTATGAGTATTTTA
TTAGATACACCAGCGATCACAAAATTGCCTACTTTTGATATCGAAGGAGACACTGGTGTCATTGATTCT
AGTACCAGTGGACGAGTTTAAATAAACGAAAATTAGGTGATTGATAAATACAATAGGTGTTGATGAA
GGGGATGGTAAGACCAGTATTGATGGGAATGTGGAGGAATTTTGTGTTGATTGCTGATGAATTTATT
CATTGAGTGACAAGTTTGTCTGCTGGTTAGCAAAACATAGAAAGGTGGATAGTATAGAGGCAAGAGAT
GTTCAACTACATTTGGATAAGAATTGGAATATCAAGATTCTCGTTTATGCAATGGATGAGATTCGAAAC
ACAAGAAAAATACAACCTAGTAATAGTTATAGTCAGAAAGTACAAGGTGTCGAAGTTTCGAAAGCTGTG
AATGATGATAATGCTTAA

YDR145W_homolog 511aa (SEQ ID NO 468)
MERFNQIRQKLETVQRRVQLLEQTKKTGNVTPEQIQIDKEIIECKAKFQQYQKVGIIYRNQLVLQAKA
QQQRQLQQRRQQQQQQQQNNLKSANQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQ
VQQQQFMGNSQQQQQQQQQLRNANKSALQGQAPSQAPTPLPVRPTPQSQPTAQAGVASQAATPGFRAS
QPTPSQTSRTGSALQQRAPSRQASSTPQSQFPPLPSESRRHSATTSEKPLPQQPGSGTAKSPSVAATP
AQNNGTVTARSASPVATTTDSATTGRSGTPQQQSRSSRSGSSLNLAGITRQSVPSLPISSSINVKQPTIT
TFNSINDTRPSLTGGAANPMSILLDTPAITKLPTFDIEGDTGVIDSSTSGRVLNKRKLGLDLINTIGVDE
GDGKTSIDGNVEEFLDLADEFIHSVTSFACRLAKHRKVDSEIARDVQLHLDKNWNKIPGYAMDEIRN
TRKIQPSNSYSQKVQGVESKAVNDDNA

YDR154C_homolog 333bp public: 1..333 (SEQ ID NO 469)
ATGATGTCGTTCCAAAGACTGCTGAAAATTTCAAGAGCTTTATGTACTGGTGAAAAAGGTTTGGTTACA
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GTACTGGTGGTAAAAGTATTTACGGTACCAAAATTTGCTGATGAAAACCTTTGTCAAGAGACATGACAGAC
CAGGTTTGTGTTCTATGGCCAAATGCTGGTCCAAACACCAATGGTTCCCAATTTCTCATACCACCGTTC
CATGCCCATGGTTGGATGGTAAACACGTTGTTTTCGGTGAAAGTCACTGATGGTTTAG

YDR154C_homolog 110aa (SEQ ID NO 470)
MMSFQRSSKISELYVSVKKVLVTKVLFSTESSHNSCFKVVISPTLTVSVVKVFTVPNLSMKTLSRDMTD
QVCCLWPM SVQTPMVPNSSLPFFAHGWMVNTLFSVKSSMV

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YDR216W_homolog 4257bp public: 1..4257 (SEQ ID NO 471)

ATGATTTTCACCAACTCACCAGAGTCAATACCTTAATTTATTTTGTCAACCCAGTTTAAATGACTGAGTCC
GGAGATATTATTGATAGTGTCTACTGGTACAAACAACACGACAGCAAACATGTCAAATACAACAATAGAT
GCGCCTACTCCCGCCTCGACTACCAAGAAATTATAAGCACAAAAACAGAATACCAATACTGGAACATCC
ATGTCGCCAAGTAATTTCAATAAATTCACAAACAACAAATGCAGCAGCAGCAGCAGCAACAACAACG
TCAAAAAAGTCCAAAGACATCCCATTTAGAGTTGACTGCATTTGGTACAACCCCTCTGGGAAACCACGT
TTATTTGTGTGTCAAGTCTGTACAAGAGCATTTGCTAGGTTAGAATCTACGTAGACATGAAAGATCA
CACACAAAGGAAAAACCATTTAGTTGTGGTGTGTGTCAACGGAAGTTTAGTCGTGAGATTTATTGCTA
AGACATGCACAGAAATTACACGCTGGCTGTACTGATGCAATAACAAGATTAAGAAGAAAATCAATTAAG
AAATCTCAGGATGGGGACGATGATGATGACGATGATGACGACGATGAAGAAATGGCAAATCTGAAGAC
GAAAACGATCATGATGAATCGGGCAATGCAAGCACAAAGAAATGGTAAAAAGGATAAAAAAGATCCACCA
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TTGGCTAAATTTATCAACAACGACATCAAGGAAAAATTCACCAATCTACGAGAAAAAACTCCAGCTCT
TTGCACAAGCAGGTTCTTGATCAACGTCAAAGGCTGCCGTTAATACAAAAATTTGATCAAGTACCAAA
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GCTCAATCGGGTGCCAACATATGCCATCAACATACCTGAGTTTAAATGATATATATCCACAATCTGATAAT
GTTGAATTTTCAACCCCTCAATTTCTTACCATCTTCATTTGGATAATGAAATGACGTGGCTAAATAATAT
CCAAACATTTCCGGATTGTCTGATTCTGTGTGCTGCTGCAAACTTGATGCGTCAGAATTCATAACAAAT
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TCAGCTACCGATATGGGACAAACAAGATCCGAAAGTGTAAACAGTTTAAACACTCCATTTGATGGTTCC
TACATGATGCCAACGGTAACAATAAGCAATCAAGAAATCCAAATGGTGTGCTGCTCATCATCATCAT
CAACAACAACAGCAGCACCAGCAGCACAATCATCAACATCAACCAAAATCAGTCTCTGCTCGGGTTATCG
AGAAATGACATGTTAAGTGAAGTCACTATGGCTATTTCAATTTTATGATATCCCGGAGAATATTTCTCAAT
TTCCCAATGGATTCTATATCAACAACCTTCAATGCTCTTTCGGGCCAAATTCAAAACCTTTAAACCA
TTATCGCCTATCACACAAGAAATGAACATGAGATTACTCCAAGAATTGATGGAAGAATTGGGGATTTC
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TCTGTTCTTTACGGATTATTTTCAGATAATGAAAATAATGTTTATATTGTTATCCGTCAATTGAACGCC
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GAAGAATTTATAATAAGTTAAATTTCTCATGATAATGGTACTTCTTATTTTCCAATAATTTGAATGAT
GAAATGCGATACAAAAATAATATAAACATGCAATCTCAAACGAGAATAGTATTTATCATTTATCGGTTG
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CAATTGCAGAATCTTTGTAAATATGGATTCAATTTGTTGGTGCATGGTATATATGAAATCAACAAATAT
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TATCAAGATTTAACTCAAAATTTATCATCGTCTTTTGGATGCTCACAGTACTGGGAATCCACTTAATTCA
ATTAATGATTATGATTTATTTGAACTTGCTGATTGTGTGATTTCTGGTACTCAAATTTGATATTATTTAAA
GTTGAGGATTCCAACAGTAATAGTAGAAATCGAAGCAAAAATGATCCAACAAATGAAATCAATAACAAA
CTCAACAACAACAACAACAATAACAATGATGATAATAATAACAGTAATGGTGTATCAATTAATTTCT
GCCTTTGACTAGTATTTTGGATATTTGAATATGGATAATAATGGTTATGCCAAAAAGAAGATTTTAA
CGATTTCATGATGATGATTGGCGATGATAAAGAAAAACAGATGTCAATTTTGTATTAACATATTTAAA
CTTGATATATTTGAAGAAGTTGAGAAATCAAGTAATTTGATACAAGCACAAATGTTATTTCCATGCATTT
TCCGTATTTATCGATTTTTCGGTTTATGTTATGCGTAAAAATGATAATAATTCATCACCATTGCTAAT
ACTGATTTAATATTTGAATTTGAATCATAGATATAGTATGGTCTTATAGATTATTAGAAAAGACTTGAACCT
TTTTTGAATTTGAGATATCAACATCAGCAGGAGGAGGGGGAGGAGGTGTTAAACAATAACAATAACAAC
GCCTTATCTATAAAATTAGAACAAGAAATTCACAACTTGTATCTTTACAATGGGAATGTATTATCTTCA
GATCATAATACAAATACAAATACCACCAATACTATTTACTACTACTACTACTACAGACAATGGTACTAAA
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GTTTTGAATTTATATTTATGATTTAAATTTAAAAGTTTGGGTATTTAAGAAATGGGTGATAGTTTATCA
GAAATTAGAAAATATTTAATTTGATAATGAATCTACTTTGAATGGTTAA

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YDR216W_homolog 1418aa (SEQ ID NO 472)
MISPTHQSQYLNYFVNPVLMTESGDIIDSVTGTTTTANMSNTTIDAPTPASTTKNYKHKKQNTNTGTS
MSPSNSINSTNNAAAAATTTTSKKS KDIPLELTAFGTTTPSGKPRLFVCQVCTRAFARLEHLRRHERS
HTKEKPFSCGVCQRKFSRRDLLLRHAQKLHAGCTDAITRLRRKSIKKSQDGDGDDDDDDDEEMANSED
ENDHDESGNASTKNGKKDKKDPPEFNLNLFNSKQKPTKANTTKSKVAKLSTTTSRKNSTNPTRKNSSS
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VEFSTPQFLPSSLDNEMTWLNNIPNIPGLSDSVAANLMRQNSITNSADHVTPPVNVSQHGSFSSHQSTF
SATDMGQTRSESVNSLNTPPFDGSYMMPTVTISNQEIQNGVAAHHHHQQQQQQHQQHNHQQPNQSSGLS
RNDMLSEHYGSFYDIPENILNFPMDISSTTSNAMSSGPIQNFKPLSPITQEIEHEITPRIDGRIGDF
QNNNTNDNPIHQNIYDLNLFHTIDDIGQDVISKFMGGYSFYGDNNVSATSSANDYNPNIVSPSQ
QNNQFALHNQSSHPGASPHLNQAMMNKMLHNYSSNKLFTNHIRHMINKALGKYPISGIMTPTIPSN
KLEFYLSVFIQSFLAHLPIHPSKLNVEIMAMTGNEDINNESARVCLPLLTATMGALLANNKNDAEHL
YEASRRTIHIYLESRKTNSTNDKNYKNGKDKSSSGNPLWLLQSLMLSVLYGLFSDNENNVYIVIRQLNA
LNSLVKTSIKNGPIFFSNNGEDEELYNKLNSHDNGTSLFSNNLNDEMRYKNNINMQSQTRIVFIIYRL
TNFLMMYNVPLTFSINDINQLAVTSKDEETLWNFKNYQEFQEFSHKNNKTLLDDYLNKNEPIIFRELL
LTVIKFGISDSNISPEIEKKVTHQLQNLCKYGFNCLVHGIYEIKQYQEMKEVDTFKVLDYLTKFYPTND
GLGFNCFRLPANKDLEKIDYALLVDFTKISSIIDLKLLKEQSWLKNYQDLTQNYHRLDAHSTGNPLNS
INDYDYLKLADCCISVLKILFKVEDSNSNSRNRKNDPTNEINNKLNNNNNNNNNDMNNNSNGDQLIS
AFD TDFGYLNDNNGYAKKEEFLRFTDDELRYDKENTMSYFDKHIKLDIFEEVEKSSNLIQAQMLFHAF
SVLSIFSVYMRKNDNNSSPFANTDLIFELNHRYSMVLRLLERLETFLKLRYSQAGGGGGGVNNNNNN
ALSIKLEQEFNTLYLYNGNVLSDDHNTNTNTNTNTTTTTTTTTDNGTKQNQHHSQDFGLEKTLYLKMGEN
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YDR224C_homolog 393bp public: 1..393 (SEQ ID NO 473)
ATGGCCCCAAAAGCAGAAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAA
ACCGCTTCCACCGATGGTGCTAAAAAGAGAACCAGCTAGAAAAGAACTTATTCCTCATATATATAT
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GTTAACGATATTTTCGAAAGAATTGCCACCGAAGCCTCAAATTAGCTGCTTACAATAAAAAATCCACA
ATTTCCGCTAGAGAAATCCAAACTGCTGTTAGATTAATTTTGGCAGGTGAATTGGCCAAACATGCCGTT
TCCGAAGGTACCAGAGCCGTCACAAAATACTCATCTGCTTCTAGTTAG

YDR224C_homolog 130aa (SEQ ID NO 474)
MAPKAEKKPASKAPAEEKKPAAKKTASTDGAKKRTKARKETYSSYIYKVLKQTHPDTGISQKAMSIMNSF
VNDIFERIEATEASKLAAYNKKSTISAREIQTAIVRLILPGELAKHAVSEGTRAVTKYSSASS

YDR342C_homolog 1653bp public: 1..1653 (SEQ ID NO 475)
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TATATTGGTATTAGTATTTTGTGTTTCTTATTGCTTTGGTGGTTCGTTTTCGGTTTCGATACCTGGT
ACATTTCTGGTTTCTTAACATGACTGACTTTTTAGAAAAGATTGGTGGTACTAAAGCTGACGGTACT
CTTTACTTTTCCAACTTAGAACTGGTTTATTGATTGGTTTGTTCATGTGGGTTGTGCCATTGGTGCA
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AGTTACGGTACTAAGAAATATTCTGACTCCAGACAATGGAGAATTCCATTGGGTTTATGCTTTGCTTGG
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ATTGACGATGCTAAGATTTCACTTGCCAAAATAACAAGGTTTCTCCAGAGGACCCTGCATTATACCGT
GAACCTCAATTAATCCAAGCTGGTGTGAAAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTA
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TCTGAACCTTATCCATTAAAAGTCAGAAGTAAGGCTATGGGTTTTGCTAATGCATGTAAGTGGTGTGG
GGTTCTTGTATTCTTCTTCACTTCATTTACTGATGCTATCCACTTCTATTATGGTTTGTGTTT
ATGGGCTGTTTAGTGTTTCCATTCTTGTGTTTACTTTATGATTACGAAACTAAAGGCTTACTTTA
GAGGAAATTGATGAATTATACTCTACCAAGGTTGTTCCATGGAAATCAGCCGGTTGGGTTCCACCTTCT
GACGAAGAAATGGTTTCGTGCAAAAGGCTATACTGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

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YDR342C_homolog 550aa (SEQ ID NO 476)

MSLDNSTENRDLEEKKEEIPKNEHNEQGEQENNEHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG
TISGFINMTDFLERFGGTKADGTLYFSNVRTGLLIGLFNVGCAIGALFLSKVGDYGRRVGIMTAMIY
IVGIIVQIASQHWYQIMIGRIITGLAVGMLSVCPLFISEVSPKHLRGTLVYCFQLMITLGIPLGYCT
SYGTTKYSDSRQWRIPLGLCFAWALCLLGMVRMPESPRYLVGKDRIDDAKISLAKTNKVSPEDPALYR
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGMLQSLQQLTGDNYFFYYSTTIFKSVGLNDSF
ETSIILGVINFASTFVGIYAIERLGRRLCLLTGSVAMSICFLIYSLIGTQHLVIDQPGGPTRKPDGNAM
IPITALYVPPFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLISFFTSFITDAIHFFYYGFVF
MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVVPWKSAGWVPPSDEEMVRAGYTGDIHADEEQV

YDR343C_homolog 1641bp public: 1..1641 (SEQ ID NO 477)

ATGTCTCAAGACAACGTCTCATCAACATCTACAGCTGAGGCTGTAAATAATGAAATCAAAGTCAAAGAT
GAATTCGACAAGAAGAACAAGCTCATACTAGTTTAGAAGATAAACCTGTGAGTGCATACATTGGTATC
ATCATTATGTGTTTCCCTTATTCGCTTTGGTGGTTTCGTTTTCGGTTTCGATACGGTACTATTTCCGGT
TTCATTAAATATGTCTGACTTTTTAGAAAGATTCGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCC
AATGTCAGAACTGGTTTAAATGATTGGTTTGTTCACCGCTGGTTGTGCCATTGGTGCATTATCTTGTCT
AAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATTGCTATATTGTTGGTATT
ATTGTTCAAATTCCTCTCAACATGCTTGGTATCAAGTCATGATTGGTAGAATTATCACTGGTCTTGCC
GTTGGTATGTTATCAGTTTTATGTCTTTTGTTCATTTCCGAGGTTTCTCCAAAACATTTGAGAGGTACT
TTGGTGTGCTGTTTCCAATTGATGATTACCTTGGGTATCTTCTTGGGTATTGTTACTACCTATGGTACT
AAGAGTTACTCAGACTCTAGACAATGGAGAATTCATTAGGTTTATGTTTGTCTTGGGCTTTATGTTTG
GTTGCTGGTATGGTTAGAAATGCCAGAATCTCCAGCTTACCTTGTCCGTAAGACAGAATGAAGATGCT
AAAATGTCTACTTGTCAAACAAAGTTTCCCGAGGACCCAGCCTTATACCGTGAACCTTCAATTA
ATTCAAGCTGGTGTGAAAGAGAAAGATTAGCCGGTAAGGCATCTTGGGGTACTTTATTCAATGGTAAA
CCAAGAATCTTTGAAAGGGTTGTTGTTGGTGTCTATGTTACAAGCCTTACAACAATTGACTGGTGATAAC
TATTTCTTCTACTACAGTACCCTATTTTCAAGTCCGTTGGTATGAATGATTCTTTCCAAACTTCTATC
ATTATTTGGTGTATTAACTTTGCGTCCACTTTTGTGGTATTTATGCTATTGAAAGAATGGGTAGAAGA
CTCTGTTGTTTAACTGGTTCCGTTGCCATGTCTGTCTGTTTCTTAATCTATTCTTGGTGGTACTCAA
CATCTTTTATATTGACAAACCAGGTGGTGTAGTAGAAACCAGATGGTGATGCCATGATCTTTATGACT
TCACTTTATGTGTTCTTCTTTGCTTCTACATGGGCTGGTGGTGTCTTACTCCATTATTTCTGAACCTTAT
CCATTGAAAGTTAGAAGTAAGGCTATGGGTTTAGCTAATGCTTCCAATTGGACCTGGGGTTTCTTAATT
TCTTTCTTTACTTCAATTTATTACTGATGCTATCCACTTCTACTACGGTTTCGTCTTTATGGGATGTTTA
GTTTTCTCCATTTTCTTTGTCTACTTTATGGTTTACGAACTAAAGGTCTTACCTTGAAGAAGAAATGAT
GAATTGTACTTCCAAAGTCTTCCATGGAATCAGCTGGTTGGGTGCCACCTTCCGAAGAAGAAATG
GCAACCTCTACGGGATATGCTGGTGTATGCCAAACCAGAAGAGGAACACGTTTAA

YDR343C_homolog 546aa (SEQ ID NO 478)

MSQDNVSSTSTAEAVNNEIKVKDEFQRQEEQAHTSLEDKPVSAIYIGIIMCFLIAFGGFVFGFDTGTISG
FINMSDFLERFGGTKADGTLYFSNVRTGLMIGLFNAGCAIGALFLSKVGDYGRRVGIMTAMIVYIVGI
IVQIASQHWYQVMIGRIITGLAVGMLSVCPLFISEVSPKHLRGTLVCCFQLMITLGIPLGYCTTYGT
KSYSDSRQWRIPLGLCFAWALCLVAGMVRMPESPRYLVGKDRIDAKMSLAKTNKVSPEDPALYRELQL
IQAGVERERLAGKASWGTLFNGKPRIFERVVVGVMQLALQQLTGDNYFFYYSTTIFKSVGMNDSFQTSI
IIGVINFASTFVGIYAIERMGRRLCLLTGSVAMSVCFIYSLVGTQHLVIDKPGGASRKPDDGAMIFMT
SLYVFFFASTWAGGVYSIISELYPLKVRSKAMGLANASNWTWGFLISFFTSFITDAIHFFYYGFVFMGCL
VFSIFFVYFMVYETKGLTLEEIDELYSTKVLWPWKSAGWVPPSEEMATSTGYAGDAKPEEEHV

YDR544C_homolog 1700bp (SEQ ID NO 479)

CTAAAGTCCAAAGTTGGTTCAATTTTTGGCAGAAAAAAGAAGAAGGAAAAATTCCTGGA
GCTGATTCAATTGCTGAAGATGAATCATTATCTGAGGTTTCTTTGCCACCTACAAGAACT
AGGAATTCATCGGTGTTGTCTCGCAGTAACCTCAACTAGAAGATCTTTTATTGACCGCTTC
CATAGAGATGAGTCTAGCACTGGCATTAGCAGACAACATGAGCAGCACCAGCAGCCTTTG
AGTGATCCTTTGCCTCACGCAGAGAAGCCTCAACCGGAAATTCCTCAATCACCAGAAGCT
CCACAGGCCAAATCACTAGAGCCTGTATCAGAAGTACTAAAAGAAGTGTTCACCTATG
CAAAACGGGTCCGAAAGGAAAGGTGAAAATCAGCAGTCGAGAGTTGATGTATCCTCTCAA
ACCTTGTACACAGTTACTCCTACTCAGGATGGATTGGTGGTTCTGTAAACCATTACCA
GAACCTGTTGATTCTCCAAATGTGATTAAATACAATGACTCGGACGACTCTTCTACAGAA
GAACGTAGAGGCTCGTTACTTGAAAAACACAATTTAGAAGTACAACCTGTATCTTCCCA
TTCATACTCAACCGCCAGCACCTGTGCCACAAGAATCCAGATCTAGACAAAGCAGTGAT
GGCATTTACTCGTTTGAAGCGGGTGATGATTCCAACCAATCTCGGCTACTCCAAGATCC
GAGCAAAATGTGTTTGGACAGATGCCAGACCCAAATTTGTCTCCTGAAAAGACTCTTGCT
CCACCACCACCACCTTCGAGAAAAGTTTGCACCATGAAGAACCAACTGTAAGGGATTCA

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GCTCTTTTCCACAATTTACCTGCTGCCTCCCATTCTGGAAGAGATTCCGGTAATGGCTCCA
TTAGCAAGTCAAGACAGGGGTCATTCTGTTGTTGAAAAATGATTTCAAACACGAAAACCTTG
GCATCCACCCTCGGATTGAGCTCTTCTATTGCTGAAGTCATCAATGCCAGCTTTAAGGAT
GGACAGTTGATTAAATCACAAGTAGTTGGTGAAGTGGCCTTCAATTATAATGGTAATGCT
TCCGATCCACTTGTGGTCACTATTCTTAATAGTTTCGATAAAGTACTCGTGAACAAGACT
TTTATTGAGGATTTAGGTCAAAGCAAGTATAAAGTGAACCAACTTCAATTACGTCTAAA
ACTCTTGGTGGGTTGAAATATCTTTTGAAACCAACACAGGTACCAGTGATAATTCAACAA
ATATGGAAATTTGAACCTCATCAGTCAAGTTTGATGGTTAGCATTCTGTTCAACTACACCT
TTGGTATTGGAAAATTTTGTGTCTCTGTAGCTTTGAATCAAGACATTGAAGCAACATCT
GCTTCCTCAAAGCCTCAAGGTGCGTTTAATAAAGAGAAAAACAGAATAACATGGAGATAT
CCACAGTCCCTCGCATTGAATGGTGTAGAGCGTTTGATAGCTAGATTTATGACTAATGGA
TTGGGTTCCGAACATGAGTCTGGTGTGAGATTAAATTTCAAGTTAAGGATCCACAAGTC
AAGTACTGTAGTATTTACAGTGAGAAATGGCGAAGAGATTCTACGTTTAGAAATTTGGTT
AGCGGTAGTTATAGTGGTCATCTTTAAGTTATCTGTTTTGAGATTAGTCTCTTGTGAAT
TGAAAAAACGTGA

YDR544C_homolog 548aa (SEQ ID NO 480)

LKSKVGSIFGRKKKKEKFTGADSLAEDESLSVSLPPTTRNSSLRSNSTRRSFIDRF
HRDESSTGISRQHEHQHQQPLSDPLPHAEKPQPEIQSPEAPQAKSLEPVSEVLKELFPFM
QNGSERKGENQQSRVDVSSQTLSPVTPTHDGFSGSVKPLPEPVDSPNVIKYNDSDDSSTE
ERRGSLLEKHNLVQPVSSPFTTQPPAPVPQESRSRQSSDGIYSFEAGDDSNPISATPRS
EQNVFGQMPDPNLSPEKTLAPPPPSRKVLHHEEPTVRDSALFHNLPAAHSGRDSVMAP
LASQDRGHSLLKNDKFHENLASTLGLSSSIAEVINASFKDGLIKSQVVGEVAFNYNGNA
SDPLVVITPNSFDKVLVNKTFIEDLGQSKYKVNPTSITSKTLGGLKYLKPTQVPVLIQQ
IWKFEPHQSSLMVSIRSTTPLVLENFVVSVALNQDIEATSASSKPOGAFNKEKNRITWRY
PQSLALNGVERLIARFMTNGLGSEHESGVQIKFQVKDPQVKYCSIYSENGEEIPTFRNLV
SGSYSGHL

YEL071W_homolog 1584bp public: 1..1584 (SEQ ID NO 481)

ATGCAGAGGAGATTAGTACAGACTGCTTCGTATTTGATTAGACGAAACAACGTGGCATGTAGATTCAGT
CGTTATAATGGTTTGCCCGTTGCATCTTATTCTACAAAAACAGTACCTTTTACGGCAGATACTTATTCC
CAAAAAGTCCAACGTGATGCAAAATTCAGCAACTTGAATCTCAAGACATCGAATACTTTAAAAGTGTA
TTACCTGAGAATTCATTTACTGATGAAGACGACTTATTGTTTTCACGAAGACTGGATGAGAAAG
TATAGAGGTCAATCACAATTTGGTPTTTGAAACCGAAAACCAACCGAACAAGTCGCTTCTATCTTAAAGTAT
TGTAATGATAACAAGCTAGCTGTGTACCACAGGGTGGGAATACTGGGTGGTAGGTGGATCTAATCCA
ATTTTTGATGAAATCATCATTTCTTGTGCGCCATGAATAAAATCAGATCGTTTGTATCTGTCAGCGGT
ATATTGAAAGTCGACGCTGGTGTATTPTTGGAAACAGCTGATCAGTATTTGGCTGAGCAGGGCTACATT
TTCCCGCTCGACTTGGGAGCTAAAGGGTCGTGTATGTTGGTGGCAATGTTGCATGTAATGCTGGTGGT
TTGCGTTTGTACGATACGGTCTTTGTCATGTTCTGTTTATAGGTTTGAAGCTGTCCTTGCCCGACGGT
ACAGTTTATAACTCTATGCATTCATTGCGTAAAGATAATACTGGTTATGATTTGAAGCAGTTGTTTATT
GGATCTGAAGGTACTTTGGGTATTATACTGGTGTTCGATTCTATGTCCATCAAGACCACAAGCGCAA
AATGTGGCATTMTTAGCTGTATCGAGTTATGAGGCCGTTTCAAAAAGGTTTGTCCAGGCTAGAAAAGGAG
TTGCAAGAAATTTATCGGCTTTTGAATTCATGGACAACACCTCACAAAAGTTGACTGCTAAGCATTTA
GGTTTGGAGCACCTTATTGAAAGCGGTGACTTCCCATTCTATGTGTTAATTGAAACCTCTGGCTCCAAC
AAAGAGCACCAGCAGCAAAAATTTGAAACATTCCTTGGGGAATGCAATGGAAGAAGGTTTAGTCGACGAT
GGGATTATTGCACAAGATGAGGCTCAAATACAATCATTATGGTTCATGGAGAGAAATCCATCCCTGAAGCA
ACCATTATTGGAGGCGGTGTTTACAAGTATGACGTTTCTATTCCATTGGCAGATCTTTACGGGTAGTT
GAGGACATCAATACCAGGTTAAATGATGCTGGAATGCCAGCTTGGACGATGAATCGAAACTTGTGCTT
GCTGCATTGGGTTATGGTCACATTTGAGATGGGAATTTACACTTGAACGTTTCTGTGAGAAAGTATTCT
CCTGAAATTTGAACTATCTTGGAGCCATTTGTCTATGAATGGATCGCAAAAAAATGGATCCATTTTCG
GCTGAACATGGGTGGGATTCCAAAAGAAAACTACATTTGGGTATTTCAAGAATGAGATTGAGGTCAA
TTAATCAAAGAAATCAAACAACATTACGATCCAAATGGAATCATGAACCATATAAATACGTGTAA

YEL071W_homolog 527aa (SEQ ID NO 482)

MQRRLVQTASYLIRRNNAVCRFSRYNGLPVASYSTKTVPFTADTYSQKVORDAKFKQLESQDIEYFKSV
LPENSIITDEDDLFFNEDWMRKYRQSQLVLKPKTTEQVASILKYCNDNKLAVVPQGGNTGLVGGSNP
IFDEIIISLSAMNKIRSFDPVSGILKVDAGVILETADQVLAEQGYIFPLDLGAKGSCHVGGNVACNAGG
LRLRLRYGSLHIGSVLGLAVALPDGTVVNSMHSRLKDNTRYDLKQLFIGSEGLGIITGVSIILCPSRPQAQ

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NVAFLAVSSYEAVQKVFVQARKELQEILSAFEFMDNTSQKLTAKHLGLEHPIESGDFPFYVLIETSGSN
KEHDEKLETFLGNAMEEGLVDDGIIAQDEAQIQLSWSWRESIPEATTIGGGVYKYDVSIPLADLYGLV
EDINTRLNDAGIASLDDSKLVLAALGYGHIGDGNLHNVSVRKYSPEIETILEPFFVYEWIAKNGSIS
AEHGLGFQKKNYIGYSKNEIEVKLIKELKQHYDPNGIMNPKYK

YER177W_homolog 795bp public: 1..795(SEQ ID NO 483)

ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA
ATGGTTGAAAACATGAAAGCCGTTGCTTCCTCTGGCCAAGAATTGTCTGTTGAAGAACGTAATTTATTA
TCTGTTGCTTACAAGATGTCATTGGTGCTCGTCTGCTTCTTGGAGAATTGTTTCATCAATTGAACAA
AAAGAAGAAGCCAAAGGAAATGAGAGCCAAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT
GAATTGTCTAAAAATTTGTGAAGATATTCTCTCTGTGTTGAGCGACCATTTAATTACATCTGCCCAAAC
GGTGAATCAAAAGTATTTTACTACAAGATGAAAGGTGATTACCACAGATACCTTGGCTGAATTTGCTATC
GCTGAAAAACGTAAGGAAGCTGCTGATTTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTGCTGTG
ACCGAGTTGCCACCAACCCATCCAATCAGATTAGGTTTAGCATTGAACTTCTCTGTTTCTACTATGAA
ATTTTGAACCTCCAGATAGAGCTTGTCAATTAGCTAAACAAGCTTTCGATGATGCTGTTGCTGATTTA
GAAACCTTATCTGAAGATTTCATACAAGGATTCAACTTTGATTATGCAATTATTGAGAGATAACTTGACT
TTATGGACCGATTATCTGAAGCCCCAGCTGCCACTGAAGAACAACAACATCCAGTCAAGCTCCAGCT
GCTCAACCAACAGAAGGTAAGGCTGATCAAGAATAG

YER177W_homolog 264aa (SEQ ID NO 484)

MPASREDSVYLAKLAEQAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ
KEEAKGNESQVALIRDYRAKIEAELSKICEDILSVLSDHLITSAQTGESKVFYVKMGDYHRYLAEFAL
AEKRKEAADLSLEAYKAASDVAVTELPPHTPIRLGLALNFSVFYIEILNSPDRACHLAKQAFDDAVADL
ETLSSESYKDSLIMQLLRDNLTLWTDLSEAPAATEEQQSSQAPAAQPTEGKADQE

YGR192C_homolog 1008bp public: 1..1008(SEQ ID NO 485)

ATGGCTATTAAAAATTGGTATTAAACGGTTTCGGTAGAATCGGTAGATTAGTCTTAAGAGTTGCTTTGGGC
AGAAAAGACATTGAAGTTGTGCGCCGTCAACGATCCATTGCTTCCAGACTATGCTGCTTACATGTTT
AAATACGATTCTACTCACGGTAGATACAAGGGTGAAGTCACTGCTTCTGGTGACGACTTGGTCATTGAT
GGTCACAAGATTAAAGTTTTCACAAGAAAGAGACCCAGCTAACATTCCATGGGGTAAATCTGGTGTGAC
TACGTTATTGAATCCACCGGTGTTTTCACCAAACTCGAAGGTGCTCAAAAACACATTGATGCTGGTGCC
AAAAAAGTTATCATCACTGCTCCATCTGCTGATGCCCCAATGTTTGTGTTGTCGGTGTAAACGAAGACAAA
TACATCCAGACTTTGAAGATTATCTCCAATGCTTCTTGTTACCACCAACTGTTTGGCTCCATTAGCTAAA
GTCGTCAACGACTTTTCGGTATTGAAGAAGGTTTGATGACCACTGTCCACTCCATCACTCCCAA
AAGACCGTTGACGGTCCATCCCACAAGGACTGGAGAGGTGGTAGAAGTGTCTTGGTAACATTATCCCA
TCTTCCACTGGTGTGCTAAAGCCGTTGGTAAGGTTATTCAGAAATTGAACGGTAAATTGACTGGTATG
TCTTTGAGAGTCCCAACCACCGATGTTTCCGTTGTTGACTTGACTGTGATGATGAAGAAAGCTGCTTCT
TACGAAGAAATTGCTCAAGCTATCAAGAAAGCTTCTGAAGGTCCATTGAAGGTTGTTTGGGCTACACT
GAAGATGCTGTTGCTCCACCGATTCTTGGGTTCAAGCTACTCATCTATCTTTGATGAAAAAGCCGGT
ATCTTGTGTGCTCCCAACTTTGCTCAAAATTGATTTCCTGGTACGATAACGAATACGGTTACTCCACCAGA
GTTGTTGACTTGTGTTGAACACGTTGCTAAAGCTTCTGCTTGA

YGR192C_homolog 335 aa (SEQ ID NO 486)

MAIKIGINGFRIGRLVLRVALGRKDIEVVAVNDPFIAPDYAAVMFKYDSTHGRYKGEVTASGDDLVID
GHKIKVFQERDPANIPWGKSGVDYVIESTGVFTKLEGAQKHIDAGAKKVIITAPSADAPMFVVGVNEDK
YTPDLKIIISNASC'TTNCLAPLAKVVNDTFGIEEGLMTTVHSITATQKTVDGSPSHKDWRRGTASGNIIP
SSTGAAKAVGKVIPELNGKLTGMSLRVPTTDVSVVDLTVRLKKAASYEEIAQAIIKASEGPLKGVLYT
EDAVVSTDFLGSSYSSIFDEKAGILLSPTFVKLISWYDNEYGYSTRVVDLLEHVAKASA

YGR243W_homolog 399bp public: 1..399(SEQ ID NO 487)

ATGGCTTCAACAGTTCAACACGCATCCAAATTCACAGTMTTTTAAATTTCAGAGACCGGTCTTAGAACC
GTGCATTTTGGGCTCCAGTGTTCAAATGGGCCCTTAGTTGCTGCTGGACTTAATGACATACAACGTCCT
GTTGAAAAATTGAGCGGAACCAACAGATAGCATTGTTTGGCCACTGGTGCCATATGGACTAGATGGGCC
GGGTTTGTATATAAAACCAAGGAACATGCTTTTGGCATCAGTGAATTTCTTTTGGGTGGAGTTGCTGGT
TACCAATTGTTAAGAATTGTCAACTACAGAAGAGATTGGGTGATTCCCAATGCAAGTATTTAATTAT
ATCTTGAACGGTGATGCAGCTGCTGTAAAGAACCAGAACCAGCCAAGAATTAA

YGR243W_homolog 132aa (SEQ ID NO 488)

MASTVQHASKFQRFLNSETGPRTVHFVAPVFKWALVAAGLNDIQRPEKLSGTQQIALFATGAIWTRWA
GFVIKPRNMLLASVNFLLGGVAGYQLLRIVNYRRDLGDSPMQVFNYILNGDAAVKEPEPAKN

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YHL021C_homolog 1224bp public: 1..1224(SEQ ID NO 489)

ATGTTAAGACAACCATTACGCCAAATCCGTTTCCACTCGAAATGGGCACCTGTCAGGATACAACAGCAAA
GAAGTGACAGTCACCATCAACGGCAGAACCTGTACATTCAACAACGTGTTTTTGAGAGACGCATGCCAA
AGCCCAGACTCGGTAGACCCCATTTCTAGCCAAAACTATTCACTACAGCAGATGCAGCAACCGGCTTG
CAAAATTAACGCACCCCGAGTGGTAGAGGATTCCCTCATTGAAAAATCCAATGGAGCAACAATGGCAAACTC
ACCAACTCAGTCTACCCCGTGTCTATTCTTAGAAAACTACTCCACCAACAACGACTCGGCAAAATTCTTT
GACAAAGATAGAAAGTTATGGGACAAACAAGAACTCGAAAAACAATTTGCCTCCCTCAACATGGACTAC
GACGACATTCTCACCACGACAACCTCTTTCTTCCAGACGTTGTACAACCTGAATAGGTACGGGTTAAACA
TTTGTCAACAACATCCCCACCCACAAATTTCTGACATGACAGAGGACAACGCCACGCAATGGCCAGTG
TACAAGATCGCCGAAAAGTTTGGCTACATCAAGAAAACATTCTACGGGACATTATTCGACGTCAGAAC
AAGAAGGAAAAAGCAACCAACATTGCCTACACCAACACGTTTTTGGCATTGCACATGGACTTGCTCTAC
TACGAGTCACCCCGGGATTACAGTTGCTACACGCTATCCAGAACTCTACGTTGGGCGGCGAAAAACATC
TTCTGTGACTCGTACCTTGCTGTGCTGAGCATGTCCGGAACCCGACCCAGGGCATAACGGCACTCACC
CAGACCCCAATCACCTTCCACTACGACAACAACAACGAGTACTACTACTACAAGCGGCCGTTAATCGTT
GAAGACCCCGAGGTTGGCGACGGGTTCCCGAAAATCGCGTCCATCAACTATGCCCGCCATTCCAGGGC
CCATTGAGGTTGACCCCAACCCAGACTTTATCCGCGGAATGCAGTTATTCGAAACCTTCATCAACGAC
CCGGCAAAACCACTTTGAAATCAAAATGCCAGAAGGCACCTGTGTCAATTTTCGAAAACAGAAGAGCCCTT
CACTCGAAGAACGCATTCTCCGACCTGAACAACGGCGACAGATGGTTAATGGGCACTTATGTTGACGGC
GACAGTTTTAGATCAAAATTACGTATAGGCTATAGAAAAGTACATACCTAA

YHL021C_homolog 407aa(SEQ ID NO 490)

MLRQPLRQIRFHSKLALAGYNSKEVTVTINGRTCTFNNVFLRDACQSPDSVDPISQKLETTADAATGL
QINAPPVVEDSSLKIQWSNNGKLTNSVYPVSFLENYSTNKRGLKGFDFDKRKLWDKQLENNFASLNMDY
DDILITNDSFFQTLNLRNRYGLTFVNNIPTQISDMTEDNATQWPVYKIAEKFGYIKKTFYGLFDVKN
KKEKATNIAYTNTFLPLHMDLLYESPPGLQLLHAIQNSTLGGENIFCDSYLAAEHVVRKTDPRAYTALT
QTPITFHYDNNNEYYYYKRPLIVEDPEVGDFPKIASINYAPPFQGPFEVDPHPDFIRGMQLFETFIN
PANHFEEKMPEGTCVIFENRRALHSRNASDSNNGDRWLMGTYVDGDSFRSKLRIGYRKVHT

YHR162W_homolog 354bp public: 1..354(SEQ ID NO 491)

ATGTCATCATTTTAAAAAATTCAGTATTTTTTATTTTCAAAACAATCCCTTAGATATGTCTGTACAAC
CATTTTTGGGGTCCAGTATCAAATTTGGGATTCCTATAGCTGCTATTTTAGATTGAAAAAAGATCCT
GATTTAATTAGTGGACCAATGACTGGTTCATTAATACTTTATTCTTTAGTGTATGAGGTATTCATG
GCAGTTACTCCTCAAAATTATTTATTATTTGGGTGTCAATTTGTTAATGAATTGGCACAATTGAGTCAA
GGATTTAGATGGGTTAAACATCACTATGATACTTCTTCAAATGATGGTGAAGATACCAAAAAGATAACT
CAAAATTGA

YHR162W_homolog 117aa(SEQ ID NO 492)

MSSFKKFTDFLFSKQLSRVCTTHFWGPVSNEFGIPIAAILDLKKDPDLISGPMTGSLILYSLVFMRYSM
AVTPQNYLLFGCHFVNELAQLSQGFWRVKHHYDTSSNDGEDTKKITQN

YLR109W_homolog 531bp public: 1..531(SEQ ID NO 493)

ATGACTGACGGTAAATTCCTCAACTAACATTGAACCAAAATACATTCCCTTATTTCTAAAGATCATGCAAGT
TTAACTGCTTGTGCTAATCCAATACCATGGATTAAAATCTTTATTTCCAAATAATACTGTTGTTGTC
ACTGCTGTGCCTGGTGTCTTTACCCCAACTTGTACTGAACAACATATCCCTGATTATTTGAAACATTTG
AAAGATTTCAAAGACAAGGGCGTCAAAAAAATCATGTTTTATCTGCCAATGATCCATTTGTAATGGCA
GCTTGGGCTAAAGCTTTGGGTATAGTGAAGAAAATTATGTTATTTTGTCTACTGATCCTAATGCT
TCTATTTCTAAAGAATTGGGTGATGGATTTGTTGCTGATTTGACTCTGGCAGGTATGGGATTAAGATTA
CAAAGATATGCTAGTATTGTTGTTAATGGAGAAATCACTTATTTGGAACTGAAGATAGTTTGGGATTC
CTGGAAATTTCTAGTGCTGAAACCATTTTAAAGAGAATCCACAATTAA

YLR109W_homolog 176aa(SEQ ID NO 494)

MTDGKFPTNIEPKYIPYSKDHASLTACANPIPLDLKSLFPNNTVVVTAVPGAFTPTCTEQHIPDYLKHL
KDFDKGVKKIIVLSANDPFVMAAWAKALGYTDEENYVIFATDPNASISKELGDFVADLTSAGMGLRL
QRYASIVVNGEITYLETEDSLGFSEISSAETILKRIHN

YLR206W_homolog 879bp public: 1..879(SEQ ID NO 495)

ATGAGAAAAACAAAATAACAATTTATTGGATTTGAATGATGAAACACCACCACAACAACCTCAATATTAT
TTAGCAACCGGATTTATCAACAACAACCAAAATTTATGCCCAGCAACCTCAATCGCAACAATTCCAA
CAATATGATATGTTTGGGAACCCAATACAGAATCCAATGGACACAGGATTATATAATCAACAGGCCTAT
TATCAACAACCACAACAGCAGCAACAACAGTTTCAACCAAAACAGTTTACTGGTTTTAACTATGGACAA
CCACAACAACCACAAGCGCAACCAAGAACCTTTACCAACCATGAAAACAGGATCCAAATAATCCATTTGCC
ATGTCTTCTGGGTCAGACAATACCAACAAGCCACCAACTCAATCCTTAAACAGTTTACTGTAACAGCAA

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CAACAGCAACAGCAGCAGCAACCACAATTTTTTACTCAGCCAACTACTGCTCCACTCAAACAACAAAAC
ACATCATCATCAAGGTTTAATGAACTCATGAGTTGAATGATTTTAACTCAAGGAAC TGGATTAGAT
ACATTCGGTAACACTGGAGATACTAGAATCCCACATCAACATACAAAGACACAAAATTTTATAAATTCA
AGTGGAACTGGATATAAACAACACTGGTAATGAACCAATTAGATTAAAGTTCTAATGCTACAGGTAATCCA
TTTCTTAATACTGGTATTGGATATCAAGGTGCTACACAACAGCAAGTGCCACAACAGCAAGTGCCACAA
ATCAATCCTGCTTATACTGGGTATGGATTGGTAACGCTCAACCTCAACAACACCAGCAATACCAACAA
CAACAACAATCACGTAATGGTAATGATGGCCCAAGTTTAATAGATATTTAA

YLR206W_homolog 292aa (SEQ ID NO 496)

MRKQNNNLLDNDLDETPPQQPQYYLATGFYQQQPQFYAQQPQSQQFQQYDMFGNPIQNPMDTGLYNQQAY
YQQPQQQQQQFQPNQFTGFNYGQFPQPPQAQPEPLQPLKTGSNNPFAMSSGSDNTNKPPTQSLNSLAEQQ
QQQQQQQQPQFFTQPTTAPLKQONTSSSRFNETHLNDLLTQGTGLDTFGNTGDTRI PHQHTKTQNFINS
SGTGYKQTGNEPIRLSSNATGNPFLNTGIGYQGATQQQVPQQQVPQINPAYTGYGFGNAQPPQHQQYQQ
QQQSRNGNDGPSLIDI

YMR043W_homolog 789bp public: 1..789 (SEQ ID NO 497)

ATGGCTATTAAAGAAGAAACAAATGAATTTAGTCAAGGTAATGAGGGGAATTCCTATTCAACCAATAAC
AACAATAACAGCAACAACAGCAACAGCAACAACAATGCTGATGTTTCTGCACCAGTAGATGATGACGAT
GATGACGATGGTACTTCTCAAGGTAAAACCTCAAAGGAAAGAAGAAAAATTGAGATCAAATTCATTCAA
GAAAAATCAAGACGTCATATTACTTTTTCGAAAAGAAAAGCTGGGATTATGAAGAAAGCTTATGAATTA
TCAGTATTGACAGGTACTCAAGTGTTATTATTAGTTGTTTCAGAACTGGTTTGGTTTATACTTTTACC
ACTCTAAATTACAACCTTTGGTCACTAAATCTGAAGGGAAGAATTTGATTCAAGCATGTTTGAATGCT
CCTGAAGAAGGATTGGGTGATGATCAAGAGAATCAAAGTGATGGAATAACAGGAGATTCACCTGATCAA
AGCCCTGCTCCAGCAACCAATCCAATGTCACTGGGTGCTGAGGTCTGCTCATCATCATCAACAACAA
CAACAGCAACAACAACAGCTCAACAGCAAGCTCAGCAACAATGGCACCAATGCCTTCTCATGGTTTA
CCTACACATTATTCCAATCCTCAAGGAGCTGGTAATCCTGGTGTACCTCCTCAACAACAAGGTCAACAT
CAACCTGGTATTCCATTACAAGGTGGTTATAGTGATCAATACCTGTATTTTGGTAATATTCAAAATAAC
AACATACCTAATCAACAGCAATATCAATGA

YMR043W_homolog 262aa (SEQ ID NO 498)

MAIKEETNEFSQGNENSHSTNNNNNSNNSNNNADVSAPVDDDDDDGTSQGKTQKERRKIEIKFIQ
EKSRRHITFSKRKAGIMKKAYELSVLTGTQVLLLVVSETGLVYTFTPKLQPLVTKSEGKNLIQACLNA
PEEGLGDDQENQSDGNTGDSPDQSPAPATNPNVMGAAGHAHHIQQQQQQQQAQQQAQQQMAPMPSHGL
PTHYSNPQGAGNPGVPPQQQGHQPGIPLQGGYSQYSYFGNIQNNNIPNQQQYQ

YMR256C_homolog 330bp public: 1..330 (SEQ ID NO 499)

ATGAGAATGAAACAACCAGACGACCAAAAGTCTGAGAGAGAGAGAGAGAAAAAATATCGGCTCATTATT
TTCAATTCACTTTTAATCCTAGTTAATACTATTTACTTTCTTTCTTCTAACTATCCATCCCACCATCCT
ATCTATTCAATTATGAATCCACAAAGAAATTATTGAATTACAAAAACATTATCAAAATACTCCTAAACCA
TTATGGTTAAGAGGTAGACAATCGGCATTTTATGTTTATCCATTTTATGCTTTTATGCTGTTAGTACT
GCCATCCCATTATATTATAGTGTTAGAGCTGTTGCTGGTATAAAAGATGAATAA

YMR256C_homolog 109aa (SEQ ID NO 500)

MRMKQPDQKSEREREKKYRLIIFNSLLILVNTIYFLSSNYP SHHPIYSIMNPQRIIELQKHYQNTPKP
LWLRGRQSAFLVYPFYALFAVSTAIPLYYSVRVAGIKDE

YOR267C_homolog 2091bp public: 1..2091 (SEQ ID NO 501)

ATGCCAGATAAAACATAAACTCAAACATTTTGGAAAAAATAAACACGACAAAGATGACGAATTGTCCTTG
TCAACGTCAAACCATTTCTCACGGAAGTACACGGAAGTTTTTAGGATTTTCAATTTGGAAGACATGAATCG
GGCGACTCGTTGACTTCTCCAGTTATGAGCAATTCATCCGAAAGTCATCATCACAGCCATCACCCCTCAT
CAAGCCAAATCAAGTGCAAACCATCGTAACCCCTCTCCAGTTTCAATCACTGGTACTGCCACTACC
ATTCCATCAATACAAATCACCACAACCTCAAGCATCTGGATTACACCGCGGGGACTCCGATAAAAAATCA
TCTGGCTCAGTTGTTGATTTTGAAAAAATTTCTCAAAACAAAGAAAACTTCAAATCCAAAGAAAGGAAGGA
CATAGTATTTTGGGACAATATAGCAATCAGCTCCATTCACCACCACCAATGGCGCAGGTTTATTCGCCT
GGTGCAGGCTCGGGGAACGGCAGTGCCTTGCAATCACGTGAACAATCATCTACGTCATTAGCCACTTTA
ATCAATCAAACATCTTCTCAACTTTTGTACAATGCTTCACATTTCTGTCAAATAGCAATCGAGATCCCTTC
ACGGACGCAACTCTCCATTTGGTGAAGAAGTATGGTAAGATCGGGAAAGAGTTGGGCAGTGGAGCCGGT
GGGTCCGTCAAATTAATCACCAGGCCAGTGACTCCAAGACGTTTGCTGTTAAAGAAATTTAGAGCGAAA
AGATCTACTGAATTACATGAAAGATTACACTAGGAAATGTACTGCTGAGTATTGTTATTTGTTTCTACTTTG
AGGCACCCAAACATCATTTAAACCATCGATATTATCCATGAAAAACAATCGTTATTTTGAATTTATGGAA
TATGCACCTATAGATTTCTTTGCTGTTGTTATGAGTGGAGAGATGCTCGAACGGAAATCAATTTGTTGT
TTAAAGCAAAATTTATGAAGGTGTGGCATATTTACACAAATTAGGGTTGGCCCATCGTGATTTGAAATTG
GATAATTGTGTTATAACGAATGAAGGGATTTTGAAGATTATCGATTTTGGTAGTGCTGCTCATTTTCAAG

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TATCCCTACGAACAGTTTGGTAACAACAATTCTATTTCAGCCGTGTCATGGTATTGTTGGATCTGATCCT
TACTTGGCCCCGAGGTTTTGAAATCTCCTAATAGCTACAACCCACAACCTGTGGATTTATGGTCTATT
GCCATAATTTACTGTTGTATGACTTTTGAAGAGATTTCCTTGGAAAATACCTAGTCAAGAAAAGGATAAC
AGTTTCCGACTTTATTGTCATGTATGATGATAATTTCCATGATTATTATTTGAGTAACGAATGTCATAAA
CTTTTGTGTC AACAGCGTAAACTAAAGAATACAAATGTTAGACTGAACAAAAGGAAAAAGCAGCTAGAA
GAGGAAAAGGGCGACAAGCCTGAAGAAGACGAAGAAATGAAAGATGCCGATAGTGCACCACAGCAACAT
CATCATTTCTCATGATGTAGAGCTGGGAAAAACTGGTGGATCTACGGTTGGCAAAGACAAGTCAAATGAA
GCTGTTACCGTTTAAACAGATGAGCAAGCAGAAGAGATTATGGCACAATTAAATGAGATTGATAGAAAA
CTACAAGAGTTTGAAGATAAAAAAGAAATCAACTTAAAGAGAAATATGAGGCTTTGCGAGATGCTGATCCT
AGATATCAAAAAACAGTTGGCACAATTCACGAAGAGGAAGAAAAAGCAAAGACTAAAAAGATGCCGAGCAC
GGTCCGATGAGAAAAAGAAATCACATCATAACAGATTTCATGGTCCGTATAGATTGATGAGATTGTTG
CCACATGCTTAGACAGTCAATCAAGATTATTTGGAGGTTGATCCAAAGAAAAGAGCAACTATGGAA
GAAATTCAGAAAGATGAATGGATTAAAGAAATTCATGCTGTACAGTTAAGCCAGTTTCAAAATCAACA
GATGCAACATTAGATTTTATTGAGGATGAGGACGAAGTATTGGTGAAAGGAGTACCTCCACACGAGCAT
ACAATTGTGAAAGAAGGTTGA

YOR267C_homolog 696aa (SEQ ID NO 502)

MPDKHKLKLFEGKNKHKDDDELSTSNHSHGSTRKFLGFHIGRHESGDSLTSFVMSNSSESHHHSHHPH
QANSSANHRNPSFVHSNTGTATTIPSIQSPQASGLHRGDSDDKSSGSVVDLKKFFKTKKTSNPRKEG
HSILGQYSNQLHSPPPMAQVHSPGAGSGNGSALQSREQSSTSLATLINQTSQLLYNASHSVNSNRDPF
TDDNSPLVKYKIGKELGSGAGGSVKLITRPSDKTFAVKEFRKRSTESLKYDTRKCTAEYICGSTL
RHPNIKTIDIHENNRYFEIMEYAPIDFFAVVMSEMSRTEINCCCLKQIIEGVAYLHKLGLAHRDLKL
DNCVITNEGILKIIDFGSAVIFKYPYEQFGNNNSIQPCHGIVGSDPYLAPEVLKSPNSYNPQPVDLWSI
AIIYCCMTLKRFPWKIPSQEKDNSFRLYCMYDDNFHDYLLSNECHKLLQLQQRKLKNTIVRSNKRKKQLE
EEKGDKPEEDEEMKDADSAPQQHHSHDVESGKTGGSTVGKDKSNEAVTVLTDEQAEIEMQLNEIDRK
LQEFEDKKNQLKEKYEALRDADPRYQKQLAQIHEEEKQRLKDAEHGADEKKKSHHKQIHGPYRLMRL
PHAARPVISRLLEVDPKKRATMBEILEDEWIKIQCCTVKPVSKSTDATLDFIEDEDEVLVKGVPPEH
TIVKEG

YOR374W_homolog 1500bp public: 1..1500 (SEQ ID NO 503)

ATGTTTAAAAAGGCCCTTACCATTAGTCAGCAAGCTCACAACACCAAAAGGTATCACTTATAACCAACCC
CTTGGGTTATTTCATCAATAACGAATATGTTTACCCCAAAGCAACAAAAGACATTTGAAGTTATTTCCTCCA
TCCACTGAAGAAAAAATAACTGATGTTTACGAAGCTTTAGAAGAAGATATTGATACTGCTGTTGAAGCC
GCACAAGCCGCATACCACAATGGTTGGGCTCAAGGGCCACCAGAACAAAGATCAAAAGTTTGTGTTCAAA
TTAGCCGCTTGATTGAAGAAAATGCCGAATTATTAGCTCAAATTGAAACTTGGGACAACCGGTAAATCC
TTACAAAATGCCAGAGGTGATGTTGCTTGCAGAGCTGCTTACTTCAGATCCTGTGGTGGTGGCCGAC
AAAATTTTGGGTTCCCAAATCAATACTGGTAACACTCATTTCAACTACACTCAAAGAGTCCCATTTAGTC
TGTGGTCAAATTATTCTTGGAAATTTCCTATTATTGATGGCTTCTTGGAAATTGGGACCAGTCTTGGCT
ACTGGTTCTACCAGTGTGTTGAAGACTGCTGAATCCACCCCATTTATCTGCTTTATATCTTTCCCAATTG
TTAGTCGAAGCCGGTATGCCAAAAGGTGTTATCAACATTGTTTCTGGTGGTGGTGGTGGTGGTGGTGGT
GCCATTGCTAAACATCCAAAGATTGAAAAAGTTGCTTCTACTGGTCTACTGCCACCGGTAAAATTATC
ATGAAATTGGCTGCTGAATCAAACCTGAAAAAAGTTACTTTGGAATTGGGTGGTAAATCTCCAAACATT
GTTTTCAACGATGCTGATTGGACAAGACTATTCAAACCTTGATTGTTTCTATCTTCTACAATTCTGGT
GAAGTCTGTTGTGCTGGTCTCTCGTCTTTTGATTCAATCCGGTGTTCAGACCAAGTTGTTGAAAAATTC
AAAGAAGCTGCTGAAAGTGTCAAGGTTGGTAACCCATTTCGACGAAGACACTTTTATGGGTGCCCAAGTT
TCTGACGTCCTAATTGTCAAAATTTTGAATACTGTTGAATCTGGTAAATCTCAAGGTGCTACTGTTGTT
ACCGGTGGTGTAGAGCTGATGGTAAAGGTTACTTTGTCAAACCAACTATTTTCGCTGATGTCAAGAAA
GATATGGATATTGTCAGAGAAGAGATCTTTGGTCCAGTTGTCACTTTGATCAAATTTGATAGTGTGAC
GAAGCCGTTGAATTGGCCAATGATTCCGATTATGGTTTGGCTGCTGGTATTCACTCTGCTGACGTTAAC
AAATGTATTGATGTGGCCAACAGAGTTAAAGCCGGTACTGTTTGGGTCAACACTTATAACGATTTCCAC
CCAATGGTTCCATTCCGAGGATTCAAGTCTTCAAGTATCGGTAGAGAAATGGGTGAAGAAGTTTGCAT
GAATACACTCAAGTCAGAGCTGTGAGAATGAAAATCAACCCACCAACTAA

YOR374W_homolog 499aa (SEQ ID NO 504)

MFKKALPLVSKLTPPKGITYNQPLGLFINNEYVHPKQKTFEVIISPSTEEKITDVYEALIEDIDTAVEA
AQAAHYHNGWAQGPPEQRSKVLFLADLIEENAELLAQIETWDNGKSLQNARGDVALTAAYFRSCGGWAD
KILGSQINTGNTHFNQYQVRPLVCGQIIPWNFPLLMASWKLGPVLATGSTTVLKTAESTPLSALYLSQL
LVEAGMPKGVINISVFGATAGAAIAKHPKIEKVAFTGSTATGKIIMKLAESNLKKVTLLELGGKSPNI
VFNDADLDKTIQNLIVSIFYNSEVCCAGSRLLIQSGVYDQVVEKFKEAAESVKVGNPFDEDTFMGAQV
SDVQLSKILKYVESGKSQGATVVTGGARADGKGYFVKPTIFADVKKMDIVREEIFGPVVTLIKFDTV
EAVELANDSDYGLAAGIHSADVNCIDVANRVKAGTVWVNTYNDFHPMVPFGGFSASGIGREMGEVLH
EYTVQRAVRMKNIPPN

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YPL089C_homolog 1836bp public: 1..1836(SEQ ID NO 505)

ATGGGTAGAAGAAAGATTGAAATAGAACCATGTGACAGACGATAGAAATCGTACAGTGACTTTTGTGAAG
CGTAAGGCAGGGTTATTTAAAAAAGCTCATGAATTAGCTGTGCTCTGTCAAGTGGATTTAACGGTTATTT
ATCGTTGGCAATAATAATAAAGTATATGAATATTTCTACTGTTGAGGCAAATGAGATTTTAAATGCCTAT
AATAAAACCATTAAGTCAAGTACAGTACATGAATCGAAGTCTCCAGAATATTATTCGAAATTTAGA
AAGAAACGACATTTAAATGAACCACTTATGAATAAATCAGGGTCTGTAGTTGGCACTAATACACATTG
AACGATGAAGACTATGATCATAATGTTTCATGAAGCGGGCGATGAGGATTCGGAATATGAAAGCGATGAT
AATTCGCCAACCTAAACGGCACAAAAGATCAGAGTCGGTTAAAAAAGAGCAAAACCCCAAAGTGT
AATAGTACCAACCTCCACCACCGCTCCACCACCTCATATATCTTTAAATAATGTTCCAAACATTTACC
AACCCCAAAATTTACAAAAACAGATTGATGAGACAAATAACACTTCGGCACCGCCCGCTACTGGGACA
AAAAATGAACCAACGATGCAACGACCAGTATTGAGGGTACAAATACCGAATGATGCCAAGAGCAATACG
AATAATTCCTATAGTGGTGTAAATAATAGTGTGGCAAGGACACGGCGAGAACAGTGCAGCGCAGTTCGAC
AATAGTGCAACCAACCAAAACACTCAATCGAGCAATACAACATCAGGTACAGGGACTGCTGATACCAAT
TCATCGCAACTAAATTCAAATGGTAATAGTAATTTAGTGCCCGGAATGTTCCAAATACCAGATTTTCG
GGATATTCATCGTTTCGATCACCAGACTCAGAAAACCAACATTACCGTTACCTTTGCAAAACCAATCA
CAAACGTCATCTCCAGCTAGTGTGTAGCACCAGGTTTACCATTGACAGGAGGAAGCAATGCATATTTT
GCAGGAATGCAACATCACCCTGGGTGGTTCGTATGTCAATTATCCAGCCCAAGTATATCAGCAGTAT
CAACAGTTCCAAATCAACTACAACACAAAGAACCAACAGCAACAGCAACAGCAACAGCAACAAACAA
CAATCTCAGCCGAGCCATCATCGCAACTGGTTGGAAATCAAAATGCACAATTGGAAATCAGCAGCAGCA
TTCCGTTTCGGTTTACCGACAGGGACACAATTTAATAATGGTGAACAAACACCAATTTTCAGGATTGCCA
TCAGGATACGTTAATGATATGTTCCCTTCCCATCTCCATCAAACTTTCTTGCACCTCAAGATTGGCCA
TCAGGTATAACACCAACTACTCATCTACCACAGTATTTTGTGAATATGCCATTGAGTGGAAATGGACTG
CAACAACGCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA
CAACA
CAACAGCAACTGCAAGTACCTGTTATCCCAATACAACAACAACAACAACAACAACAACAACAACAACA
AATCACAATCAGCTAATCTAATACCAGGGTTTTTACAAAACCCAAACACAAGCCACTGGAAATTCGGCA
AATGCTTCCAAGCTGAGTGATGCTGGTGATGGTACTAATCCAACCACAGCAGGAAGTTCAAGTTCAGCA
GATGTCAATAACCAACAATGGACCTAATAAAAATACATAA

YPL089C_homolog 611aa(SEQ ID NO 506)

MGRRKIEIEPLTDDRNRVTFTVVKRAGLFKKAHELAVLCQVDLTVIIVGNNNKVYEYSTVEANEIFNAY
NKTIKVRKQVHESKSPEYYSKFRKKRHLNEPLMNKSGSVVGTNTHLNDEDYDHNVEAGDEDSEYESDD
NSPQPKRHKRSESVKKEQNPKVFNSTQPPPPPPPHISLNNVPTFTNPQNYKKQIDETNNTSAPPATGT
KNEPTLMQRPVLRVQIPNDAKSNTNNSHSGVNSDGDARTVTAVDNSATNQNTQSSNTTSGTGADTN
SSQLTNSNGNSALVPGNVNTRFSGYSSFRSPDSRKTLPLPLQTKSQTSSPASAVAPGLPLTGGSNAYF
AGMQQSPVGGSYVNYPAQVYQQYQQFQNLQLEQQQQQQQQQQQQQKQSQPQPSSQSVGNQNAQLESAAR
FRSGLPTGTQFNNGEQTPISGLPSRYVNDMFFPSPSNFLAPQDWPSGITPTTHLPQYFVNMPLSGIGS
QQSQQQNAQQQSQVPVPIPIQTQTSQMASTT
NHKSANLIPGFLQNPTQATGNSANASKSSDAGDGTNPPTAGSSSSADVNNNTNNGPNKNT

YAL003W_homolog 693bp public: 1..693(SEQ ID NO 507)

ATGAGTGACAAAGAAGATTTAAATCTTATATCTGACAATAATAGAGTTATTTCAATGAGACAATTGATT
TTACAATTACTGACTACAGGAATAAACAACAAAATATAAACGATATACTAACATGTTTGATAGTACTACT
GCCACTCAAGCTGATGTCACTGTCTACAAAGCTTTCCAAAAGGAATTCCCAACAATTCACCAGATGGTTC
AACCACATTGCTTCATTCACTGAAGAATTGCAAGACTTGCCAGCCGGTAAAGCCCCAGCCGCTTCTGGT
TCTGCTGCTGCCGCTGCTGAAGAAGAAGATGACGAAGATGTCGACTTGTTCGGTTCTGATGATGAAGTT
GATGAAGAAGCTGAAAAATTGAAGCAACAAGATTAGCTGAATACGCTGCTAAGAAGGCTGCTAAAGGT
CCAAAACAGCTGCCAAATCTATTGTCACTTGGATGTCAAACCATGGGATGATGAAACTGATTGGAT
GAATTATTGACCAACGTCAAAGCTATCGAAATGGAAGGTTTGACTTGGGGTGCTACCAATGGATTCCA
GTTGGTTTTCGGTATTAAAAAATTACAAATTAACCTGGTTGTTGAAGATGCTTTAGTCTCATTGGATGAC
TTACAAGCTGCTGTTGAAGAAGATGAAGACCACGTCCAATCTACTGATATTGCTGCTATGCAAAAATTG
TAA

YAL003W_homolog 230aa(SEQ ID NO 508)

MSDKEDLNLISDNNRVISMRLILQLSTTGINKKYKRYTNMFDSTTATQADVTVYKAFQKEFPQFTRWF
NHIASTFEEDFLPAGKAPAAASGSAAAAAEEEDDEDVDFGSDDEVDEEAELKQQLAEYAACKKAAGK
PKPAAKSIVTLDPKPDDETDLDELNTNKAIEMEGLTWGAHQWIPVGFGIKKLQINLVVEDALVSLDD
LQAAVEEDEDHVQSTDIAMQKL

YAL060W_homolog 1185bp public: 1..1185(SEQ ID NO 509)

ATGAAGGCAATTGTATACCACGATAGAGGAGATATTAGATACGACCCCAATTTCCCTGATCCACAAATC
ATTTCGACTGGATGATGTCAAATCAAAGTTCATTATTGTGGGATTTGCGGTACTGATTTAAAGAATAT
AGTGATGGGCCGATTTTTTTCCACCAGAAAGGTGAATTGAATGAAATTTCTCAAATGGAATCAATTCAA

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GTCATGGGTCATGAAATTAGTGGTGAAGTAATTGCTATTGGGGATGATGTAACCAATGTTAAAGTGGGT
GATAAAGTTGTTGTGAAAGTGACAGGAACCTGTTTAGATAGACATCGTTACCAAGATCCTAAAAATGGC
GATCTGCCATAAACCAAAATTGTCCAAGTTGTGTTTCGGGTAACATATAATGCGTGTGATTAATCTTGCTTTA
ATTGGTTGTGGATTGTGTAATGGTGGATGTGCAGAATATTTAGTTGTTGCTAGTCTGAAAGTTATTGCA
TTCGATCAGAATAAAATCCCTATGGATATTGCCGCAATTAATTCACCAATAGCTGTTAGTTGGCATGCT
GTTAAAGTATCAAAATTTTAAACCCGGTCTTAATGCATTAATTTTAGGTGGTGGCCCCATTGGATTAAACA
ACAATTTTGTCTTTGAAAGGTAATCAAGTCTCCCAAATTTGTTTAAAGTGAACCAAGACGT
CAATTTGCGAGAGAAATTAGGAGTTATTACTTATGACCCTACGGGTAAATCAATCGAACAATGTGTTGAA
GACTTAAAAAAATTATCCCCGGGAGGTTATGGTTATGAATATTCATATGATTGTTCTGGAGTTAAGGCA
ACTTTTGAAACTGGATTGAAAACCTTTGAAAATTCGTGGATGTGCAACAAATGTGCCATTGCGGCTCAT
AAATCAATTCATTATATCCTATGGAAATTACCTTTTCAAAAAAATGTTAACTGGATCAATTTGTTTTT
GTTAAAAAAGATTTTGAAGAATCAATTAAAGCAATTGAAAATGGTTTAAATATCGATTGATGAATTGAAA
ATGTTGATTACTCTGAAAATTCATTTACAAGATGGAATTGAAAAAGGGTTTTTGGAAATTAATTAATCAC
AAGGAAAAACATATTAATAATATGTTTTCTCCGAAAAGTGAATATTTACTATGCAATGGAGTAAATGAT
TCCAATAAATAA

YAL060W_homolog 394aa (SEQ ID NO 510)

MKAIVYHDRGDIRYDPNFPDPQIIRSDDVKIKVHYCGICGTDLKEYSDGPIFFPPKGELNEISQMESIQ
VMGHEISGEVIAIGDDVTNVKVGDKVVVEVTGTCLDRHRYQDPKNGDSPKPNPCSCVSGNYNACDYLAL
IGCGFANGGCAEYLVVASSKVIAFDQNKIPMDIAALIQPIAVSWHAVKVSNFKPGSNALILGGPIGLT
TIFALKGNQVSQIVLSEPALARRQLAEKLGVTYDPTGKSIEQCVEDLKKLSPGGYGYEYSYDCSGVKA
TFETGLKTLKIRGCATNVAIWAHKSIPLYPMEITLSEKMLTGSICFVKKDFEESIKAIENGLISIDELK
MLITSKIHLQDIEKGFLELINHKEKHILFSPKSEYLLCNGVNSNK

YBL058W_homolog 1116bp public: 1..1116 (SEQ ID NO 511)

ATGTCTGAAATACTCCAGATTCCCAATTGATTGCTGAATTTGTATCTATAACAAATCTTCTACATAC
CTTGCTGAACAGTATTTACTGAGAAACAGCAATGATTTAGTGAAGCAGTTGAGGATTTCTATGCCAAC
AATGAACCATCTCAAAAATCAGAAACCAAAAAATCTTCTTCTTAATGCTAAAGGCTCTGGTGTAAAA
ACATTTAGAGACTTGAACGATGAAGATGATGAAGAGGATGACAAGACCAATACCAATTTCTTTACT
GGAGGAGAGAAATCAGGATTGCAAGTTGAAGATCCCAATAAAGATAAGGATAATGACAGATCAATAATT
GATCAAAATTTTCAAAAAGCCAGAGAACAATGCAACAACCAGATGATAGACCAAGTGCTTCTCAAGAT
GATCAACCATCACCAATTAAATTTTCAGGCAAAGGGTTCAAATTTGGGTGACGGGAATGAACCAAGTCAA
GTAGTGGAGGATCCTAATGCCAGTGCTAAAAAATTCAGACCTAGTAAAGTGACTAGAGAAATTACATTT
TGGAACAAGGTTTACAGTAGGTGATGGACCTTTGCATAGATACGATGATCCAAGAAACGCCAGTGTT
TTGCAAGAATTGAACCAAGGAAGAGTTCCAATGCTCAATTTAGATGTTGAATTTGGCCAAGATGTTGAT
GTTTCTGTATACAAGAAAACCGACGAAGATTGGACACCTCCGAAAAGAAAAATTTGGTGGTTATCACGGT
GCAGGTCATAGACTAGGCTCACAGTACCTGGGGAAGTACTTGTAAATAATGAAGCATCATCTCAACCT
GATATCAAAACCGAACTGAAATTTCTAAACCAAAAGACGAAGGCGAAGGTGACTCCACAGTTCAAATA
AGATTTGCCAATGGTAAAGAATCATCACAAATTCATTTCTCGGATTCATTCTCAAGGTTTATGAA
TTTGTAAAAATCATGAATATAATTTGAACCTACTAGACCATTCACTTTAAGTCATGCATTCCAGTC
AAACCAATAGAAGAAAGTAGTGACATTACAATTTCTGATGCTAAATTGAAAAATGCAGTGATTGTTCAA
AGATGGAAATAG

YBL058W_homolog 371aa (SEQ ID NO 512)

MSENTPDSQLIAEFVSITNSSTYLAEQYLSRNSNDLVEAVEDFYANNEPSQKSETKKSSSSNAKSGSVK
TFRDLNDEDDDEDDKTNTNFTTGGESGLQVEDPNKDKDNDRSIIDQIFQKAREQMPPDDRPSASQD
DQPSPIKFSKGPKLGDGNEPSQVVEDPNASAKFRPSKVTREITFWKQGFVGDGPLHRYDDPRNASV
LQELNQGRVPMISILDVEFGQDQDVSVYKKTDEDWTPPKRKIGGYHGAGHRLGSPVPGVVLNNEASSQP
DIKTETEISKPKDEGEDSTVQIRFANGKRTSHKFNSSDSILKVYEFVKNHEYNSEPTRPFTLSHAFPV
KPIEESDITISDAKLKNAVIVQRWK

YBR039W_homolog 804bp public: 1..804 (SEQ ID NO 513)

ATGCGTCTTAAATCCATTAAAAACATTGAAAAATCACCAATACCATGAAGATTGTTGCCTCTACTAGA
TTGAGTAAAGCTCAAAAAGCCATGGCTTCATCTCGTGTGTTTCAATGAAACTGATAAAGAATCTTGCT
AATGCTGAACCAAAACCAATTGAAGAAGAAGCTTCTAAATCTGATGACAAAACTTTATTGATTGTTGTT
TCTTCCGATAAAGGTTTATGTGGTTCTATTCATCTCAAGTTTCCAAAGCTGCCAGAAAGAGAACTGAA
GAATTAATGGTAATGTGATATTGTTTGTATTTGGTGATAAAGTCAAGCACAATTTTGAGAACTTAT
GCTGACAAAGTTAAATTTGGCATTCAATGGTGTGTTGTAAGAAGAACCAATTTCACTGAAGTTGCCCTTA
ATTGCTGATGAAATTTGCTAAATTAGGTAACATGAAATGTTGAAATTTCTTTACAACAAATTTGTTTCT
GGTGTGTTTCAATTTGAACCATCTAAATTTTCCATTTAGCTGCTGATGCCATTGCTAACTCTCCAGGTTTA
AGCAAAATATGAATTGGAATGAAGAAATCACTTCTGATGTTGCTCAATTTCTTTAGCTAACAACTTG
TTGACTGCTATGGCTGAAGGTTATGCATCTGAAGTTTCTGCTAGAAGAAATGCTATGGACAATGCCCTCC

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AAGAATGCTGGTGATATGATCAACAGTTACTCTATTTTGTATAACAGAACTAGACAAGCCGTCATTACC
AACGAATTGGTTGATATCATTACTGGTGCCTTCCTCATTGGACTAG

YBR039W_homolog 267aa(SEQ ID NO 514)

MRLKSIKNIEKITNTMKIVASTRLSKAQKAMASSRVFNEDKEFLSNAEPKPIEEEASKSDDKTLILIVV
SSDKGLCGSIHSQVSKAARKRTEELNGNVDIVCIGDKVKAQILRTYADKVKLAFNGVGKEEPNFTEVAL
IADEIAKLGNVENVEILYNKFVSGVSFEPKFSIYAADAIANSPLSKYELENEEITSDVAQFSLANNL
LTAMAEGYASEVSARRNAMDNASKNAGDMINSYSILYNRTRQAVITNELVDIITGASSLD

YBR062C_homolog 450bp public: 1..450(SEQ ID NO 515)

ATGTTATCTGCATCTAACGAAGAAGCCATAGCATCAGCATTGCGACAATTGAGTGAATCAGAAGGATCA
ACACTTGTCTCAATCACTCATGGATCTGCTTGGTGAACAAAAGACATCGAAGGGGGTCACTGACGAATAC
TTGGATACTTTGAACGTATTCCAGTAAAACAAATTACTGATAAAGACGCATCTTGTCCAATTTGTACA
AATCGATTCAAAGATGATAAGCATCCATTGATTGTGAGATTGCCCTTGTGGTCACTGGAGTCAATCATATT
TTTGATTGGGAATGTGTTGGGCCGTGGTTGCAAATGAATCCACTTGTCCAATGTGTGCAACCAATATC
TTAGAGGTAGAAGCTAATAGAAGGAAAATAATAGATGAAGAAATAAAAAAGGCCCAAGAAGAAGATTCC
GAGGAAGAAGAAGAAGGTTGGGATATATATGGATAA

YBR062C_homolog 149aa(SEQ ID NO 516)

MLSASNEEAIASALRQLSESEGSTLAQSLMDSLGEQKTSKGVTDYLDTLERIPVKQITDKDASCPIC
NRFKDDKHPLIVRLPCGHGVNHIFDLECVGPWLQMNSTCPMCRNILEVEANRRKIIDEIikkaQEE
EEEEEGWDIYG

YBR101C_homolog 855bp public: 1..855(SEQ ID NO 517)

ATGGAAAAATTATTACATTGGACAATTGCACAACAATCAGGGGATAAAGCAGCTCTTGAAAAGATTGGA
GAACCCGATCAAAAGGCACTTAATCAATTATTTGGTGGTCCCGATGAAGCCACTTTAATGAAGGAAAGT
ATAAAAGTTGTTGAATCAACCGATGTTTCATTAGAAGATAAAGAGATCGCCTTGAAAAATTCGAAATG
TTGATTGAAAATTTAGATAAATGCAAATAATATTGGTAATTTGAAATTATGGAATCCATTGATTGACATT
TTAGCCAAAGAAGATACCCCTGTTGAATTGAAAGTACTTATTTGTGGAATAATTGGAACCGCTGTACAA
AACAACCCCAAATCTCAAGAAGATTTCAATGAACTGAAGGATTGAGTGAATTGATAGAATTAGCACAA
GATGACAAAAAATTTGAATTACAATGAAGGCATTGTTTGCTATTTCTTCATTATCAGAAAATTTCAA
CCTGGATATGCAAAGTTTGAGAAATTCGAAGGTTTGAAGTCAATTAATTTTGATAACAAGAACAACAAG
TATCAATTGAGAATTTTATCATTAAATATCATCCATTTTGAGTAATGGGTTAGACGATAGCTTGAAAGCA
CAATTCAAAGAAGCAAAATTAACCTCACTATTTAGCCTCGGTATTGAATGAGGATTCAAACACTAGTTTG
GTGGACAAATCTTTAAACATTGTTTCTCAATTGAATCAATTAAGTATGAGTTTAGCTTAGAAGAAAA
TATGAAATAAATAGAGGAATCCAAGTGGTTGAAGGGTTGAGTGAGAACTTAATATTGATGATCTCAAT
AATGCCAAACAGGCCACATCCTCTTAG

YBR101C_homolog 284aa(SEQ ID NO 518)

MEKLLHWTIAQQSGDKAALEKIGEPDQKALNQLFGPDDEATLMKESIKVVESTDVSLLEDKEIALENFEM
LIENLDNANNIGNLKLWNPLIDILAKEDTPVELKVLICGIIGTAVQNNPKSQEDFNETEGLSELIELAQ
DDKKFELQSKALFAISSFIRNFQPGYAKFEKLQGLKLINFNKNKYQLRILSLISSILSNGLDDSLKA
QFKEAKLPHYLASVLNEDSNTSLVDKSLNIVSQNLQNLNIEFSLEEKYEINRGIQVVEGLSEKLNIDDLN
NAKQATSS

YBR139W_homolog 1653bp public: 1..1653(SEQ ID NO 519)

ATGCAATTATCTACATTAGTCACTTGGTTGGCTGCTTTAACTGTCGGTGACAGGCAGTATCATTCGGC
AACAATTTAAAGATCAGATTATATTGGATTCTGAGGAAAGCTCCCCAGATTTATATTGGAGTCAGTG
TTCAAAGACTTGGGTTCAATGCGAGTTGATTTGATTACTGCTTGGGCAGAAATGCAATCTGAATTATCA
CCTGAACAAATTGCCAAATTAATCAATCAATATGAGTCTAAAAATGAAAAACCAAAGAAAAATAAGTTT
AATCCAATGTCGACATTTCTTCACCAAGTTCCAAGTTTGAAAAGCTTTCCAATGATAAATTTGCTGGT
TATTCAATGCGGTGATAAAGAGAGTTTCCCAGAAATTTGGGTCTTGATACAGTGAAACAATACACTGGG
TATTTAGATATTGACTCATTAGATAAACATCTTTTCTATTGGTTTTTTGAAAGTAGAAATGATCCAAG
AATGATCCTATTATTTTATGGCTCAATGGTGGTCCAGGTTGCAGCTCTTCAACGGGATTATTTTTTGAA
TTAGGACCATCCTCGATCAACAAAACCTTTACACCCAGTTTACAACCCATATTCCTTGGAATTCGAATGCG
TCGGTTATTTCTTAGATCAACCCGTTGGAGTTGGATATTCGTATACAGGAGGAGATGAAGTTAAGAA
ACTCTCACTGCTGCTAAAGACGTTTATGTGTTTTTTGGAAATGTTTTTCCAAAAATTTCCACAATTTTTG
ACTAATAAGTTTCAATTTGCGCGTGAATCTTACGCCGTCATTATATACCAGCATTGTGCTTCAGAAATC
ATTAACAATGCCGATAGGTCAATTTGAGTTGGCATCTGTGTTGATTGGTAACGGTATCACCGATCCATTG
ATTCAAGATGGTTCCCTATAAACCAATGGGCTGTGGTGAAGGTGGTTACAAACCTGTTTTGACAACCTGAA
CAGTGTGATCAAATGGAAGGGATTATCCTAGATGTGCTAAATGACTAAATTTATGTTACAGTTTCCAA
TCTGCCCTTGACTTGTGTTCCAGCTCAATACTACTGTGATTCCCGTTTATTTCAACCTTATGCTCAACA
GGATTAAATCCTTATGATATCAGAAAGGATTGTGCCGAGCAAGGTGGTAATTGTTACGTAGAAATGGAT

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TACTTGGATGAATACTTGAATCTCGATTATGTGAAAGAAGCTGTTGGTGCTTCTAATATTGACATTTTT
ACTTCATGTGATGACACCGTGTTTAGAACTTTATTTTAGATGGTGATGAAATGAAACCTTTCCAACAA
TATGTTGCTGAGTTATTGGACAATAATGTACCTGTATTGATTTATGCTGGTGACAAAGATTATATTGT
AATTGGTTGGGTAACTTGGCATGGGTAAACGAAATTGGAATATTCAAGATAGTGAACATTTTGCACCAAAA
CCATTACAATTATGGAAACAAGATGGCAAGAAAGCTGCTGGAGAAGTCAAGAATCACAAACATTTTACA
TTCTTGAGAATTTATGACGCTGGTCACATGGTTCCCTTTTGATCAACCAGAAAATGCTCTTAGTATGGTT
AATACTTGGGTACAGGGAGATTATCTTTTGGTTTAGAGGGTAATAAATTATCTGAAGCTGATTAA

YBR139W_homolog 550aa (SEQ ID NO 520)

MQLSTLVTWLAALTUGAQAUSFGNNLKDQIILDSESSPDLYLESVFKDLGSLPVDLITAWAEMQSELS
PEQIAKLINQYESKNEKPKKNKFNPMSTFSSPSSKFEKLSNDKFAGYSMRVKESFPEILGLDTPVKQYTG
YLDIDSLDKHLFYWFFESRNDPKNDPIILWLNGGPGCSSSTGLFFELGPSSINKTLHPVYNPYSWNSNA
SVIFLDQPVGVGYSYTGDEVKNTLTAAKDVVFLLEFFQKFPQFLTNKFHIIAGESYAGHYIPAFASEI
INNADRSFELASVLIGNGITDPLIQDGSYKPMGCGEGGYKPVLTTEQCDQMERDYPKCAKLTCLCYSFQ
SALTCVPAQYYCDSRLFQPYAQTGLNPDYDKDCAEQGNCYVEMDYLDEYLNLDYVKEAVGASNIDIF
TSCDDTVFRNFILDGDEMPPFQYVAELLDNNVPLIYAGDKDYICNWLGNLAWVNELEYSDSEHFAPK
PLQLWKQDGGKKAAGEVKNHKHTFLRIYDAGHMVPFDQPENALSMVNTWVQGDYSFGLGNKLSEAD

YCL052C_homolog 1446bp public: 1..1446 (SEQ ID NO 521)

ATGAGACAAAGAACAACCATTTATAATCCTTATTCTAGTCATGATGGAATCATAACTAATCTTAATCGA
ACAAATTTCCAATTATCAAGCATACCTAATCATTTATTACAAATTGAGAATAAATATACCATCACCACC
ACCACCACACAACCTAACAAATCATCTATATCTGGCAATTAAAGAATTAAGAATTCAAACGAAATTC
AATAATAATGAATCAGGTATACCAATTTTTCATTATTGAAATTAAGCAAGGACTTAATATTTATGCTGTA
CCACAATCTAATGTGCACAAATAGAAATTTGGCAACAAGTTGAACAATTGATAATGGAATTATTAGGG
ATTAAATTATCTTCACAACAATGGATTGCTAATGTTAATTCTTTTATTATCATGATATTCAACCTCAA
CCATTATTGAATTTGAAAGAAGGATGGAAATTCATTTACATCCTAAATCCAATTATGATTATATATAT
AATCAAGATAAAATTATTATTCGGAATTTGTTAACAATGTGTGAGAAATAGAATTTAATCTTGAACCTG
GGTATTTATAAAGAAATTTGGTTTGTTTTAAATTGATGAAAAAATCTCAACTAATGATGATTGAATTA
ATGGTATTAGAGTGATATTAGATGAAGATAGTAATACTAATAACAAGAAGAATCGATACATAAGACA
ATGTTTCATATAAAACCAAGACATAGGAGTTTGTATGATTCTACCACCATCACCACCACCAAGATCATT
CCACAAGGATTACATCCTATTTTGAAGTACTGAACCTAACACAACAACCTATTGTTATTCCAACCTGATTTT
GATGTTGAAGAATGTAAATTTTATTATTTTGAATTTAAATAAATCATTAATATTTGATCAATTTCAA
AACATTCCAATAGGATCGCAATTAATTATTAATAATGGGAATAAAATTTAGAATTACCAGAAATATAAA
ATTAATCAATGGGGTAATGAACCTTTTATTGAATTTGAATTTGATAATGATAATGATATCCCTCATCAT
ATAAATTTAAGATTCATTCAGATATCAATTACCTCAAAATAATCATTTCCCATTTCCAAATTAGTAAT
GTTTTAAATTCGTTACCAATATTTTATAGGTTGTAATGTCAAAGAAGGAAATTTATTAGATAAATCA
CCTTTTGATACTAAAAGAGATGTTAAATTTGGTGGTAATTATGAAATTTATTTTACTGAAGATACAGTT
TTTTATCATTTACAGAAATCCGACAATTCGGCAATTCGGGTAGTTCAACATTATTAGAAATTAATATT
CCTCATGGGAAACTACATTTGATAGAGTCAATAATATAACTTCACTTGGTTTATTAATTGGTGTATTG
ATGATTTTATATGCCATTTCAATAAGAGTTTTCATGAGTACCACCTCAAAGACGAAAAGGGATTAA

YCL052C_homolog 481aa (SEQ ID NO 522)

MRQRTTIYNPYSSHDGIITNLNRTNFQLSSIPNHLFTIENKYTITTTTQPNKSSLYSAIKELRIQTKF
NNNESGIPIFSFIYEPGLNIYAVPQSNVDKLEFWQVEQLIMELLGIKLSSQQWIANVNSFYHYHDIQPO
PLNLKKEGWKFNHLPKSNYDIYNQDKIIIRELLTNVSEIEFNLESGIYKEIGLEFLIDEKISTNDDLNL
SGIRVILDEDSNTNNKEESIHKTMFHIKPRHRSFDDSTITTTKIIPOGLHPILSTELNNTTIVIPDF
DVEECKFYYYLNLNLSLIFDQFQNIPIGSQLIINNGNKNLELPEYKINQWGNELLFEFEFDNDNDIPHH
INLTVHSRYQLPQNNHSHSQISNVLNSLPNIFIGCNVKEGNLLDKSPFDTKRDVKIGGNYEIFYTETDV
FYHLQNSDNGSGSSSTLLEINIPHGKTTFDRVNNITSLGLLIGVLMILYAIISIRVFMSTTSKTKRD

YCR009C_homolog 882bp public: 1..882 (SEQ ID NO 523)

ATGTGGAAAAAGAAAAAGAGGGAATTTTTTTTTTGTCAATCATTTTTTTTTTTCTTTTATCTCGCACAT
TTCTTTCTTCAACTAGACATGCTCTGGGGAGGATTAAAGAAAGCAATCAATCGAGCTGGCGCATCTGTT
ATTGTCAAGGATGTTGACAAGACTATGGATAAGGACTTTGATGTGGAGGAGAGAAGGTACAAGACCTTA
AAGACTGCAGGACGAATTTACAGAAAGCTGCCAAGGGGTATTTGGACAACATCAGAGCAATCACGAAT
TCCCAAGTCACAATTGCCGAGATTATTTATAACTTGTACGAGGAGTCGAAGCAGGGACAATCGCTCTAC
TCGAATGTTGGGACTTATTACATGCAGAGTGTCAAGGAGTTTGATGAGGAGACTGTGAAACAGATTGAT
GGCCCGTATAGGGAGACTGTTTTGGATCCAATTTGGAAGGTTTCCAACTACTTTAGTGAGATTGACGAA
GCAATCAAAAAGAGAGCACACAAGAAGATTGACTATGAGCAGTGCAAAGCCAAAGTTAGACGGTTAGTC
GATAAACCTGCCAAAGATGCCGCCAAGTTGCCACGCCCGAGAAGGAATTGTCGATGGCCAAAGAGATT
TACGACGAGTTGAATGACCAGCTCAAGGCCGAGTTGCCCGAGTTGATTGCATTGAGGGTGCCTTTCTAC
GATCCGTCGTTTGGGCGTTGGTCAAGATCCAGTTGAGGTTCTGTACTGAGGGGTACTCGAGATTGGCA

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CAGATCCAACAGTACTTGGACCCAGCGTCCAGAGACGAGTATGCCAATGGGTTGTTGGACGGCAAGATT
GATGATATGTTGGCACAAATGCAAGGTTTGAGTATAACTTCTTTAGGAAAGTAG

YCR009C_homolog 293aa (SEQ ID NO 524)

MWKKKKREFFFFCHSFFFFFYLAHFFLQLDMSWGGFKKAINRAGASVIVKDVDKTMDKDFDVEERRYKTL
KTAGTNLQKAAKGYLDNIRAITNSQVTIAEIIYNLYEESKQGQSLYSNVGTYMQSVKEFDEETVKQID
GPYRETVLDPGKFSNYFSEIDEAIKKRAHKKIDYEQCKAKVRRLVDKPAKDAAKLPRAEKELSMKEI
YDELNDQLKAELPQLIALRVFPYDPSFEALVKIQLRFCTEGYSRLAQIQYLDPASRDEYANGLLDGKI
DDMLAQMQGLSITSLGK

YCR010C_homolog 858bp public: 1..858 (SEQ ID NO 525)

ATGTCAGCTGATTTAGAAATCAACAACCACACATCATCTTATTATTGAAACAAGGGTGATAAC
AGTAGCAACCACCACCACACACACAAACAAATCAACATCACCTTATGATCCTCATCATCCAATTACTAAA
ATTGAAACTGATGGAGATTATGTTACTTTTGGTAATGAAAGATATTTACGTTCTGATTTAGTTGAAGCA
TTTGGTGGTACTTTAAATCCAGGGTTAGCTCCACCACCTAAAAATGATTTTGCTAATCCTGCTCCATTG
GGATTATCGGCATTTGCTTTAACAACATTTGTTTTAAGTTTAATTAATTGTGAAGCTAGAGGGGTTACT
ATTCCTAATATTGTTGTTGGATTGGCATTTCCTATGGTGGTGGTGGTCAATTAGTTGCTGGTATGTTT
GAATTGGCCGTTGGTAATACTTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
GCTGCTATTCAAGTTGATTTCATTTGGTATTAAAGCTGCTTATGCTAATAATACTGAAGAATTACATTAT
GCTGTGGGGATATTTTTAATTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
ACTGTGGCATTCTTTTTAATATTTTCTTTTTAAGTATTACATTTTATTATTGGCAATTTCTGATTTT
ACTGGTAAAGTGGCAATTAAGGCGGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
AATGCTTATGCTGGTATTGCTAATCCTCAAAATAGTTATATTACTGTTAAAGCTATTCCATTACCAGAT
TTACAAGATCCAACAAGAAAAATAAATAA

YCR010C_homolog 285aa (SEQ ID NO 526)

MSADLENQQPQDHHLLIENKGDNSSNHHHHNNNSTSPYDPHPITKIETDGDYVTFGNERYLRSDLVEA
FGGTLNPLGAPPPKNDNFANPAPLGLSAFALTFVLSLINCEARGVTIPNIVVGLAFFYGGAAQLVAGMF
ELAVGNTFGGVALSSYGGFWGAWAAIQVDSFGIKAAYANNTEELHYAVGIFLIGWFIPTFFLMLLTVKS
TVAFFLLIFFLSITFLLLAISDFTGKVAIKKAGGVFGLITAFVAWYNAYAGIANPQNSYITVKAIPLPD
LQDPTRKNK

YCR021C_homolog 1029bp public: 1..1029 (SEQ ID NO 527)

ATGTCGCGTGTGTTTCAACTTTATCCGATATCATCAAACGTAATGATGCTGTTAACGTGAACCCACCA
AACCAATTAATTGATTTACATATCACTGAACATGGTAGTGATTGGCTTTGGGCTGTTTTTTCAGTTTTT
GCATTAATTTGCAATTTGTCATGGATTTCATTTACATTTTACTGACGTTAGAAAATCTGGTTTGAAGAGA
GCTTTATTGACTATCCCATTAATTAAGTGTGCTGTTTTGCTTTGCTTACTATACCTTATGCTTCTAAC
TTGGGCTATACTTGGATTTGACAGAATCAACCATGCTGGTACTGGTTTTAGACAAATCTTTTATGCA
AAATTTGTTGCTTGGTCTTGGGTTGGCCATTAGTGTGGCTATTTCCAAATTAATCACCATACCAGC
TTTACTACTACTGAAGATGAGTCTGATTTGCTTAAGAAATTCATTTCTTTGTTTGAAGCTTTGTTTACT
AGAGTTTGGCAATGAAGTTTTCGCTTTGGGTTTATTTGATTGGTGGTGGTGGTGGTGGTGGTGGTGGT
TGGGTTTATTTCACTTTTGGCTGTGTGTTCCAAATTTGTTGCTATTTATTTAGTCATTAATGATGTGGT
GTTTCAATTTGGTTCATCTTCTCATTCAGTCTTTGGCAATGCTCTTATCCTTGGCTTTTGTATTGTTTGG
ATTTTGTACCCAGTTGCTTGGGTTTGGTGAAGGTGGTAATGTTATTCAACCAGATTGAGAAGCAGTG
TTCTATGGTATTTGGATTGATCACTTTTGGTGTATTCCAATTAATCTTGACTTGGATTGCCATTAAT
AACGTTGATGAAGAATCTTCAACAAAATATGGCATTTCATTTGAAACCAGAAAATGAACATGCTCCA
ACTGCTACTGAAGATGTTGAAAAGCAGTTGGTGAACCCCAAGACATTTCTGGTGATCTGCTGTGTGCT
CCATCAGGTGTTCCAGACACTGGTGTGCTCAAGCACAGCCGAAGCTGAAGAAGCTATTTAA

YCR021C_homolog 342aa (SEQ ID NO 528)

MSAAVSTLSDIKRNDAVNPNPNPIIDLHITEHGSDDLWAVFSVFALFAIVHGFYISFTDVRKSGLKR
ALLTIPLFNSAVFAFYTYASNLYTWILTEFNHAGTGFRQIFYAKFVAVFLGWPLVLAIFQIITNTS
PTTEDESDLLKFIISLFEALFTRVLAIEVFVLGGLLIGALIESYKMGYFTFAVVFQLFAIYLVINDV
VSFGSSSHSVFGNALILAFVIVWILYPVAVWGLEGGNVIQPDSEAVFYGILDITFGVPIPIILTWIAIN
NVDEEFFTKIWHFHLKPENEHAPTATEDVEKAVGETPRHSGDTAVAPSGVPDGTGAQAQAQAEAEERI

YDR178W_homolog 510bp public: 1..510 (SEQ ID NO 529)

ATGATTTCAACTTATTCACGTATTGGTTTAAACCACTTAACTAAATCATCATCATCATCATTAACCT
ACTACTGTTAGACCATTATTATGGCCAATTTTACTAGAGGAATTAACCTATTCTCAACCACCAGGT
TATATTGTTGGTACAGTTAATGATGCTTATGTACCACCACCACCACATAAATTAGAAGGTTTATTACAT
TGGACTAGTGAAAGGATTGTTGCTATTGGTATGTTACCATTAGTTTTAGCACCATTTATTACTGGTGGT
GGTGGTTCGACTTTAATTGATTCCACCATGTGACGATTATTATTATTTTATTGTCATACTGGTTTCCAA
AGTTGTATTATAGATGATATTCCTAAAAGAGTTTATGGATCTTATCATAATTATGCCATGTATTTATTG

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ACTTTTGGTACTGGTATTGCTGGTTATGGTATTTATCAAATTGAACTAAAGAAGGTGGTGTTCCTCAAT
ATTATTTCAAACCTTTGGAAAGCTTAA

YDR178W_homolog 169aa (SEQ ID NO 530)

MISTYSRIGLTTTLTKSSSSSSSLTTTVRPLLLANFTRGIKTIPQPPGYIVGTVNDAYVPPPPHKLEGLSLH
WTSERIVAIGMLPLVLAPFITGGASTLIDSTMSALLLFHCHTGFQSCIIDDIPKRVYGSYHNYAMYLL
TFGTGIAGYGIYQIETKEGGVSNII SKLWKA

YDR202C_homolog 387bp CDS: 1..>387 public: 1..387 (SEQ ID NO 531)

ATGACAGCAAATATCTTGAATAATAAACATTCATAGATACTGTATTATCAATACAATCAACTCAAAAT
GATAAAGAATTACATTTGGTATATTATAAATATAATTTTACCCGATTTACCTCAAATCATAGAGACTTTA
CAGATTTGTTCAAATTTGTTGATGTACAATTCACCACAAGAACCCTGATTCCAAACAATGTATTGAAAAA
GGTCCATCTATCAAGCTACCTTTTGTCTTTAACCATCAACAAGATTCTGTCAATGGGATAATAACCCGA
GATGGACCATATATCACAGATCTTAATTTGACGGTTAAGAATCATTTATTTCAACAAGCATTTCCATAAG
TTGCGCTTAATAAAGCCAATGGTTTTAGAACAACTTGTTAAT

YDR202C_homolog 129aa (SEQ ID NO 532)

MTANILNNKTFIDTVLSIQSTQNDKELHWYIINIILPDLPQIIETLQICSNLLMYNSPQEPDSKQCIEK
GPSIKLPLSLTNQQDSVNGIITRDGPYITDLNLTVKNHVFNKHFHKLRLIKPMVLEQLVN

YDR256C_homolog 1458bp public: 1..1458 (SEQ ID NO 533)

ATGGCTCCAACATTTACGAATTC TAACGGTCAACCAATTCAGAACCATTGTCCTCAAAGAGTTGGT
CAACACGGTCCATTTGTTGTTACAAGATTTCAACTTGATTGATTCATTTGGCCCATTTTCGATAGAGAAAGA
ATCCCAGAAAGAGTTGTCCACGCTAAAGGTTCCGGTGCCTTATGGTGTTTTTGAAGTCACTGACGATATC
ACTGATATTTGTGCTGCCAAATTCCTGGACACTGTTGGTAAGAAAAC TAGAATCTTCACCAGATTCTCT
ACTGTTGGTGGTGAATTAGGTTCTGCTGATACTGCTAGAGATCCAAGAGGTTTGTCTACCAAATTTTAC
ACTGAAGAAGGTAACCTGGATTTGGTTTACAACAACACTCCAGTGTTTTCAATTAGAGACCCATCTAAA
TTCCACATTTTCATCCACACCCAAAAGAGAAAACCCAGAAACTCACTTGAAGGATGCTAACATGTTTTGG
GATTACTTGACTAGCAATGAAGAATCCATTCATCAAGTTATGGTTTTATTCTCCGACAGAGGTACTCCA
GCTTCTTACAGAGAAATGAATGGTTACTCTGGTCACACTTATAAATGGTCCAACAAAAAAGGTGAATGG
TTTTACGTTCAAGTTCAATTCATCAGTGACCAAGGTATTAAGACTTTGACCAACGAAGAAGCTGGTGTCT
TTAGCTGGATCTAACCCAGATTACGCCCAAGAAGATTTGTTCAAGAACATTGCTGCTGGTAACTACCCA
TCATGGACTGCTTACATTCAAACCATGACTGAAGCCGAAGCTAAAGAAGCTGAATTTCTGTGTTTGAT
TTGACCAAGTTTGGCCACACAAGAAATACCCATTTGAGAAGATTTGGTAAGTTCACTTTGAATGAAAAC
CCAAAGAACTACTTTGCTGAAGTTGAACAAGCTGCTTTCTCTCCAGCCACACTGTTCTTACATGGAA
CCATCTGCTGATCCAGTCTTGCAATCAAGATTGTTCTCCTATGCTGATACTCACAGACACAGATTGGGT
ACCAACTATACTCAAATCCCAGTGAAGTGTCTGTCAACCGGTGCTGTTTTCAACCCACATATGAGAGAT
GGTGTATGACTGTTAATGGTAACTTGGGTAGCCATCCAACTACTTGGCCAGTGATAAGCCAGTTGAA
TTCAAACAATTTTCTCTTCAAGAAGACCAAGAAGTTTGAATGGTGTGCTGCCACTCCATCCACTGGAAA
GCCACCCAGCTGATTTTCAAACAAGCTCAAGAATTTGGGAAAGTGTGTAAGAGATATCCAAACCAACAA
GAACATTTGGCCCAACATTGCTGTACATGCTGCTGGTGTGCTGATGCTGCTATCCAAGACAGAGTGT
GCATACTTTGGTAAAGTCTCTCAAGACTTGGCTGATGCTATCAAAAAGGAAGTTTGGAAATTATCTCCA
AGAAAATAA

YDR256C_homolog 485aa (SEQ ID NO 534)

MAPTFTNSNGQPIPEPFATQVRVGHGPLLQDFNLIDSLAHFDRERIPERVVHAKGSGAYGVFEVTD
TDICAAKFLDTVGKKTRIFTRFSTVGGELGSADTARDPRGFATKFYTEEGNLDLVYNNTPVFFIRDP
FPHFIHTQKRNPETHLKDANMFWDYLT SNEESI HQVMVLFSDRGT PASYREMNGYSGH TYKWSNKKGEW
FYVQVHFISDQGIKTLTNEEAGALAGSNPDYAQEDLFKNIAAGNYP SWTAYIQMTTEAEAEAEFSVFD
LTKVWPHKKYPLRRFGKFTLNENPKNYFAEVEQAAPSPAHTVPYMEPSADPVLQSR LFSYADTHRRLG
TNYTQIPVNC PVTGAVFNP HMRD GAMTVNGNLGSHPNY LASDKPVEFKQFSLQEDQEVWNGAATPFHWK
ATPADFKQAQELWKVLKRYPNQ QEHLAHNIAVHAAGADAAIQDRVFAYFGKVSQDLADA IKKEVLELSP
RK

YER103W_homolog 1971bp public: 1..1971 (SEQ ID NO 535)

ATGTCTAAAGCTGTTGGTATTGATTTAGGTACAACCTATTCTTGTGTTGCTCATTTTGCCAAATGATAGA
GTTGAAATTATTGCTAATGATCAAGGTAATAGAACTACCCCTTCATTTGTTGCTTCACTGATACTGAA
AGATTGATTGGTGTGCTGCCAAGAAATCAAGCTGCTATGAACCCAGCAAACACTGTTTTCGATGCTAAA
CGTTTAATTGGGAGAAAATTTGATGATCCAGAAGTTATAAATGATGCTAAACATTTCCCATTTAAAGTC
ATTGATAAAGCAGGTAAACCAGTGATTCAAGTTGAATATAAAGGTGAACTAAAACATTTTACCAGAA
GAAATTTCTTCAATGGTTTAAACAAAATGAAAGAAATTGCTGAAGGTTATTTGGGTCTACTGTATAA
GATGCCGTTGTTACCGTTCCAGCTTATTTCAATGATTCTCAAAGACAAGCCACCAAAGATGCTGGTACT

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ATTGCTGGT'TTGAATG'TTTTAAGAATTATTAATGAACCTACTGCTGCTGCCATTGCTTATGGT'TTAGAT
AAAAAAGG'TTCCAGAGGTGAACATAATG'TTTTAATTTTCGATT'TGGGTGGTGGTACT'TTTGATG'TTCA
TTATTAGCCATTGATGAAGGTATTTTCGAAGTTAAAGCCACTGCTGGTGATACTCATTTGGGTGGTGAA
GATTTTGATAACAGATTAGTCAACTTCTTTATTCAAGAAATTCAGAGAAAGAACAGAAAGATATTTCC
ACCAACCAAGAGCT'TTAAGAAGATTAAGAACTGCTTGTGAAAGAGCCAAGAGAACTTTGTCTTCTTCT
GCTCAAACCTCAATTGAAATTGATTCC'TTATATGAAGGTATTGACTTCTACACTTCAATCACCAGAGCC
AGATTTGAAGAATTGTGTGCTGACTTGTTCAGATCCACTTTAGATCCAGTTGGTAAAGT'TTTAGCTGAT
GCCAAGATTGATAAATCTCAAGTTGAAGAAATTGTCTTGGTTGGTGGGTCCACCAGAAT'TCCAAAGATT
CAAAAATTGGT'TTCTGATT'TCTTTAATGGTAAAGAATTGAATAAATCTATCAACCTTGATGAAGCTGTT
GCTTATGGTGGTGGTCTTCAAGCTGCCATTTTAAGCTGGTGATACTTCTTCCAAGACTCAAGATATTTTG
TTATTGGATGTTGCTCCATTGTCTATTAGGTATTGATAAATGGTTAGTGAAGCTGAAAAATTCAAAGAAGAAGATGAA
AGAAATTCTACTATTCCAAC TAAGAAATCAGAACTTTCTCCACTTATGCCGATAACCAACCAGGTGTT
TTGATTCAAGTGT'TTGAAGGTGAAAGAGCTAAACTAAAGATAACAAC'TTGT'TGGGTAAATTTGAATTA
TCTGGTATTCCACCAGCTCCAAGAGGCGTCCCTCAAA'TTGAAGTTACTTTCGATATTGATGCTAATGGT
ATCTTGAATGTTTCTGCTTTAGAAAAAGGTACTGGTAAACTCAAAAGATTACTATCACCACGATAAA
GGTAGATTATCCAAAGAAGAAATTGATAAATGGTTAGTGAAGCTGAAAAATTCAAAGAAGAAGATGAA
AAGGAAGCTGCTAGAGTCCAAGCCAAGAATCAATTGGAATCTTATGCTTATTCAATTGAAAAACACAATC
AATGATGGTGAATGAAAGATAAGATTGGTGCAGATGATAAAGAAAAATTAAC TAAAGCCATTGATGAA
ACTATTTCTTGGTTAGATGCATCTCAAGCTGCTTCTACTGAAGAATACGAAGATAAACGTAAAGAATTA
GAATCAGTTGCTAATCCAATCATTAGTGGTGTCTTATGGTGTGCGCGTGGCGCTCCAGGTGGTGCAGGC
GGATTCCCAGGTGCTGGTGGCTTCCCAGGTGGTGGCCAGGTGCCCGTGGTCCAGGTGGTGTCTACTGGT
GGTGAATCAAGTGGACCAACTGTTGAAGAAGTTGATTAA

YER103W_homolog 656aa (SEQ ID NO 536)

MSKAVGIDLGTTYSCVAHFANDRVEIIANDQGNRTTPSFVAFDTERLIGDAKNQAAMNPANTVFDK
RLIGRKFDDEPVINDAKHFPFKVIDKAGKPIQVEYKGETKTFSPPEISSMVLTKMKEIAEGYLGSTVK
DAVVTVPAYFNDSQRQATKDAGTIAGLNLVRIINEPTAAAIAYGLDKKSGRGEHNVLI FDLGGGTDFDVS
LLAIDEGIFEVKATAGDTHLGGEDFDNRLVNFPIQEFKRKNKKDISTNQRALRRLRTACERAKRTLSSS
AQTSIEIDSLYEGIDFYTSITRARFEELCADLFRSTLDPVGKVLADAKIDKSQVEEIVLVGGSTRIPKI
QKLVSDFFNKGELNKSINPDEAVAYGAAVQAAILTGDTSSKTQDILLLDVAPLSLGIETAGGIMTKLIP
RNSTIPTKKSETFSTYADNPQGVLIQVFEGERAKTNDNNLLGKFELSGIPPAPRGVPQIEVTFDIDANG
ILNVSALEKGTGKTQKITITNDKGRLSKEEIDKMVSEAEKFKEEDEKEAARVQAKNQLESYAYSLKNTI
NDGEMKDKIGADDKEKLTKAIDETISWLDASQAASTEYEDKRKELESVANPIISGAYGAAGGAPGGAG
GFPAGGFPFGAPGAGGPGGATGGESSGPTVEVD

YGR086C_homolog 954bp public: 1..954 (SEQ ID NO 537)

ATGCATAGAACTTATTCTTTAAGATCCACTAGAGCTCCAAGCTGCATCTCAATTACAAGCTCCACCTCCA
CCACCATCATCTACCAATCCAAATTTTGGTAAAGGTTTCGATTAGTCATACTTTCCGTAAACAAGCT
GCTGGTGTCTTAGGTCCAGAATTGTGCGAGAAAATTGGCCATTTTAATTAATAATGAAAAAAATTTAATG
AGATCAATTGAAATCACTTCTCGTGAAAGAAAAGATGTTGCTAAACAATTATCTTTATGGGGTGAAGCT
AATGAAGATGATATTAGTGATATCACTGATAAATTGGGGGTTTAAATCTATGAAGTTGGTGAATTGGAA
GATCAATTTATTGATAGATATGATCAATATAGAATCACTTTGAAATCTATTAGAGATATTGAAGGTTCA
GTTCAACCAAGTAGAGAAAGAAAACAAAAAATTACTGATCAAATTGCTTATTTGAAATATAAAGATCCT
CAATCACCAAAAATTAATGTTTTAGAACAAAGAAATGGTTAGAGCTGAAGCTGAATCTTTAGTTGCTGAA
GCTCAATTGAGTAATATTACTAGAGAAAATGAAAACCTGCTTTAATTATCAATTTGATTCTATTAGA
GAACACGCTGAAAAAATTGCTTTAATTGCTGGTTATGGTAAAGCTTTATTAGAATTATTAGATGAAAGT
CCAGTCACTCCAGGTGAACTAGACCAGCTTATGACGGTTATGAAGCTTCTAAACAAATATTATTGAT
GCTGAAAACGCTTTAGCTTCTTGGACTTTTGATTCTGCCGTTGTTTCGTCCAACCTTTATCATTAGCTGCT
CATGATGAAGAAGCAGAAGAAGATTTAGAAGGTGCTTATGAAGATGATGAATTGGCTAATGAAGCTGAA
AATTTAAGAATTGCTGAAAAAGATTTTGATGAAGTTGAAGCTAAAATTGCTGCTTAA

YGR086C_homolog 317aa (SEQ ID NO 538)

MHRTYSLRSTRAPTASQLQAPPPPSSTKSKFFGKGSISHTFRKQAAGALGPESLRKLAILIKMEKNLM
RSIEITSRERKDVAKQLSLWGEANEDDISDITDKLGVLIYEVGELEDQFIDRYDQYRITLKSIRDIEGS
VQPSRERKQKITDQIAYLKYKDPQSPKINVLEQELVRAEAESLVAEAQLSNITREKLKTAFFNYQFDSIR
EHAEKIALIAGYGKALLELLDESPVTPGETRPAYDGYEASKQIIIDAENALASWTFDSAVVRPTLSLAA
HDEEAEDLEGGAYEDELANEENLRIAEKDFDEVEAKIAA

YGR197C_homolog 1536bp public: 1..1536 (SEQ ID NO 539)

ATGTCTCATGATGATTCAATCTGAATTCAAACCCAGCTCAAATCCAACCTCCAATCCTGTGTCAAAG
CCGTCTGATATGGGCAGATCAAGCAACGACAGTGGCTCCGAACCATCAATACAACATTTTACGTTAGCC
CCACTCGAACCACAAGCGGATGAAGAGGATATGGAATGGGTGAGCCAATATCACGACAATCAACCTTT
CTTGAGAGAGTACAATCTCGATATTCATTTTCCACGAGAATTTCGAGCTCAAAGAAAGGAATTGTCC

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ATGAAATATCTTAAAATTTATCTAGTCATGGCCATTGGTTGCTTAGGAGTGTTCCTATATATTGGGGT
TCAATGTATCAAAGAGAAACCCGAATTA AAAA ACTTGAAAATGTTGGTAGTTTTAGAAGATGAAGAAATT
AATGGCATCCCTCCACTTTTTGGCAATCAGCTTCGTGATTTATTGGCCACCCCAACGGCTAGAACACTC
GGCGATTGGAATAATATAACACTAGCGAATTTGAAAATATTGCATCAAAAACAACAACAATAAAT
GAAGAGGTCATTCGTCAAATTCATCATCAAAATTTATTGGGCCTCGATATATGTCAAGCAAAATTCATCT
TATAACATATACAATGCATTAGCCAATGGTAATCAGTACAATGTCAGTGAATCTGTGTATTGTTACTAT
GAAACAGGAAGACACCTAACTAGTGTGGCCCATATGTGGTGGCATCTATAGATGCCATTCAAACATATG
TGGTTGGATCAAACCTGGTGATGAGGGACATTGTGAGAATTGGTAATATAACTCTTGACAATGCAAAAC
TCGGTTGCTGTGCCACTACCGCCTTGGCATTCAAATAATTGATATGAGACCATCTACTAGTGGAGTT
TTAGTTGCAGCTTTACAAATTTGGTCTTCTTTATCTTGTGATTGTTAGTTTTTTCAGTTTCAATTTTTT
GTGATATACACCGATCAGTGGCATTAATGGTGAAGCAAGAAACTTTTTACTTTATCGAGTTTTCGCA
TCAATCATATCGTATTTTGTATCAGTTTAATGTTTGGTTTGGTTACTTTAGCGTTTCAAGTTGATTTT
GCTGTTACATTTGGTAAATCTGGCTTCTTAGTTTACTGGATGGTAACATTTTAAACAATGTGGAGTGT
GGATTGGCTAACGAATTGGCCGCTATGCTCATACTTACTATCTATCCACCAATGGTTGGGTTTGGTTG
ATCTTCTGGGTAATTATAAATATCACACCCACATTCACACCAATTGCTTTGTTACCTGAATTTTATCGG
TATGGTTACGCCATGCCATTGCATAATGCTTTTGAAATTTATTCTGTTATTTTTTCAACACGTATAAG
GGATTATAGGAAGAAGCATTTGGAATCATAATTGCATGGGTGGTATTTTAAACATTAATGGCACCATA
GTGGTGGTTTACTTTGGTAGCACTATGAGTAAAAAAGCTGCTGCTCCGCTGCTGCTGCAAAAAAGGAA
AAGGAAAAGTCAAAGTAA

YGR197C_homolog 511aa (SEQ ID NO 540)

MSHDDSNNSNSNPSSNPTSNPVSKPSDMGRSSNDSGSEPSIQHFTLAPLEPQGDEEDMEMGEPISRQSTF
LERVQSRYSFFHENLRAQRKELSMKYLKIYLVMAIGCLGVFSIYWGSYQRETRIKNLKMLVLEDEEI
NGIPPLFGNQLRDLLATPTARTLGDWKIYNTSEFETIASKHNNTINEEVIRQIHQNYWASIYVKQNSS
YNIYNALANGNQYNVSDSVYCYETGRHLTSVGPYVVASIDAIQTMWLDQNSVMRDIVRIGNITLDNAN
SVAVATTALAFQIIDMRPSTSGVLVAALQIGLLYLIVSFFSFFNFVDIHRVALMVQRNELLVYRFA
SIISYFVVISLMFGLVTLAFQVDFAVTFGKSGFLVYWMVFTLTMWSVGLANELAAMLILTIYPPMVGFWL
IFWVIINITPTFTPIALLPEFYRYGYAMPLHNAFEIYSVIFFNTRYKGLIGRSIGIIIAWVVFLLMAPI
VVVYFGSTMSKKAAPAAAAKKEKEKSK

YGR250C_homolog 1890bp public: 1.1890 (SEQ ID NO 541)

ATGTCTGCTGCTGAAACTAATCAACTTCAAGAACTCTATGGAAAAAGTTGAACATTGGTTCAACTACTGAA
GAACAATCAGCTGCTGCTGCTACTACCACCTGCTGATCAATCAGCTGAAGAACAAGGAGAATCATCTGGT
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GAAATCTTTTCTCCAATCGGTCAAGTTTCTCTATCAGAGTTTGTGCTGATGCTGCTCTTAAAAATCT
TTAGGTTATGCTTACGTCAACTACCACAAGTACGAAGATGGTGAAAAGGCTATTGAAGAATTGAACCTAC
AACCCGATCGAAGGTCGTCCATGTCGTATCATGTGGTCTCAAAGAGACCCATCTGCTAGAAGATCTGGT
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TCTCCATTCGGTAAGATTACTTCCATTTACTTGGAAAAAGACCAAGATGGGAAATCTAAAGGTTTGGT
TTTGTTAATTTTGAAGATCATGAATCTGCTGTTAAGGCTGTTGAAGAATTGAACGATAAAGAAATCAAC
GGTCAAAAGATCTACGTTGGTAGAGCACAAAAGAAAAGAGAAAGATTGGAAGAATTGAAGAAACAATAC
GAAGCTGTTAGATTAGAAAAATTTGGCCAAATACCAAGGTGTCAACTTGTTTGTTAAGAATTTGGATGAC
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GATGTTAGACGCTCTCAATTAGAACAACAAATTCAGCCAGAAACCAATGAGAATGCAAAATGCTGCT
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CCAGAACAATGGCCAAGACCAGGTCCAAATGGCCAACCAAGTTCCTGTCTACGGTATTCCACCTCAATTT
CAACAAGACTTTAACGGTCAAAACATGAGACCTCAGCAACAACAACAACAACAACCAAGAGGTGGATAC
TATCCAAACCGTAACCAAAACCAGCAAGAGAGACTTGGCTGCTATCATTTCTAGTGTTCACAAGATCAA
CAAAAGAGAATTTTGGGTGAAGAATTGTATCCAAAGATTGTTGCTACCGGTAAGGCTCAAGAACAGAA
GCTGCTGGTAAAAATCACTGGTATGATGTTAGGTTTAGAAAACCAAGAAATTTTGGATTTGTTAGATGAT
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YGR250C_homolog_629aa(SEQ ID NO 542)
MSAAETNQLQESMEKLNIGSTTTEEQSAAAATTTADQSAEEQGESSGVAENSASLYVGELNPSVNEATLF
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DGNIFIKNLHPAIDNKAHDTFSAFGKILSCKVATDEFGQSKCFGFVHYETAEEAAEAAIENVNGMLLND
REVFVGKHHISKDRESKFEEMKANFTNIYVKNIDLNYSEESFEKLFSPFGKITSIYLEKDQDGKSKGFG
FVN FEDHESAVKAVEELNDKEINGQKIYVGRAQKKRERLELKKQYEA VRLEKLAKYQGVNLFVKNLDD
TIDSEKLEEEFKPFGTITSAKVMVDEAGSKSGFGFVCFVTTPPEATKATEMTFRMINGKPLYVALAQRK
DVRRSQLEQQIQARNQMRMQPAAAGGLPGQFI PPMFYGQQQGFPPNGRGNAPYPGENPQMMMRGRGQPF
PEQWPRPGPNGQPVVPYGI PPQFGQDFNGQNMNR PQQQQQQPPRGGYYPNRRNQT SKRD LAAI I SSV PQDQ
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AGNAEEQA

YKL117W_homolog 221aa (SEQ ID NO 544)
 MSSTTTQTPTVLWAQRSSDDAAKNIIYLTIQISDPIDLKIDLKSDHLIIDS KSNDSVYSSIDYHLQID
 FFKEIDPDQSKINTENGSHIFMILRKQDQEEYWPRLTKEKLKYHYIKTDFDKWVDEDEQDEVKDDPND
 FGGPGGPGGAMDFSQMLSGMGLGCTGSGSGPGVDLSALASQLGQAGGAGGAAGLDGEEGEEGDEEAK
 KAAEEGSSNATAATEKE

YKR075C_homolog 3042bp public: 1..3042(SEQ ID NO 545)

ATGTCGTTATCAGGAGAAGTGTTTTCAGGAGGAGCAACCACCTTCTCAACATATCGAGGCACAAGATGAT
GACCAATTTTGGAAAATACAACCTTTAAATTGAAAAGAAGACTAGATCCATGGGTTTATTAGATGAATTTTATC
CCTGATAAACTAAAAGAACAAGATGGTAAATAATTCAGAAGCAAAATTCATAACAACAGCTGCATCAACA
ACCAGCTCAAGAAACTTGGCAGCTATGGCAGCTATAGCATCAAAAACAATTCGTATATGTTTAAACGAA
ACTCCAAGCAGTCAACATCATGAAACTATAGAATCCATATCTAATAACTCCGATGGCGATGTAACCCA
TCATCAGATGTAGCGCCATCATCTACATCACCTGTCAATTCACCTTCACCAACTTCCTCACCAGCATT
GATTTAAAAATCTCCAGAATTGTTGCCTCATGTATACAGATTTAGCTGTTGAACCTTCACGTCATGTT
GATTATTTATCCCAACCAATGGGATGTTTCTGATATTTGGAAGCTTGGCGATACGTTATTTCCAAAAGA
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CTCAAGACTATAAGTCCAGAAGTGGTGAATTTGGTCGAAAGATAGTGATGTTACTTGGCTTTTATGGACCA
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AGTTCGTGTTGCCGGGGATATATCTATTGGCAAAAAATGTTCCAGTAAGAATGGACCTAAACCAATATTG
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CATCCCGATGAATATTTTGATCCCGAAGCCCTTCTGAACAAAATTTAAACAGTCAATATAAGAATACAGCT
CCTACTCATAACACTAGTGTGGCCAAAATTACAAAGCTTGTGTAAGAACTCCCAATTTCTTCATCTTCTGCT
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CAAAGTCACCTATATGAAGGAGACGATGAATCCATTGAGGAAGCGGATGAAGAGGTAGAGGATGATGAA
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CCAAATAATTTTGGGCCAGCATTCAGTGCATCAACTTCTACTCCAGTGGCACCATCTTTAAGTCGTAC
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CTTCTCATAATGTCAATAATGATATTAGTAGAGGTTATGATTATTATTATGATTACAACACTGTATAC
ACATGTAATCCAAACAATTCAGTGTATGCATCTTATCAAAGTCCAGATGTTGTTGATGTTCCAGAAAAT
CTTGATATGGGATCCAAATTTGATTATGAATTTATTGAAAAATACGATAGTATCCCTGTAGTAGATACA
ACATTTTGAGAAATAATGATACCATTAATAATATGCCAATTCCTGTATAGTCTGCCGTCATCACCTTTATCA
TTGCTATTTTCCGGTGGAGGTAAAAATTTCTGGGTCACTGTTAAATTTCCCAAAATTTCCCAATAGTTAAT
GTCAACTCTAACCACGAACAACAACAACAAATCACAAGCAAAACCAAGACAAAGACAAAGGCATCTCCT

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TTCCAATTGAGTGATTTCAGAAGATGATTCAAAATAGTGATTTCGGATGATGATGGTATTTTCAGGATTATCA
ATAGGTACAAGAAGATCTAGTCAAGCTTTAGCTGAACGGTATTTCAATCATCATTGACAAGTTCTACA
CAAGAAACAGCACCACAACATTTCCCGATGCTAAAGAGATTGAACCGGTTGCTGAACATGTTTCGAGT
ATTAACCCACGATATTCTTCGACTTCGATTTCTAAGCAACCTACAAGTTCAAGTTCACTTTACAACTG
TTTTTCGGAGGTGCTGGTGGGTTAAGTAGTACTGATAAAGAGTTGTCGAAACTGTTTTTAGGAGGATCA
ACGTCAGCATCAACATCAACATCGCATGATGAGAAGACTACTACTATTGATTCTTCAAGTACTGGGTTT
TTCCAAGTACCAAATAGAGATTATACTCCTTCTCCAGATAATAATACTTTGACTCGTACATTATCTAAT
ACATCCAAGAAATCTTCACCATTACCACCACAAACAACCTTCAGAGAATGCATTTCAGAGGTGATGGACAA
CAATCACAATCACAATCACAATCACAATCACAGTTGCCACTGCAACAACAACCTGCAACCACGACGGGA
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CCAAGTCCACAATTTGGTAATGCTAGTGCACATCTTCAAGATCAAGATCAAGGTGATGAAAATGAACAT
GAACATGAACATGAAGAAAATCATAAGAATCTTGTGGTCAAGCTAGAGGTTTAGCTAAACACTTCTTT
GGATAA

YKR075C_homolog 1013aa (SEQ ID NO 546)

MSLSGEVFSGGATTSQHIEAQDDDHFFENTTFKLKRTSMGLLDEFIPDKLKEQDGNNSSEANSSTTAAST
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DLKSPPELLPHDDTDLAVEPSRHVDYLSHQWDVSDIWKSWRYVISKRKDVANAARLENASWRTWAQRRSN
LKTISPEVVNWSKSDSVTWLYGPILKDDDHVNENHSDAIETTATSSVAGDISIAKKCSSKNGPKPIL
KKRTMEQSMISHSNLLKLQLATQIHQKKREQKLKQBELKRQHQLNHPDEYFDPEALSNKLNLSQYKNTA
PTHNTSVAIKQLSLKTPNSSSSASLKDLMKDEAVVPSSEQISHDQNOEDGNVSGDVESKGERHIFND
EVMQCIADIVYSDDQRYNSDEEDYDSDDDDDDYDQYEPSNDSLALQSHLYEGDDSEIEBEADDEDE
DGSEDEEDDEGGFFLNKSNAPILGQHSSASTSTPVAPSLSRHTDITDDTASISTNSKSYKTIQL
LPSTSINYGSDESSDEANPYTSSLSHNVNNDISRGYDYDYDYNTVYTCNPNNSVYASYQSPDVVDVPE
LDMGSNFDYEFIEENNDIPVVDITFENNSTINMPSISYSSPSSPLSVAISGGGKNSGVTVNSPFPFIVN
VNSNPQQQQSQAKPKPKTKASPFQLSDSEDDSNDSDDDGISGLSIGTRRSSQALAESVFQSSLTSSST
QETAPQHFPDAKEIEPVAEHVSSINPRYSSTISIKQPTSSSSLSQSFSGAGGLSSTDKELSKSFLGGS
TSASTSTSHDEKTTTIDSSSTGFFQVPNRDYTPSPDNNTLRTLSNTSKKSSPLPPQTTSENAFRGDGQ
QSQSQSQSQSQLPSQQSQPRRGLLFDEEDSEDEDEGMVIGGKREEKKLHGQGYNALSQVAGRNGIHS
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YLR216C_homolog 1221bp public: 1..1221 (SEQ ID NO 547)

ATGTGTAAAGTGGTGAGTGTTTCGAGAACATTCCACCAGTATTTTTTCCAAATTTATATAAAAATGAG
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ATTTTCATGCAACGGCAAACCCAAGGGCCGTGTTGTTTTCAAACCTCTACGATGATGTTGTTCCATAAACA
GCAGCTAATTTCCGTTCCTTATGTACTGGTGACAAAGGTATATCACCAAAATCTGGTAAACCACTTTCC
TATAAAGACTCAATTTTCCACAGAGTGATCAAAGACTTTATGTGCCAAGGTGGTGACTTTACCGCTCCT
TCCGACCATTTTGGGAAGTGGTGGTGAGTCCATTTACGGAGAAAAGTTTGAAGATGAAAACTTTAAGTTG
AACCATAAACAAACCATTTTGTGTGTCATGGCTAACTCTGGACCAAAACCAATGGCTCTCAATTTTTT
ATCACAACAGTTCCAACACCACACTTGGACGGTAAACACGTTGTGTTTGGAGAAGTCAATTGAAGGGAAA
TCAATTGTACGTCAATTAGAGAGAAGCGAAAAGGGTGCCAATGACAGACCAGTAGAAGATTGGAAAATT
GCTGATTGTGGTGAGCTTCCAGCCAACATATGAGCCGGTTGCACTGGGTGCCGATGATGGAACGGTGAT
ACGTACGAAGAGATTTAACCGACAACGACACTATCGACATCAACAACCCGCAATCTGTTTTTCGCGGCT
GTCAGCAAAATCAAGGATATTGGTACCAAACTTTTGAAGAAGGGAAATTAGAAAAATCATACGAAAAG
TATACCAAGGCCAATAGCTACTTGAATGATTACTTTCCCGAAGGTTGTCTCCAGAAGACTTATCAACA
TTGCATGGCCTCAAATTATCGTGTTACTTGAACGCTGCGTTAGTGGCATTGAAATTGAAACACGGCAAA
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TTATACAGAAAAGGTATGGGCTATATCCTAGTCAAAGACGAAGAACAGGCTCAAAGATTCTTGAAGAA
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YLR216C_homolog 406aa (SEQ ID NO 548)

MCKVVSVFENIPPVFFPNLYKNEIKFSFSVFFHHQLMTATPVYFDISCNGKPKGRVVFVKLYDDVVPKT
AANFRSLCTGDKGISPKSGKPLSYKDSIFHRVIKDFMCQGGDFTAPSDHLGTGGESIYGEKFEDENFKL
NHNKPFLLSMANSGPNTNGSQFFITTVPTPHLDGKHVVFGEVIEGKSIVRQLERSEKANDRPVEDWKI
ADCGELPANYEPVAGADDGTGDTYEEILTDNDTIDINNPOSVFAAVSKIKDIGTKLLKEGKLEKSYEK
YTKANSYLDYFPEGLSPEDLSTLHGLKLSCYLNAALVALKLKHGKDAIAAANNALEVEQIDDKSKTKA
LYRKMGYILVKDEEQAKILEEALALEPNDAAIQKGLQEAKHNIKLRDKQKKAMAKFFS

YMR009W_homolog 537bp public: 1..537 (SEQ ID NO 549)

ATGGTCAATTTTATTTTCATGATAACAAAGATACACTTGAAAAATTTTACTGAAGATCACAATTCAGGA
GAACCAGTTAGTTTTGATCAACTAGCTGAAATGGTGTTATTTACAAGTACATTACTACCCAGGAAGAA

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TTAGACGCATTGGCTACTGAAAGAGAATACAAGAATAGAGATGTTGTTACTTTAACTTACCAGCCTTC
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GAAATTAGATATATTGCTGAAGGTGAAGGTTATTTTGATGTTAGAGATAAACAAAGATCGTTGGATTAGA
GCTAAATTATCACCTTACGATTTGTTGATTTTACCAGCAGGAATTTATCATCGTTTACATTGACTAAT
GCTGCAAAACACGTCAAGGCAGTTAGATTATTTAAAGATGAACCTAAATGGGAAGCTATCAATAGAGAC
ACAGGAAAAAATACCGAAGCTCGTGAACCTATGCTAAGACTATTGCAGTATAG

YMR009W_homolog 178aa (SEQ ID NO 550)

MVEFYFHDNKDTLENFTEDHNSGEPVSPDQLAEIGVIYKYITTQEELDALATEREYKNRDVVTLNLPAF
NNDIDAYNAKMQQFYKEHYHEDEEIRYIAEGEGYFDVRDKQDRWIRAKLSPYDLLILPAGIYHRFTLTN
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YMR011W_homolog 1641bp public: 1..1641 (SEQ ID NO 551)

ATGTCTCAAGACAACGTCTCATCAACATCTACAGCTGAGGCTGTAAATAATGAAATCAAAGTCAAAGAT
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ATCATTATGTGTTTCCCTTATGCTTTGGTGGTTCGTTTGGTTCGATACTGGTACTATTTCCGGT
TTCATTAATATGTCTGACTTTTAGAAAGATTCCGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCC
AATGTCGAACTGGTTTAAATGATTGGTTTGTTCACCGCTGGTTGTGCCATTGGTGCATTATTCCTTGTCT
AAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATTGCTATATGTTGGTATT
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CTCAAGCTGGTGTGAAAGAGAAAGATTAGCCGGTAAGGCATCTTGGGGTACTTTATTCATGGGTAA
AATCAAGATTCTTTGAAAGGGTTGTGTTGGTGTCTATGTTACAAGCCTTACAACAATTGACTGGTGATAAC
TATTTCTTCTACTACAGTACCCTATTTTCAAGTCCGTTGGTATGAATGATTTCTTCCAACTTCTATC
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CTCTGTTTGTAACTGGTTCCGTTGCCATGCTGTCTGTTTCTTAATCTATTCCTTGGTTGGTACTCAA
CATCTTTATATTGACAAACCAGGTGGTGCTAGTAGAAAACCAGATGGTGATGCCATGATCTTTATGACT
TCACCTTATGTGTTCTTCTTGTCTTACATGGGCTGGTGGTGTTACTCCATTATTTCTGAACCTTAT
CCATTGAAAGTTAGAAGTAAGGCTATGGGTTTACGTAATGCTTCCAATTGGACCTGGGTTTCTTAATT
TCTTTCTTTACTTCAATTATTACTGATGCTATCCACTTCTACTACGGTTTCGTCTTTATGGGATGTTTA
GTTTTCTCCATTTTCTTGTCTACTTTATGGTTTACGAACTAAAGGCTTACCTTGGGAAGAAATTGAT
GAATTGTACTCCACCAAGTCCCTCCATGGAAATCAGCTGGTTGGGTGCCACCTTCCGAAGAAGAAATG
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YMR011W_homolog 546aa (SEQ ID NO 552)

MSQDNVSSTSTAEAVNNEIKVKDEFQEEQAHTSLEDKPVSAIYIGIIMCFLIAFGGFVFGFDGTGTISG
FINMSDFLERFGGTKADGTLYFSNVRTGLMIGLNFAGCAIGALFLSKVGDYGRRVGIMTAMIVYIVGI
IVQIASQHWYQVMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGTLVCCFQLMTLGLIFLGCTTYGT
KSYSDSRQWRIPGLCLFAWALCLVAGMVRMPESPRYLVGKDRIEDAKMSLAKTNKVSPEDPALYRELQL
IQAGVERERLAGKASWGTLENGKPRI FERVVVMSVLQALQLTGDNYFFYYSTTIFKSVGMNDSFQTSI
IIGVINFASTFVGIIAERMGRRLCLLTGVSVMGLIYSLVGTQHLIDKPGGASRKPDGDAMI FMT
SLYVFFFASTWAGGVYSIISELYPLKVRSKAMGLANASNWTWGFLISPFITSFIDAIHFYYGFVFMGCL
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YMR110C_homolog 1986bp public: 1..1986 (SEQ ID NO 553)

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CCACAAAGCACTAACACCCCTGCTGCTGCTGTAGCAAAGTCTAATCCAAATACCAATGCAGAGCCAGCT
AAAATTCCAAACGAAAAACTGTTAAAAACAGAATCACCAGTGAAGTCAAAAACAAAACGGTGCAACAACA
ACAAAGGAAAAATCTGATGTTCTGTTGGAGACAAAATCGACGTCATCAACTACTGTCAGCAACAATAAC
TCGGTCTTACAATATACCGAGTTGTCGGAGATCCCTATTGGTGTGAAAGAATTACTAAGGCCTTCCAT
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AACCAGGAAGCTTTGTGTGACGCTTTGCAAAAGGACTTTACCCGCTTCCCTTCCGAAACAAGAACTAT
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ATTTTAGTCATTGCTGCTTTCAATTATCCGTTTFTGTCTCGATCTCACCAATAGTTGGTGCAATAGCA
AGTGGCAACACAGTTGCACTCAAGCCTTCTGAGTTAACACCCCGTTTTCAGCTTTTACTGACTTG
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TTGGAACAAAAATTTGACAAAATTTGTTTATACTGGTAGCGGTTTGGTAGGTACAATAATTGCGAAAAAG
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AGAGTTTGGTTCAATAGAGAAGGGAATGTGAGAATTGGAGGTCCACCCCTCTTGTGTTTCTGCTTGGAAAC
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YMR110C_homolog 661aa (SEQ ID NO 554)

MSKPSSIKKSKASAIKPSANSKSKTPKIETPKLQQVETRLEGEVPTTKVSIKRNSTITTESVKASEDKST
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SVLQYTELSEIPIGVERITKAFHSGKTHSLQFRLKQLRNLVFTMKDNQEALCDALQKDFHRLPSETRNY
EFATGLNELVFI MSQ LHKWSKPQPVDELPLNLSLNPVYIERIPLGTILVIAAFNYPFFVSIPIVGAIA
SGNTVALKPSLTPRFSKLFTDLLSKALDPEIFFVNGAIPETTCLEQKFDKIVYTGSGLVGTIIAKK
AAETLTPVILELGGKSPAFVLDDISDKDLATVARRIAWGRFVNAGQTCIGVDYVLVAKSKHDKFISALQ
EVIEKEFFQDVKTRNFTHMIHIDRAFEKMESILNTTSGNVIIGGKLDHGRYVGPVTIDNVTWTDSSMK
DEIFGPILPILTYTDLEKSCREIIANHDTPLAQYIFTSGPISRQYNSQINTITTLVRSGGLVINDVLMH
IALHNAPFGGVGTSGNGAYHGEFSYRAFTHERTVLEQLHWNWVWLKSRYPYPYANKKDKLIASSQQKYGG
RVWFNREGNVRIGGPPLLFSAWNNALGVAELVRDFIGAGL

YNL031C_homolog 411bp public: 1..411 (SEQ ID NO 555)

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AGATTAGTCAGAGAAATTGCTCAAGATTTCAAACTGATTTAAGATTCCAATCTTCTGCTATTGGTGCT
TTACAAGAAGCCGTTGAAGCTTACTTGGTTGGTTTATTTCGAAGATACTAAGTTGTGTGCTATCCATGCT
AAGAGAGTTACCATTCAAAAGAAAGATATGCAATTAGCTAGAAGATTGAGAGGTGAAAGATCTTAG

YNL031C_homolog 136aa (SEQ ID NO 556)

MARTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRFQKSTELLIRKLPEFQ
RLVREIAQDFKTDLRFQSSAIGALQEAVEAYLVGLFEDTNLCAIHAKRVTIQKKDMQLARRLRGERS

YNL134C_homolog 1086bp public: 1..1086 (SEQ ID NO 557)

ATGAAAGCAGCTATCATTTCTGGATCTTTCGAACCTTATCAATTAGCGGAAATTAAGATATTCCTCAA
CAAAAAATAAAAGAAAATGAAATATTAATCAAAGCAGTAGCTTTTGCAATAAACCCAACTGATTGGAAG
CACATTGTTTATCAATTGGGCAGCCAGGTGATGTTGTTGGTTGCGATGTTAGTGGGATCATGAAGAA
GTGGGTTCTCAAGTAACTGGGTTTGCAAAAGGTGACACTGTAAGTGCTTTTATAACTGGTAATAGATCA
CCTCGCACTGGAGCTTTTGCAAGATATGTAGCTGTTGATCCTGCTACTTCGATAAAGTACAATAAGAAAT
TTTGAACATTTGACTAATTTACAAGTATCTGAAATCCACTCATTTGAAGGGGCAGCAAGTATTAATTTA
GGTTTGGTTACCGTTGGGCTTTTCAATTTCTCATTACTTACGAATTGACAACAAAAGCAACCTGGGGAT
AGTATTTTGATTGTTGGGGAGGAGCAACTGCAACTGGAGTTCTAGCCATTACAGTTGCCAACTAGTGTAT
AATCTCAAAGTAATCACACAGCATCACCCAAAACACACCCTCTTGAAACAATTAGGGGCAGATTAT
GTTTTCGATTATGGAGACGCTGATGTTGTCAATAAAATTAAGAATATTGGCCAAATTAATTTGCTCTT
GATACGATTGCAACACCAGAAACGTTTCAAAAAGTTTACGACTCAACAGAGGGGTCTCAAGAAGTATTT
ATTGATTCTTAGCAGGTTTAGACTATCGATCAATTGCTGCCAATGATGCCAGAGGAGATCAAGTACAT
TGGGGGCACACCATTTGCTTGTGTTGGCATCTTTAAAAGAGAAAAGTGTGTTAATGAAAATTTATGTTCAA
ACACCTGAATTTAGATGATTTTACTCAGTGGTGGCAAAAGGTGGTCCCTCAAATAATTGATCGTATT
AAACATACAAATTTAAAGTTATTAAATGAAGGATTGACTCCGTAAGTGAAGGTTAGAATTGTCTAGA
AATAATAAACTCTCTGCTGAAAAGGTTGATTTAGAGTTCTGGATCTGTGA

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YNL134C_homolog 361aa (SEQ ID NO 558)

MKAAIISGSFEPYQLAEIKDIPQQIKIKENEILIKAVAFAINPTDWKHIVYQLGSPGDVVGCDSGLIEE
VGSQVTGFAKGDVSAFITGNRSPRTGAFAYVAVDPATSIKYNKNFEHLTNLQVSEIHSFEGAASINL
GLVTVGLSFSHYLRIDNKKQPGDSILIWGGATATGVLAIQVAKLVYNLKVITTASPKNHTLLKQLGADY
VFDYGDADVNNIKINIGQIKFALDTIATPETFQKVYDSTEGSQEVFIDSLAGLDYRSIAANDARGDQVH
WGHTTIACLASLKEKTVFNENYVQTPPELLDDFTQWWQKVVPQIIDRIKHTNLKLLNEGLDSVSEGLELSR
NNKLSAEKVFRVSDS

YNR002C_homolog 798bp public: 1..798 (SEQ ID NO 559)

ATGACGTCTTCATCTTCTCAAAAATCTGTTGGATCTTCAATCATAGATGCAAAACCAAGGACCAATAAAA
AAAGTTGAAATTGCTGGAGAGGGTGGTGAATTTGTTATTATCAATCGTCACAAGTACTACAGACATGAC
TTGATGGCTGCCTTCGGGGGTACTTTAAACCCAGGTGCTTCTCCTTGGCCAAAGATCAATATCAACCCCT
GCTCCCTCGGGTTATGTGGGTTTGCCATGACCACTTTTGTCTTATCCCTTTACAATGCCCAAGCTATG
GGTATCAAAGTTCCAAATGTGGTAGTTTCACTTGCATGTTTCTACGGTGGTGCAGCTCAATTTTTTGTCT
GGATGTTTGTAGTTTGTGACTGGAAATACATTTGGTATGACTGCATTGACATCTTACGGTGCCTTCTGG
TTGAGTTATTACAGCAATCTTGGTTGATAGTTTGGTATCGCTGCAGCCTACGAAGCTTCTGAAGAAACA
GCTTCACAGTTACCAATGCCATTGGATTTTTCTTACTTGTCTTGGGTATCTTTACATTTATGTTGTGG
TTGAACACTTTAAATCTACAGTTACTTTTCACTTCTTGTCTTATGTTTGTAAACATTCTCTTTTG
TTAGCTGGTGGTGAATTTAGTGGAAAGAGTCGGTGTACTAGAGCTGGTGGTGTCTTTGGTGTATCACA
GCCATTGTTGCTTGGTGGAAATGCCCTTAGCCGGTACTGCTACTCCAACCAACTCTTACTTCCAACCTGTT
TCTATTCCATTGCCAGGTAACGTTGTTTCAAGAAATAG

YNR002C_homolog 265aa (SEQ ID NO 560)

MTSSSSQKSVGSSIIDANQGPIKKVEIAGEGGEFVIINRHKVRHDLMAAFGGTLNPGASPWPKININP
APLGLCGFAMTTFVLSLYNAQAMGIKVPNVVSLACFYGGAAQFFAGCFEFVTGNTFGMTALTSYGAFW
LSYSAILVDSFGIAAAAYEASEETASQLPNAIGFLLAWGIFTFMLWLNTLKSTVTFSSLFLLFVTFLL
LAGGEFSGRVGVTRAGGVFGVITAIVAWWNLAGTATPTNSYFQVSIPLPGNVVFKK

YOL139C_homolog 630bp public: 1..630 (SEQ ID NO 561)

ATGTCGAAGAATTAGCTCAAAAACTGAAGAATTGTCATTAGATTCCAAGACTGTTTTTGATTCCAAA
GAAGAATTTAATGCAAAGCATCCATTGAACAGTAGATGGACATTATGGGTACACTAAACCACAAACCAAC
AAGAGTGAAACTGGCATGATTTATTAAGCCAGTTATAACTTTCTCATCTGTTGAAGAATTTTGGGGA
ATTTACAACCTCGATTCACCAGCAAATCAATTACCTTTGAAATCAGATTATCATTGTTCAAAGAAGGA
ATTAGACCGGAATGGGAAGATGAGGCTAACTCAAAGGTGGTAAATGGCAATTCTCCTTCAACAAAAAA
CTGGAAGTCAATCCAATCATAAATGATTTGTGGTTAAGAGTTTGTGTCAGTTATTGGTGAACCAATT
GAGGATGAAGAAAACGAAGTCAATGGGATTGTGTTGAATATCAGAAAGCAAGCTTACAGAGTCGGTATT
TGGACCAAAGATTGTGATGAATCCAAATTAAAGACTGTCCGGTGAGAGATTGAAGAAAGTCTTGCAATTA
AACGATGAACAAAAAGTTGAATTCATGTGCGCATGATGCTTCCAATAC TAGAGGCGCTGAACCTCAAATT
GTTTTGTAA

YOL139C_homolog 209aa (SEQ ID NO 562)

MSEELAQKTEELSLDSKTVFDSKEEFNAKHPLNSRWTLWYTKPQTNKSENWHDLLKPVITFSSVEEFWG
IYNSIPPANQLPLKSDYHLFKEGIRPEWEDEANSKGGKWQFSFNKKSEVNPIINDLWLRGLLAVIGETI
EDEENEVNGIVLNIRKQAYRVGIWTKDCDESKLKTVERLKKVLQLNDEQKVEFM SHDASNTRGAEPQI
VL

YOR120W_homolog 888bp public: 1..888 (SEQ ID NO 563)

ATGCCAGCTCAATTGCAAGTTAACTACTGATTATTTCACTTTAAACAATGGAACAAAAATCCCAGCTGTT
GGATTAGGTACTTGGCAAGCAACCAATGAAGACGAAGCTTACAGAGCCGCTCTTAGCAGCTCTTAAGAAC
GGATACAAGCACATTGATACCGCTGCAATTTATGGAATGAAGAACAAGTCGGTAAAGCCATCAAGGAC
TCTGGAGTTCCAAGAGAAGAATTGTTTGTACTACTAAATTTGGAATGCTGACCATAAAAAATATTGAA
GAAGCCTTAGAGACTTCATTGAAAAAATGGGTCTTAACTATGTTGACTTGTACTTGATCCATTGGCCA
GCTTCAATTGACAAGTCAACTAATAAACCATATACTGATTTTGATTATGTTGATACTTATAGAGGTTTA
CAAAAAGTTTATAAGAACAGCAAGAAAATCAGAGCAATTGGTGTCTTAATTTACCAAAAAAGAAATTG
GAAAGGTTATTGTCTTCGGAAGGTGTCGATGTTGTTCTCTGCTGTCAACCAAAATTGAAGCTCACCCATTG
TTGACTCAGCCTGAATTTGATGATTATTTGAAGAAAAAGGTATCGTTTTGGAAGCTTATTCACCATTTG
GGTTCTACAAACTCTCCATTATTCAAGAACGAAGCACTCGTTAAATCGCTGAAAAGAAATGGTGTGAA
CCAGCTCAAGTTTGGTATCTTGGGCAATTCAAAGAAAGACTGTGGTTTTGCCTAAATCCGTCACCGAA
TCAAGAGTTATTTCTAACTTGAACCAATTCACTTTACCTTCAGAAGATTTCGAAACATTGAACAAATTG
TCTGAAAAGATGGTGTGTGCAAGCTTGTAAACCCAGCTTTCAACAACCTTTGATGATTAA

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YOR120W_homolog 295aa (SEQ ID NO 564)

MPAQLQVNTDYFTLNNGNKIPAVGLGTWQATNEDEAYRAVLAALKNGYKHIDTAAYIGNEEQVGKAIKD
SGVPREELFVTTKLWNADHKNIIEEALETSLKKLGLNYVDLYLIHWPASIDKSTNKPYPDFDYVDITYRGL
QKVYKNSKKIRAIGVSNFTKKKLERLLSSEGVDPVPAVNQIEAHPLLTQPELYDYLKEKGIVLEAYSPL
GSTNSPLFKNETIVKIAEKNGVEPAQVLVSWAIQRKTVVLPKSVTESRVISNLKFTFLPSEDFETLNKL
SEKDGVVRTCNPAFNNFDD

YOR122C_homolog 381bp public: 1..381 (SEQ ID NO 565)

ATGTCTTGGCAAGCCTACACTGATAACTTAATTGCTAACGGTAAAGTCGATAAAGCAGCCTTATATTCA
AGAGCCGGTGACGCATTATGGGCCCAATCGGGATCATTGCAATTACAACAACCAGAAATCACTGAAATT
GCCAAAGGTTTCGATAGTGTGAAGGTTTGCAAACCAGCGGTTTACACGTTCAAGGCCAAAAGTACTTT
TTGTTAAGAGCTGACGACAGATCAATTTATGGTAAACACGAAGCCGAGGGTGTATTGTTGTTAGAACT
AAACAACTATTTTGATCGCCCATTATCCAAGTGGTGTCAACCAGGTGAAGCTACCACTCTTGTGTTGAA
AAATTAGCCGATTACTTGATCAATGTTCGGTTATTAG

YOR122C_homolog 126aa (SEQ ID NO 566)

MSWQAYTDNLIANGKVDKAALYSRAGDALWAQSGSFELQQPEITEIAKGFDSAEGLOTSGLHVQGQKYF
LLRADDRSIYKGHEAEGVICVRKQITILIAHYPGSGVQPGREATTLVEKLADYILINVGY

YOR261C_homolog 993bp public: 1..993 (SEQ ID NO 567)

ATGTCAACAACCTGCAACTAGCACAAATGAATTGGCCCTTTTGGATAAGTCAGTAGTAGTTTCTCCGTTG
GTTTTACTATCTGTGGTGGACCATTATAATAGAGTTGCCAAAGATTCTAAGAAGAGAGTTGTTGGGGTA
ATATTAGGAGATAACTCTACTGACACAATCAAAGTTACAAACTCGTACGCAATTCCTTTTGAAGAAGAC
GAGAAGAACCCTGGAGTATGGTFTTTGGACCACAATTTTATAGATTCAATGGGAGAAATGTTTAAAAAA
ATTAATGCCAAAGAGAAATTGATTGGCTGGTACCATTCAAGGACCTAAATTGAAACCATCAGATTTGAAA
ATTAATGAGGTTTTTCAGAAGATACACCGACAACCCATTGTTGTTAATTGTTGACGTTCAACCAAGAGAA
GTTGGTATTCCAACAGATGCATATTTGCCGTTGATGATATTAACCAACGATGGCTCTGCTGCTGAAAAG
ACATTTATTTCATGTCCCTTCCTTGATTGAAGCAGAAGAAGCTGAAGAAATTGGAGTTGAACATTTGTTA
AGAGACATCAGAGACCAAGCTGCTGGTAACTTGTCCTTAAGAGTTTCTGAAACACATCAATCATTATTG
GGTTTACATCAGAAGCTTGAGAGAAATTGCAAAATATTTGGATAAGGTTTACCAAAAGAAATTACCTATG
AATCATACTATTTTGGGGAATTAACAGAATGTTTTTAATTTGTTGCCAAACTTGATGCAACAACCTGGGG
AGTGATCTCGATGGTGGTTCAGACTCGTCTCATGCATTAGCCACTGCATTTACTGTCAAGACAAATGAC
GAATTGATGATCATATACATTAAGTACATTAGTTTCAGCTATTATTGCATTCCATGATTTGATCGAAAAC
AAGTTAGAAAATAAAAAGTTGAACGAAAATAAAGCACAAGCTTCCGTGGCTGAAGTGTCAATTAATAGC
GAAAAGAAAGATTCTATAGAAGATTAA

YOR261C_homolog 330aa (SEQ ID NO 568)

MSTTATSTNELALLDKSVVVSPLVLLSVVDHYNRVAKDSKKRVVGVILGDNSTDTIKVTNSYAIIPFEED
EKNPGVWFLDHNFDIDSMGEMFKKINAKEKLIGWYHSGPKLKPSDLKINEVFRRYTDNPLLLIVDVQPRE
VGIPTDAYFAVDDIKNDGSAAEKTFIHVPSLIEAEAEIEIGVEHLLRDIRDQAAGNLSLRVSETHQSL
GLHQKLGEIANYLDKVYQKKLPMNHTILGKLQNVFNLLPNLMQQSGSDLDGGSDDSSHALATAFTVKTN
ELMIYISTLVRAIIAFHDLIENKLENKKLNENKAQASVAESSLNSEKKDSIED

YPR035W_homolog 1122bp public: 1..1122 (SEQ ID NO 569)

ATGACTACTTCCCTTACAGAACAACTGCTATTTTGGCCAAATATTTGGAATTGTCTCAAAATGGTAAA
ATCTTAGCTGAATACGTCTGGATTGATGCTGAAGGTAACACTAGATCCAAATGTAGAATTTATCCAAA
AAACCAACTAGTGTGATGATTTACCTGAATGGAATTATGATGGTTCATCTACTGGTCAAGCTCCAGGC
CATGATTCTGATGTGTATTTAAGACCAGTTGCTTTTTATCCTGATCCATTTAGAAAAGGTGACAATATC
ATTTGTTTTAAATGAATGTTGGAACAATGATGGTACTCCAAACAAATTTAATCATCGTCATGAATGTGCT
AAATTGATGAAGGCTCATGCTAGTGAAGAAGTTTGGTTTGGTTTGAACAAGAATATACTTTATTTGAT
CAATATGATTATCCTTATGGTTGGCCAAAAGGTGGATTCCAGCTCCTCAAGGTCCATTCTACTGTGGG
GTTGGTACTGGTAAAGTTGTTGCTAGAGATGTCATTGAAGCTCATTATCGTGCTTGTCTTTATGCTGGT
ATCAACATTTCTGGTATTAATGCCGAAGTTATGCCATCTCAATGGGAATTTCAAGTTGGTCCATGTGAA
GGTATTGAAATGGGTGATCAATTTATGGATTGCTCGTTATTTATTACAAAGAGTTGCTGAAGAATTTGCC
GTCAAGATTTCTTCCATCCAAAACCTTTGAAAGGTGATTGGAATGGTGGTGTGCTGCTGCTGCTGCTGCT
TCTACCAATCTATGAGAGTGCCTGGTGGTATGAAAGTTATTGAATCTGCTTTGAGTAAATTTGGCCAAA
AGACACAAGGAACATATGTTATTGTATGGTGGCGATAATGATCAAAGATTAACCTGGTGGTTCATGAACT
GGTCATATGGATACTTTTTTCATCAGGTGTTGCTAACAGAGGTGCATCTATCAGAATTTCAAGACAAGTT
GCTAAAGAAGGATATGGTTATTTGCAAGATAGAAGACCAGCTTCTAACATGATCCATACCTTGGTCACT
GGTATCATGGTGGAGACAATCTGTGGTCTATTCCAGATGCTGATATGGCTAAAGAATTCCTTAGAGAA
AGCAGTGATGATAACTAA

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YPR035W_homolog 373aa (SEQ ID NO 570)

MTTSLTEQTAILAKYLELSQNGKILAEYVWIDAEGNTRSKCRTLSKKPSTSVDLPEWNYDGSSTGQAPG
HDSVYLRPVAFYPDPFRKGDNIIVLNECWNNNDGTPNKFNRHECAKLMKAHASEEVWFGLEQEYTLFD
QYDYPYGPWPKGGFPAPQGPFFYCGVGTGKVVARDVIRAHYRACLYAGINISGINAEVMPQSWEFQVGPCE
GIEMGDQLWIARYLLQRVAAEFVAKISFHPKPLKGDWNGAGCHTNVSTKSMRVPGGMKVIESALSKLAK
RHKEHMLLYGADNDQRLTGRHETGHMDTFSSGVANRGASIRIPRQVAKEGYGYFEDRRPASNIDPYLVT
GIMVETICGSI PDADMAKEFLRESSDDN

YMR099C_homolog 900bp public: 1..900 (SEQ ID NO 571)

ATGCCAGTTGAAGAGCCTGAAGACCGTGTATCATTACTGATCCAAATGACTCAACTAACAGAGCCACC
ATTTTGAAATTTGGTGCTACTGTAGTTTCTTGGAAAAACAATAATCAAGAAAAATTTGTGGTTATCAGAA
GGTGCTCATTTAGATGGAAGTAAAGCCGTTAGAGGTGGTATCCCATTTAGTTTCCAGTTTTCGGTAAA
CAAAAAGATTCAAATCATCCAACCTTTCAAATTACCTCAACATGGATTGCTCGTAATTCAACTTGGGAA
TTCTTGGGACAACTCAAGAAAGTCTATTACGGTTCAATTTGGATTAGGTCCAGAAAAATGTTGATCCA
GAACTTTGAAATTATGGAATTATGATTTCACTTTGATTTTAAGTGTAGTTTGACTAAAGATAAATTG
GTTACTTTCAATTTGACGTGGAAAAACACTGGTAAAGAAGCAATTTGAATTTAATTGGTTGTTCCATACATAT
TATAGAATCCATGACATCACCGATACATTAGTTACCAATTTAATTGACCAACAATGTTACGATCAATTG
ATTGGTGAATCATATATCGAAAAGGCACCAGTTATCAGTTTCCATGAAGAATTTGATAGAATTTATTCA
AAAGTCAGTTTGGAAAAATCCATTCAAGTCGTTGATAAAGGTCAAGTCTTTTCAATCTTCATAGAAAA
AACTTGCCTGATTCCGTTGTATGGAATCCATGGACTAAGAAAGCTGAAGGTATGGCTGATTTCCAACCA
AAATCAGGGTTTCATCAAATGGTCTGTGTTGAGCCAGGTCAATGTTAACTCAATGGTCTCTTTACCAGCT
GGTGGGAAATGGTCAGGTGGTCAAGAAATCACTATTGGCGGTGAGATTAAAGTTCAAGCTAATATTTAT
TAG

YMR099C_homolog 299aa (SEQ ID NO 572)

MPVEELEDVRIITDPNDSTNRATILKFGATVVSWKNNNQEKLWLSEGAHLDGSKAVRGGIPLVFPVFGK
QKDSNHVTFKLPQHGFARNSTWEFLGQTQESPITVQFGLGPENVDPETLKLWNYDFTLILTVSLTKDKL
VTSIDVENTGKEAFEFNWLFTYYRIHDITDLVTNLIDQCYDQLIGESYIEKAPVISFHEEFDRIS
KVSLEKSIQVVDKGQVLFNLHRKNLPDSVVWNPWTKAEGMADFQPKSGFHQMVCEP GHVNSMVS LPA
GGKWSGGQEITIGGEIKVQANIY

YBL085W_homolog 3519bp public: 1..3519 (SEQ ID NO 573)

ATGGATGGTGGCGATACTTATATATGTATAAAACAATTTAATGCCAGATTAGGCGATGAATTGAGTCTT
AAAATTGGCGACAAAATTCAAGTATTGGCTGACGATAGAGAATATAATGATGGTTGGTACATGGGCAAA
AACTTGTGACTGGAGAAGCAGGCTTATATCCAAAAACATTTACTCAATTAATAACCAACAATGATAGT
AAAACACTTCTTAGATCGAGGTCAAGAAGAATGATGGCACCTAAAAGTTCCGACCAAGAAACAACACCA
AAGGACACCCTACTCCCGTGGTGTGAGTAATCTCAATCCCAACACTCCTCCAAATTACCTCCAACA
TTGTCTATCTTCAACAGAACCTTCCCATTTAGCTGAACCAATGTCTCAGTTAAATTTAAATAAAGATTCT
CAATCTTCTCAATATACTGGGTCTCATTGTAACAGCCAAATTGATAGAGCATTACAAGAACTTCAAGGG
TCTAATGCCGACTTGACCAATTCTGGCAATAGTTTAAATGAGCACAGAAACCACCCTACAATAACAAC
ACTAATAATAATAATAATAATAATAATAATGCTGCTACTAGTAATAATTACAAACAACCACAGTTAATG
TCGAAGAAATCAATGATAGTCTTTCTAGTCAATATCAATATCAATCACAATCCCAACAACCAAAACAT
TTGAGTGGAGATAAATCTCGACAATCCTTAACTGACGATTTGGACCCTTTGAAAGCAAATACTTGGACA
CCAAAGCAAGTTTCTTCTTATTTTGCCTTGGTGTAGGGTTGATATGGATGTGGCTGGGAAATTTGCT
CAACACAAAATCACTGGAGAAATCTTGTGTAATGGATTAAATCTTTTGAAAGAATTGGATATTGAT
TCATTTGGTACCAGATTCAAATTATATAAAGAATTGGGAAATTAAAGGAATTGAATACTGAAGGAGTT
AAAGATAAACAATTGAGAACAGATTCTCTGTGCTGACTGGATCAACTGGTAAAAATGACACTACGTCATCA
GCATTAAATCTCCACCAACTGCTTCCACAACCTTTACACGATGCCGTGCCTCATATCGATGATAATAAT
ATGTTAAATAATACTGGCAAAACAACAACAACCACTAATGCCATCAGCCGTTTTGACCAACACTTCTGAC
TACAATAATAATAGTCAACAACAAGTGGTTCTCAACATCATCAGAGGAAAAGGTCACTGTGGTGGAT
GTTGCCCCACAACAATACTTGGCTTCTGATTCTACATTTATGTGCGCTAGAAGAGCTCCTCAACCACCA
TCTGGTGAGAGCCCAATTGATACAAGTTATAAATTTGGTGTGGAAGCGAATACGATAGACCACCTTCA
CACTATGGCATGTACATGACACGTAACGCTTCAAGTCATGCCTTGGGAAGTTCATCACCAGGAATC
AACTCAGACCAGCTTCATCAATTTATGATCTGTTTTCCAATCATAATAGAAATGGATCATCAACTTCA
AAACAACACCACAAGAGAAATTCATCAGTAACCAACAATAACAATAACAATAACGGTAACAGCAACCAC
AAGCATCATCACAGACGTCATTCTTCCGTTAATCTCATACCTTTCTGCTGGTAATGATGATTCGGCAAAA
CCAACACCAAAATTTAGTAGTAAGTTCCAAAGTAACAATTTGTACAAGGGTGGTGGATGATGATGAT
GGAGATTTCACTTCTTCAAGCAATAACAACAACAATAACAGTAAGTTAGTGTGCCAGCCAGCCAGATCAAG
AGAGAAACCCTAGTGGTCAATCGTCTCTTCATGAATCAGGATCCAAATCGAAAGGAAAATCACAATTT
TTTGATTTATCCAATTCACCAGTTGATATTGATGATGCCAAGTTTTCTCCAAAAAACTGAATTCGGTA
TCAGTTCCGACCAAGTCAATGGATGCAATTTGGTGGTAATGGAGACGATAGACGTGTTGCTAGTGATTCT
ACAGGATTGAGTCAATCAAAACCTAATAATTCATCAAGACTTAAAGGCATTTCGTGCCACGTCAACTCAA

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AGTTTCCGAAGTTTAAACAGGGTCGAAGAACTGAAAACATCAGCATTTCAAGAAGGTATACGTGAGATT
ACTCCTGATGAAGCCATTAAAACAGCCAGTCATAGTGGTTATATGTCTAAACGTTCAAATAACAAATTTA
GCGTGAGAAACAAGATATTTACATTACACGGTACCAGATTATCATATTTCCAATCTTTGAAAGATAAA
AAGGAAAAAGGTTTGATTGATATTACTGCTCATAAGTGATACCTATTGATAGTGCTAGTGATGATACT
GATAAAGCTGATAGATATGCTGCGATGTATGCTCGACAACATTTGCTGGTAATTATGTTTAAATTTG
GTTCCACCGGCTCCAGGGTTTAAAAAGGGGTTAACGTTTACGCAACCGAAAACTCATTTATTTTGTGTT
GAAACAGAAGAAGAAATGAGAGCTTGGGTCAAAGCATTAATGCAAGCCACTATTGATATTGATGATTCT
GTTCTGTGTTGAGTAGTTGTTCTACCCCAACTGTCAGTTTGAATAAAGCTCAAGAATTGTTAGCTAAA
GCCAGAGAAGAAACCAAAATTACGAGATGAACAACATAAAGCTAATGGCTACATTAGAAAGCTTAGAAGAT
ATCAATGATACTTCATTTCTGGCATCTTTGGATTATCTCGATATGAGTGGAGATATTGGTFTTGGTAGT
ACTTCTCCAGTAGCAGCAACTTCAGCACCTAAATTGACTCTTGATACTAATTTAATAGGAAAAGTCTCT
GGAACCTATGGGAACAACCGGGACAATAGGTACTCCAGGAACATCAGGTGGTACCGTACCAACAACACCA
CAAATACCACGATCATCAAGTCAAAGTGGTGGGTTTGTCTTCACTTATTTATTAGCTTCTGGGTTATTA
TCACCCAAATCAGGAGGTGGTGGCGGTCCAGGAGGAATGTATCATCGTCTTCTCCAATTAAATGAAAAT
GGACCTTTAAGAAAATTCAACTTCAAATTCAGAAATTTTGGTGATATTACTTTATAAAAGTTTAAACCA
CCATCTCGACAAAATTCCCAATATGCAAGTATCACTAGTGGTGGTGGCAGTATTGGGTTTGGATATGGT
TCCAACTAGTAGTGGCTAGGTGGACAGCAACAGCAATTGGAGGAGGAGGAGGAGGAGTATTATCATCA
TCCACTCCATATTCTACTGGTCTTGGATCAACAGCAAGTTCAATGAATTATAATAATCATAAACAAC
AACAACAACAACAATTTCTGTTAATAGTCCGATTAAATGAATTTAGATCTTCAAGGGATTGAAATCATCA
TCGTACCAACGACAACAACAGGTACATCTTCAACATCAGGGAACCAATCACGTAGAACATCA
GATAAAATGTTGGGATTTTCAAGTGATGCTTCAGGTAGTCATACTTTGTATTATAACCGAAAAAATAA

YBL085W_homolog 1172aa (SEQ ID NO 574)

MDGSDTYICIKQFNARLGDELCLKIGDKIQVLADREYNDGWYMGKNLLTGEAGLYPKTFTQLITNND
KTLRLSRSRMMAPKSSDQETTPKDTTTPVSSNLNPNTPPNYPPTLSSSTEPHSLAEPMSQLNLNKDS
QSSQYTGSHLNSQIDRALQELQGSNADLTNSGNSFNEHRNHHYNNNTNNNNNNNNNAATSNYKQPQLM
SKKSNDLSQQYQYQSQQPKHLSGDKSRQSLTDDLPLKANTWTPKQVSSYFALVLGFDMDVAGKFA
QHKITGEILFELDLNLLKELDIDSFGTRFKLYKEIGKLKELNTEGVKDKQLRTDSSSTGSTGKNDTSS
ALNSPPTATTLHDVPHIDNNMLNNTGKQQTQLMPSAVLTNTSDYNNNSQQQSGSQHQRKRSSSDV
VAPQQYLASDSTFMSPRRAPQPPSGESPIDTSYKFGAGSEYDRPPSHYGYMTRTNASSHALGSSSPGI
NSRPASSIYDSFSNHNRRNGSSSTSKQHHRNNSVTNNNNNNNGNSNHKHHHRRHSSVFSYLSSGNDSDAK
PTPKLLSSKFQSNLYKGGDDGHGDEFTSSNNNNNNNSKLVSPAQIKRETTSGQSSLHESGSKSGKSI
FDLSNSPVDIDDAKFSPPKSNVSVRTKSMDAIGNGDDRRVASDSTGLSQSKPNNSRLKIRATSTQ
SFRSLTGSKSKSTSAFQEGIREITPDEAIKTASHSGYMSKRSNNNLAWRTRYFTLHGTRLSTYFQSLDK
KEKGLIDITAHKVPIIDSASDDTDKADRYAAMYASTTFAGNYCFKLVPAPGFKGLTFTQPKTHYFSL
ETEEEMRAWVKALMQATIDIDDSVPVSSCSTPTVSLNKAQELLAKAREETKLREQLKANGYIRSLD
INDTSFASLDYPMMSGDIGFSTSPVAATSAPKLTLDTNFNKSSSGTMGTTGTIGTPTSGGTVPPTP
QIPRSSSQSGGFASPYLLASGLLSPKSGGAGPGGIVSSSPINENGPLRNSTSNSEYFGDITYKSLKP
PSRQNSQYASITSGGSGIFGYGSNNSLGGPATAIGGGGGVLSSSTPYSTGSGSTASSMNNNNNN
NNNNNSVNSPINEFRSSRDLSKSSSPTTTTGTSSTSGKKPQSRRTSKMLGFSSDASGSHTFVIKPKK

YBR019C_homolog 2028bp public: 1..2028 (SEQ ID NO 575)

ATGTCAAACGAATATATTCCTGTTACTGGTGGTGCAGGTTACATTGGTTCTCATACAGTTATTGAATTA
ATCAGTAATGGATATAAAGTAGTCATTGTTGATAATTTAAGTAATTCCTCCTATGATGCAGTTGCTAGA
ATTGAATTCATTGTCAAACAACATGTTCCATTCATGATGTTGATATCAGAAATTATGAGCAATTGAAT
AAAGTTTCCAAGATTATAAGATCTCTGGAGTCATTCAATTTGCTGCTTTGAAAGCTGTTGGTGAATCA
ACAAAAATCCCCCTAGCATATTATGATAAATGTATCAGGTACTGTCAACTTATTGGAAGTATGTAAA
GCCAATGATGTGAAGACAATTGTTTTAGTTCTTCAGCTACTGTCTATGGTGATGTTACTAGATTGGT
GATAATTCAATGATTCCATCCCTGAACATTGTCCAATGGATCCAACAAATCCATATGGAAGAACAAA
TTCATTATTGAGTCGATTTTAAAAGATATTTATAATAGTGATGATGCTTGGAAAGTAGCAATTTTGAGA
TATTTCAACCCAATTGGTGCCTCATCCATCTGGTTTATTAGGTGAAGATCCATTGGGGATCCCAATAAC
TTATTACCTTATTGGCTCAAGTTGCTATAGGTAGACGTGAAAAATTGCTATTTTCGGAATGATTAT
AATAGTCGTGATGGTACCCCTATTAGAGACTATATTTATGCTGTTGATTGGCAAAGGTCACATTGCT
GCATTGGCGTATTTGAAAACTTGCAATCTAAAGGCTTGATCGTGAAATGGAATTTAGGTACTGGTAAA
GGATCCACTGTTTTTGAAGTTTATCATGCATTTAGTAAAGTTGTTGGTAGAGAATTGCCCATGAAGTT
GTTGGAAGACGTGCTGGGGATGCTTGGATTGACTGCTAAGCCAGACAGAGCAACAAGGAATTGCAA
TGGAAAACTGAACCTTACCATTGATGATGCTTGTAAAGATTATGGAATGGACTACTGAGAACCCTTTT
GGATTCAACATTGAGAATTATCTTGGAAAGAAATTGATGGGTTCAATAACCGTTTGCACAGTTTGT
GCTGGTGAATTGAAAGTTAACTTAGCGAATCGTGGTGGTATGATCCAGCTATCACGTTGAAGGATCC
AATATGGTCAAAGCTTATAATAATGCTGAAGATTCAAATCTGAAACTAACCCATTTTTTCGGTACCCT
GTTGGTAGATATGCCAATAGAATTTCCAATGGAGAAATTTAAATGAATGGAAAAGGTACAAATTAAC
AAAAATGAAGGAGCAACAACCTTGATGGTGGTGAATGGATTGATAAACAAGATTTCTTTGGTCCA
GTTGTGAAAAGTCGTGATGGTAAGTTTTCTGTTGATTCTGTTGGTTGATAAAGATGGTAATGATGG

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TTCCAGGTGAGCTTGAAGCTATCGTACATTACACAATTGATGACTCCTCAGTGGAATTGAATATGAA
TGTCATTATTATCTGGTGAAGCAACAATTGTCAATATGACTAACCATAGTTATTTCAATGTTTCCAAC
TCAGACACTATTGAAGGAACCGAGGTAAAATTGATTACTGATAAAATGTTAGAAGTGGATTACAAATTA
TTACCAACTGGTAAATTTATTGAAAATGAAAAAGCTGCTAGCCCAATTGTGTTAAATGAGAATGACGTA
TTTGACAATTGTTTTATTGTTGATGAAGAATGTGGTATAGATACTCGTGATAAACCTTTGAAACAAGTC
TTTGAAGCAACTAGTTTGTGCACAAACAACAATTGAAGATATCCACCACTGAACCAGCTTTCCAATTT
TACACTGGTGACGGTGTAAATACTAAAGGTTTTGGGAAAAGATGTGGTTTCTGCGTGGAACCAAGTAGA
TTTATTAATGCAATCAATCACAAGAATGGTCTAATCAAGTCATCTTGAAAAAGGTGATGTTTATGGA
AGTAAATTAATATGAATTTCAATAG

YBR019C_homolog 675aa (SEQ ID NO 576)

MSNEYLLVTGGAGYIGSHTVIELISNGYKVVIVDNLNSSYDAVARIEFIVKQHVFPFYDVIDIRNYEQLN
KVFQDYKISGVIHFAALKAVGESTKIPLAYYDNNVSGTVNLLVCKANDVKTIVFSSSATVYGDVTRFG
DNSMIPIPEHCMPDPTNPYGRTKFIIESILKDIYNSDDAWKVAILRYFNPIGAHPSGLLEDPLGIPNN
LLPYLAQVAIGRREKLSIFGNDYNSRDGTPIRDYIHVVDLAKGHIAALAYLKNLQSKGLYREWNLGTGK
GSTVFEVYHAFSKVVGRELPHEVVGRAGDVLDTAKPDRANKELQWKTELTTIDACKDLWKWTENPF
GFNIENYSWKEFDGFNNRLHSFVAGDLKVNLANRGALQAITLKDSNMVKAYNNAEDFKSETNPFPGTT
VGRYANRLSNGEFKLNKGVYKLTKNEGANNLHGGANGFDKQDFFGPVVKS RDGKFFVDFLLVDKDGNDG
FPGELEAIVHYTTIDSSVEIEYECQLLSGEATIVNMTNHSYFNVNSDTEGTEVKLITDKMLEVDSQL
LPTGKFIENKAASPIVLNENDVFDNCFIVDEECGIDTRDKPLKQVFEATSFVTNNKLKISTTEPAFQF
YTG DG VNTKGFGRKCGFCVEPSRFINAINHKEWSNQVILKKGDVYGSKIKEYEQ

YCR005C_homolog 1194bp public: 1..1194 (SEQ ID NO 577)

ATGAGAGGTATCAAAGGTTTAGTTTGGGAAGGTTCTGTTTTGGACCCAATTGAAGGTATCCGTTTCAGA
GGAAGAACCATCCAGACATTCAAAAAGAAATGCCAAAAGCACCAGGTGGTGAAGAACCATTACCAGAA
GCTCTTTTCTGGTTGTTGTTGACTGGTGAAGTTCCAACCTGACGCCCAAACCTAAGGCTTTATCCGAAGAA
TTTGCTGCTAGATCAGCATTACCAAAGCACGTTGAAGAAATGATCGACAGATCTCCATCTCACTTGCAC
CCAATGGCTCAATTTCTCCATTGCCGTTACTGCTTTTGGAAATCTGAATCCCAATTTGCCCAAGCTTATGCT
AAAGGTGCCAACAAATCCGAATACCTGGAATAACACTTACGAAGATTCATCGATTGTTAGCTAAATTG
CCAACCATGCTGCTAAGATTTACAGAAACGTTTTTCCACGATGGTAAATTGCCAGCTGCCATTGACTCC
AAATTTGGATTACGGTGCTAACTTGGCCAGTTTGTAGGTTTTTGGTGACAACAAGGAATTTGTTGAATTA
ATGAGATTGTACCTTACCATCCACTCTGACCACGAAGGTGGTAACGTCCTGTCACACACCACCCACTTG
GTTGGTTCCGCTTTATCTTCCCCATTCTTGTCTATTAGCTGCTGGTTTGAATGGTTTAGCTGGTCCATTA
CACGGTAGAGCTAACCAAGAAGTTTTGGAATGGTTGTTCAAATTAAGAGAAGAATTAACCGGTGACTAC
TCCAAGGAAGCCATTGAAAAATACTTGTGGGAAACCTTGAACCTCCGCTAGAGTTGTGCCAGGTTACGGT
CACGCTGTCTTGAGAAAGACCGATCCAAGATACACTGCTCAAAGAGAAATTTGCTCTTAACCATATGCCA
GACTACGAATTTCAAATTTGGTTTCAAACATTTACGAAGTCGCTCCAGGTGTTTTGACCAACACGGT
AAGACCAAGAACCCTATGGCCAAATGTGGACTCCCACTCTGGTGTCTTGTTACAATACTACGGTTTGACT
GAACAATCTTTCTACACTGTCTTGTTCGGTGTTCCTCAGAGCCTTTGGTGTCTTGCCACAATTGATCTTG
GACCGTGGTATCGGTATGCCAATTGAAAGACCAAAATCTTTCTCCACTGAAAAATACATTGAATTGGTC
AAAAACATCAACAAAGCTTAA

YCR005C_homolog 397aa (SEQ ID NO 578)

MRGIKGLVWEGSVLDPIDIEGIRFRGRITPIDIKELPKAPGGEEPLPEALFWLLL TGEVPTDAQT KALSEE
FAARSALPKHVEELIDRSPSHLHPMAQFSIAVTALESESQFAQAYAKGANKSEYWKYTYEDSIDLLAKL
PTIAAKIYRNVFHDGKLPAIDSKLDYGANLASLLGFNDKEFVELMRLYLTIHSDHEGGNVSAHTTHL
VGSALSSPFLSLAAGLNLGAGPLHGRANQEVLEWLFKLREELNGDYSKEAIEKYLWETLNSGRVVPYG
HAVLRKTDPRYTAQREFALKHMPDYELFKLVSNIEYVAPGVLT KHGKTKNPWPVNVD SHSGVLLQYYGLT
EQSFYTVLFGVSRAGVLPQLILDRGIGMPIERP KSFSTEKYIELVKNINKA

YDR345C_homolog 1653bp public: 1..1653 (SEQ ID NO 579)

ATGTCATTAGATAAATTCAACAGAAAACCGTGATTGGAAGAAAAGGAAGAAATTC AAAGAACGAACAT
AACGAACAAGGCGAACAAAACAGAGAACAATGAGCATATACCTACTTTGGAAGATAAAACCATTGAAGGAA
TATATTGGTATTAGTATTTTGTGTTTCCTTATTGCCCTTTGGTGGTTTCGTTTTCGGTTTCGATACTGGT
ACCATTTCCTGGTTTCATTAACATGACTGACTTTTTAGAAAGATTTGGTGGTACTAAAGCTGACGGTACT
CTTTACTTTTCCAACGTTAGAAGTGGTTTATTGATTGGTTTGTTC AATGTGGGTGTGTCATTGGTGCA
TTATTCCTTGCTAAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATCATTAT
ATTGTTGGTATTATTGTTCAAATTTGCTTCTCAACATGCTTTGGTATCAAATCATGATTGGTAGAATATC
ACTGGTCTTGGTATTGGTATGTTATCAGTTTTGTGTCCTATTATTTATCTCAGAGGTTTCTCCCAATCAT
TTAAGAGGTACATTAGTTTATTGTTTCCAATTGATGATTACCTTGGGTATTTTCTTGGGTTACTGTACC
AGTTACGGTACTAAGAAATATTCTGACTCCAGACAATGGAGAATTCATTTGGGTTTATGCTTTGCTTGG
GCCTTGTGTTTGTCTGGTGGTATGGTAAGAATGCCAGAATCTCCACGTTACCTTGTCTGGTAAAGATAGA
ATTGACGATGCTAAGATTTCACTTGCCAAAACCTAACAAGGTTTCTCCAGAGGACCCTGCATTATACCGT

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GAACCTCAATTAATCCAAGCTGGTGTGAAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTA
ATCACTGGTAAACCAAGAATCCTTGAAAGAGTTATTTGTTGGAGGTATGTTGCAATCATTTGCAACAATTG
ACTGGTGATAACTATTTCTTCTACTACAGTACCACCATTTTCAAGTCTGTGGGTTTAAATGATTCCCTC
GAAACATCTATTATCCCTTGGTGTTCATCAACTTTGCTTCCACTTTTGTGGTATTTATGCCATTGAAAGA
TTGGGTAGAAGACTCTGTTTATTAACCTGGTTCCGTGCCATGTCCATTTGTTTCTTAATTTACTCATTTG
ATTGGTACTCAACATCTTTACATTGATCAACCAGGTGGTCCAAACCAGAAAACCAGATGGTAACGCTATG
ATTTTCATTACTGCACCTTTATGTTTCTTCTTCCGCTTCTACATGGGCTGGTGGTGTCTACTCCATTGTT
TCTGAACCTTTATCCATTAAAAGTCAGAAGTAAGGCTATGGGTTTGTCTAATGCATGTAACCTGGTTGTGG
GGTTTCTTGATTTCCCTTCTTCACTTCATTTATCACTGATGCTATCCACTTCTATTATGGTTTGTGTTT
ATGGGCTGTTTAGTGTTTTCCATTTCTTTGTTTACTTTATGATTTACGAAACTAAAGGCTTACTTTTA
GAGGAAATTGATGAATTATACCTACCAAGGTTGTTCCATGGAAATCAGCCGGTTGGGTTCCACCTTCT
GACGAAGAAATGGTTCTGTGCAAAAGGCTATCTGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

YDR345C_homolog 550aa (SEQ ID NO 580)

MSLDNSTENRDLEEKEEIPKNEHNEQGEQENNEHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG
TISGFINMTDFLERFGGTKADGTLVSNVRTGLLIGLFNVGCAIGALFLSKVGDYGRVRVIMTAMIY
IVGIIIVQIASQHAQWYQIMIGRIITGLAVGMLSVLCPFI SEVSPKHLRGLTVYCFQLMITLGI FLGYCT
SYGTTKYSRQWRIPGLGLCFAWALCLLGGMVMPESPRLVVGKDRIDDAKISLAKTNKVSPEDPALYR
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGGMLQSLQQLTGDNVFFYYSTTIFKSVGLNDSF
ETSIILGVINFASTFVGIYAIERLGRRLCLLTGVSAMSI CFLIYSLIGTQHLVYIDQPGGPTRKPDGNAM
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLISFFTSFITDAIHFFYGVFV
MGCLVFSIFVYFMIYETKGLTLEEIDELYSTKVVPWKSAGWVPPSDEEMVRAGYTGDIHADEEQV

YDR545W_homolog 1194bp public: 1..1194 (SEQ ID NO 581)

ATGGCATCCGAAGGTATTACTGAAATCGACTCTGGTTTAATTGAAACCAATTACGATAACGTCGTCTAC
AAGTTCGACGATTTAAACTTGAACCAAAACATTGTTAGAGGTATTTTGGTTACGGGTATGAAACTCCA
TCCGCTATTCAACAAAGAGCCATCTTGCCAATCACTGAAGGTAGAGATGTTTTGGCTCAAGCTCAATCC
GGTACTGGTAAAACCGCTACCTTTACCATTTCTGCATTACAAAGAATCAATGAAAATGAAAAGCCACT
CAAGCTTTAATCTTGGCCCCAACCAAGAGAATTGGCTTTGCAAAATCAAGAATGTTATCACTGCTATTGGT
TTGTACTTGAAGGTTACTGTCCATGCTTCTATTGGTGGTACCTCAATGAGTGACGATATTGAAGCTTTT
AGATCTGGTGTTCAAATTGTCTGGTACTCCAGGTAGAGTCTTAGACATGATTGAAAGAAGATATTTT
AAAACCGATAAAGTCAAGATGTTTCAATTTTGGATGAAGCTGATGAAATGTTATCAAGTGGATTTAAAGAA
CAAAATTACAACATTTTCAAGATTATTACCAGAAACCACCAAAATTGTCTTATTATCTGCCACCATGCCA
CAAGACGTTTTGGAAGTCACCACCAAAATTCATGAACAACCCAGTCAGAATCTTAGTCAAAAAGATGAA
TTGACTTTGGAAGGTATCAAAACAATCTATATTAATTTGAATTAGAAGATTACAAATTCGATTGTTTG
TGTGATTTGTACGATTCTATTTCTGTCAACCCAAAGCCGTCATTTTCTGTAACACTAGATCCAAGGTTGAA
TTTTTAACCAACAAATTGAGAGAACAACTTTACTGTCTCTGCCATCCACGCTGATTTGCCACAAGCC
GAAAGAGACACCATTATGAAAGAATTCAGATCTGGTCTTCAAGAATCTTGATCTCTACTGATTGTGTA
GCTAGAGGTATTGATGTCCAACAAGTTTCTTTAGTTATCAACTACGATTGGCCAGCCAACAAGGAAAAC
TACATTCATAGAATTGGTAGAGGTGGTCTGTTTCGGTAGAAAGGGGGTTGCCATCAACTTTGTCACTGAC
AGAGATGTTGGTATGATGAGAGAAATTGAAAAATCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT
ATTGGTGCTTTATTGCTTAG

YDR545W_homolog 397aa (SEQ ID NO 582)

MASEGITEIDSLIETNYDNVVKFDDLNLKPNIVRGIFGYGYETPSAIQQRAILPITEGRDVLAAQAS
GTGKTATFTISALQRINENEKATQALILAPTRELALQIKNVITAIGLYLKVTVHASIGGTSMSDDIEAF
RSGVQIVVGTGPRVLDMIERRYFKTDKVKMFI LDEADEMLSSGFKEQIYNIFRLLPETTQIVLLSATMP
QDVLEVTTKFMNPNVRILVKKDELTLGKIKQFYINVELEDYKFDCLCDLYDSISVTQAVIFCNTRSKVE
FLTNNKLREQHFTVSAIHADLPQAERDTIMKEFRSGSSRILISTDLLARGIDVQVSLVINYDLPANKEN
YIHRIGRGRFRGRKGVAINFVTDVDRVGMREIEKFYSTQIEEMPADIGALFA

YIL057C_homolog 606bp public: 1..606 (SEQ ID NO 583)

ATGGCGGGAAGAAAGTCTAAGCTGAAGCTTTACCATTAGATTAGACAATATTAAACCAATGGAT
CATTTACAACAGTCCCTAAAACAAGATCATCATCAATTACCTCAATTGAAAGTGCTGATGAACCAGGT
ACTATGAAACAAGTGTTGTTACCACCTACAATCAAAGAATTTGACGAATTGGAACAATTTGAATCATTT
GTTCTGTGATGAAACTTGGGATAATGATTTTGATTATTTCCATGGTAGATTACATTATTATCCACCATTT
GTTATGAAGAGTTGTCAAAAATAATCTTGAAAAATCAAGCCTACCATGAATAAAACTCCAAGAAATTT
AGACGTGATTTACAACATCATATTCAAAAACATTAATTAAGATTAGAAAAATGTTGTGGTTACGAG
TTGAATTTGGTAAAGGAGAAGTTGTTGAGACTGATAATAAAGTTACTTGGAATTTAAAGACGAAACT
GATCATGTTTGTAGTAAAGAGAAGAAGATATGTATGATAGACATTGGAGATTGGAATTTGGATGTTTCT
TGACAAATGAATCAGCTATGGTTGATGTTGAATATAAATCCATTCCAATGTAA

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YIL057C_homolog 201aa (SEQ ID NO 584)

MAGKKKSKSEALPLDLNLIKPMHLQVPKTRSSSITSIESADEPGTMKQVLLPPTIKEFDELEQFESF
VRDETWDNDFDYFHGRHLHYPPFVMSKQNNLEKIKPTMNKNSKKFRRLQHHIQKHLIKDLEKCCGYE
LNFSGKEVVEVDNKVTKWFKDETDHGFPSKEEEDMYDRHWRLELDVSVCTNESAMVDVEYKSIPM

YKR097W_homolog 1662bp public: 1..1662 (SEQ ID NO 585)

ATGGCTCCCTACTGCTGTTGAATCTTCAATCAATTTCCGAGGTCACCCAACTATCAAATCCACTCAA
GACCCATTGGTCCAAAAGTTGCTCTTAATACCGACACTGTGATCAGACACAATGCTCCACCTCCAACC
TTATACGAAGATGGTTTATTAGAAAAAGGTACTACTATCTCATCTACTGGTGCTTTAATGGCTTACTCT
GGTAACAAAACCGGTAGATCTCCTAAAGACAAGAGAATTTGTCGACGAATCCACCTCATCCCATAAACATT
TGGTGGGGTCCAGTGAATAAACAAGTTGACGAATTAACCTTGGAAAGATTCTAGATCAAGAGCTTTGGAT
TACTTGAGAACTAGAGAAAAAGTTGTTTGTGTTGACGCTTATGCTGGTTGGGATCCAAGATACAGAATC
AAGGTCAGAATTATCTGTGCTAGAGCTTACCATGCTTTGTTTCATGACCAATATGTTGATCAGACCAACT
GAAGAAGAATTAaaaaaactTTGGTGAACCAGATTTCACCATCTACAATGCTGGTCAATTTCCAGCCAAC
ATCCACACTAAAGGTATGACTTCTGCCACTTCTGTTGAAATCAACTTTAAAGATATGGAAATGGTTATC
TTGGGTACTGAATATGCTGGTGAATGAAGAAAGGTATCTTACTGTTATGTTCTACTTGTATGCCAATC
AAACACAAGGTTTTGACTTTGCACCTCCTCATGTAACCAAGGGTTGAAAAAGGTGATGTCATTTGTTTC
TTTGGTCTTTTCTGGTACTGGTAAGACCCTTTGCTGCTGATCCACAAAGAAAGTTGATTGGTGTATGAC
GAACATTGTTGGTCCGACAAATGGTGTGTTCAACATTGAAGGTGGTTGTTACGCCAAATGTTTGGACTTG
TCTGCTGAAAAAGAACAGAAATTTTCAACTCCATCAAGTTTGGTGTCTATTTTGGAAATGTTGTCTAC
GACCAATCACCAGGTTGTTGACTACGAAGATTCAATCAATCACTGAAACACTAGATGTGCATACCCA
ATTGATTTTCAATCCATCTGCCAAGATTCCATGTTTGGCCGACACCCATCCAACCAATATTATCTTGTTA
ACATGTGATGCTTCCGGTGTGTTGCCACCACTTCCAATTTGACTAATGCTCAAGTTATGTATCATTTTC
ATTTCTGGTTACACCTCCAAGATGGCAGGTACTGAAGAAGGTGTTACTGAACCACAAGCTACATTCTCC
GCATGTTTCCGTCAACCATTCTTGGTGTGTCACCAATGAAATATGCTCAACAATTTGCTGACAAGATT
TCCGAACACAATGCCAACGCTTGGTGTGTTGAACACTGGTTGGGTTGGTTCTTCTGTTGCTCAAGGTGGT
AAGAGATGTCCATTGAAATACACCAGAGCTATCTTGGATGCTATCCACTCTGGTGAATTGTCTAAAGTC
GAATACGAAAAAGTTCCAGTTTTCAACCTTAATGTTCCAACCTTCTTGTCTGGTGTTCAGAGTGAATTT
TTGAACCCCAATAAAGCTTGGACCCAAGGTACTGATTCAATCAACAAGGAAATCAAATCTCTTGCTACC
AAGTTTGCTGAAAACTTCAAGACATACGCTGATCAAGCTACTGCTGAAGTTAAAGCTGCTGGTCCAGAA
GCATAA

YKR097W_homolog 553aa (SEQ ID NO 586)

MAPPTAVESSINFGGHPTIKSTQDPLVQKLSLNTDPTVIRHNAPPPTLYEDGLLEKGTTSISSTGALMAYS
GNKTGRSPKDKRIVDESTSSHNIWWGPVNKQVDELTKWISRSRALDYLRTREKLFVVDAYAGWDPYRI
KVRIICARAYHALFMTNMLIRPTEEELKNFGEPTIYNAGQFPANIHTKGMTSATSVINFKDMEMVI
LGTEYAGEMKKGIFTVMFYLMPIKHKVLTLSHSCNQGVKEGDTVLFGLSGTGKTTLSADPQRKLIGDD
EHCWSDNGVFNIEGGCYAKCLDLSAEKEPEIFNSIKFGAILENVVYDPITKVVDYEDSSITENTRCAYP
IDFIPSAKIPCLADTHPTNIIILLTCDASGVLPPVSKLTNAQVMYHFLSGYTSKMAGTEEGVTEPQATFS
ACFGQPFVLVHPMKYAQQLSDKISEHNANAWLLNTGWGSSVAQGGKRCPLKYTRAILDAIHSGELSKV
EYKVPVFVNLNVPTSCPGVPSEILNPTKAWTQGTDSFNKEIKSLATKFAENFKTYADQATAEVKAAGPE
A

YOL126C_homolog 1014bp public: 1..1014 (SEQ ID NO 587)

ATGGTCAAAGTCGCTATTTTAGGAGCTGCTGGTGGTATTGGTCAACCATTATCTTTATGACCAAATTA
AACCCAAATGTTGATGAATTGGCATTATTTGATGTCGTCATGTTCCAGGAGTTGGTGTGATTTATCT
CATATCAATTTCTGATTTCTAAACTCAATCATATTTACCAAAAGATAAAGAAGATAAACTGCATTAGCT
GCTGCATTTAAAGGTTCTGATTTAGTCATTATCCAGCTGGTGTTCAGAAAACAGGATGACCAGA
GATGATTTATTCAATATTAATGCATCAATCGTTCAAGGTTTAGCTGAAGGTATTTGCTGCCAATTTCTCCA
AAAGCTTTTGTCTTGGTGATTTCTAATCCAGTCAATTTCTACTGTACCAATTTGTTGCCGAAACTTTACAA
GCTAAAGGTGTTTATGATCCAGCTAGATTATTTGGTGTACTACTTTGGATATTGTTAGAGCCAATACT
TTTATTTCTCAATTTATCCTAGATCAAACTAAACCATCTGATTTCAATATTAATGTTGTTGGTGGCCAT
TCTGGTGAAACCATTTGTTCCATTATATTCATTAGGTAACTCTAAACAATATTATGATATATTATCTGAA
GAACAAAAGAGGAATTAATCAAAAGAGTTCAATTTGGTGGCGATGAAGTTGTTCAAGCCAAGAATGGT
GCTGGTTCCGCCACTTTATCCATGGCTTATGCCGTTATAGATTAGCCGAATCAATTTTAGCTGCTGTT
AATGGTAAACATGATATTGTTGAATGTACTTTCTTGAACCTTGATTCTTCAATTAAGGTGCTTCTGAA
GCTAGAAAAATGTTAAAGATTTAGATTTCTTTTCAATACCAGTTCAATTAGGTAAAAACGGTATTACT
GAAGTTAAATATGATATCTTAAATCAAATTTCTGATGATGATGATGATGATGATGATGATGATGATGAT
CAATTACAAAAGAAATATTGAAAAAGGTGTTTCAATTTGCTAAGAAATAA

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YOL126C_homolog_337aa (SEQ ID NO 588)

MVKVAILGAAGGIGQPLSLLTKLNPNVDELALFDVVNVPGVGADLSHINSKTSYLPKDKEDKTALA
AALKGSDLVVIIPAGVPRKPGMTRDDLNFNINASIVQGLAEGIAANSPKAFVLVISNPNVNSTVPIVAETLQ
AKGVYDPAFLFGVTTLDIVRANTFISQLFLDQTKPSDFNINVVGGHSGETIVPLYSLGNSKQYYDILSE
EQKKELIKRVQFGGDEVVQAKNGAGSATLSMAYAGYRLAESILA AVNGKTDIVECTFLNLDSSIKGASE
ARKLVKDLDFSLPVQLGKNGITEVKYDILNQISDDEKKLLEVAIEQLQKNIEKGVSPFAKK

YBL072C_homolog_621bp public: 1..621 (SEQ ID NO 589)

ATGGGTATTTCTAGAGATTCACGTCACAAAAGATCCGCCACTGGTGCCAAAAGAGCCCAATTCAGAAAAG
AAGAGAAAAGTTTGAATTAGGTAGACAACACAGCCAACACCAAGATTGGTCCAAAAGAATTCACTCTGTC
AGAACCAGAGGTGGTAACCAAAAATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTGGGGTTCC
GAAGGTGTTTCCAGAAAAACCAGAAATGCTGGTGCTGTTTACCATCCATCTAATAACGAATTGGTTAGA
ACCAACACCTTGACCAAAATCTGCTGTTGTTCAAATTGATGCTACTCCATTAGACAATGGTACGAAAAC
CACTACGGTGCTACTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCACGCTGCTGAAGTTGCCGAT
GCCAAGAGATCAAGAAAAGTCGAAAGAAAATGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCT
GTTGACTCTCAATTCCGTTCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGA
TGTGATGGTTACATCTTGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAAGTCTAAGAAATAA

YBL072C_homolog_206aa (SEQ ID NO 590)

MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVRTRGGNQKFRALRVETGNFSWGS
EGVSRKTRLAGVVYHPNNELVRTNLTLSAVVQIDATPFRQWYENHYGATLGKKKGGGAHAHAHAEEVAD
AKRSRKVERKLAARSAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFYLRRLTAKK

YBR009C_homolog_318bp public: 1..318 (SEQ ID NO 591)

ATGTCAGGTACCGGTAGAGGAAAAGGTGGTAAAGGTTTAGGAAAAGGTGGTGCTAAACGTCACAGAAAA
ATTTTAAGAGATAACATTCAAGGTATTACAAAACAGCTATCAGAAGATTGGCCAGAAGAGGTGGTGTT
AAACGTATTTCTGCTTTGATTTATGAAGAAGTCAGAGTTGTCTTGAAACAATTTTGGAAAACGTTATC
AGAGATGCTGTTACTTACACTGAACATGCTAAAAGAAAAACCGTCACTTCATTGGATGTTGTTTACGCT
TTGAAGAGACAAGGTAGAACCCTTGATGGTTTCGGTGCTTAA

YBR009C_homolog_105aa (SEQ ID NO 592)

MSGTGRGKGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVVKRISALIYEEVRVVLKQFLENNI
RDAVITYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YBR189W_homolog_489bp public: 1..489 (SEQ ID NO 593)

ATGGCCGGTGAATACCGGTTTAAAAACAAGGGGGGAATCTACAGAATTGGGGTTCCAAATGTCCATAAA
ATCAGAAGAGCTGCTCGTGAATTTGTAACCAGAGGTGAAAAAGGCCCCAAAAAGATTATTCGGAAGGTA
ATGGCTTTGATCAGAAGATTAGTCAGATTGGTTTCTTGTCTGAGGACAAAATGAAATTGGATTATGTC
TTGGCTTGGAACCCAGAAGTTTCTTGAACAGAAGATTCCAACCCCAAGTTTCAAATTAGGTTTAGCT
AGATCTATCCCCACGCCAGAGTTTGTATCACCAGCCACATTGCTGTTGGTAAACAAATTTGTTACC
ATCCCATCATTTACTGTCAGATTGGACTCTCAAAAACACATTGACTTTGCCCACAACTCTCCATACGGT
GGTGGTAGAGCCGGTAGAGTTAAGAGAAAGAACCAAGGTAAAGGTGGTGAAGAAGGTGCCGAAGAAGAA
GAATAA

YBR189W_homolog_162aa (SEQ ID NO 594)

MAGEYRFKKQGGNLQNWGSKCPKIRRAAREFVTRGEKGPKKIIRKVMALIRRLVRFGLSEDKMKLDYV
LAWNPEVFLNRRFQPQVFKLGLARSIPHARVLITQSHIAVGKQIVTIPSTVRLDSQKHIDFAHNSPYG
GGRAGRVKRNQKGKGEEGAEEEE

YBR191W_homolog_330bp public: 1..330 (SEQ ID NO 595)

ATGCCACACAAATACTACCACGGTAAGACTGGTATTGTTTACAACGTTACCAAATCCTCCGTTGGTGTT
ATCATTAACAAAGTTGTTGGAACAGATACATTGAAAAGAGAGTTAACTTGAGAGTTGAACATGTTAAA
CACTCTGCTTGTCTGTCAGAAATTTCTGAACAGAGTTAAATCTAACGCTGCTAAAAAGAGAGAGCTAAA
GCTAACGGTGAAACCGTTTACTTGAAGAGACAAGCTGCCAAGCCAAGAGGTTCAAGAATTATCTCCACT
GAAGGTAACATTCTCAAACTTTGGCTCCAGTCGCTTACGAAACTTTCAATTTAA

YBR191W_homolog_109aa (SEQ ID NO 596)

MPHKYYHGKTGIVYNVTKSSVGVINKVVGNRYIEKRVNLRVEHVKHSACRQEFNLRVKSNAKKKREK
ANGETVYLRQAAKPRGSRIISTEGNIPQTLAPVAYETFI

YCL035C_homolog_384bp public: 1..384 (SEQ ID NO 597)

ATGATAGACAAAATGCTGCTGATTCTTGCCCTGGGGATTCAATTTGTGGTATCAACCACCTCCACCTACT
GCACAACTGAGAAAAGAAATCGAACACACTATTAAGTCTCACAAGATTGTTATTTATTTCTAAAACCTTAT

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TGTCCATTTTGTGACCAAACCAACATCTATTAAATGAACAATATCCACAAGAATCGTACGAAGTCATA
AAC TTGAATATTCTCGATGACGGATTGACTATTTCAGAATCAATTGTATGCTAATACTGGTCAATATATG
GTGCCCATAACTTTCATAAACGGACAACACGTTGGAGGAAATTCAGAAGTTCAGCAATTGCACACCAAT
GGGAAATTGCAAGAATTATTGAATCCTCAGAAATATTGA

YCL035C_homolog 127aa (SEQ ID NO 598)

MIDKMSSILAWGFNLWYQPPPTAQTEKEIEHTINSHKIVYISKTYCPFCDDQTKHLNEQYPQESYEV
NLNILDGLTIQNQLYANTGQYMPPIIFINGQHVGGNSEVQQLHTNGKLQELLNPQKY

YDL004W_homolog 486bp public: 1..486 (SEQ ID NO 599)

ATGTTTCAGACAAGTTTTCCGTCAGTTACCAAACAATCAATTCAGTGGGGTTAAGAGAACTTATGCCACC
GAGGCCGCGCGTGTCTACAGATGCTTTGAAATTATCCTTGGCATTGCCACACCAAACTTATACAACGAC
TCCGAAGTCCAACAAGTAACTTGCCATCTGTCAACGGTGATTGGGTATTTTGGCCAACCATTTCCA
ATTGTCTGAACAATTGAGACCAGGATTGTTAGAAATCATTTCAAAAACGGAGACTCTGACCAATACTTT
GTCAGCGGCGGTATCGCCATGGTCCAACCAGGAAACAAGTTGACTATTTCCGCCATCGAAGCATTCAAG
ACCGACCAAATTGATCTCTCTGCCGTCAAAACTTGATTGCCGATGCCAAAAGAGAGCTGAATCTAGT
GATGAAAAGGTCGCTGCTGAAGCCAACATCGAATTGGAAGTGTAGATGCTTTACAACATTTTACTAAG
TAA

YDL004W_homolog 161aa (SEQ ID NO 600)

MFRQVFRQVTKQSFTGVKRTYATEAAVSTDALKLSLALPHQTLYNDSEVQQVNLPSVNGDLGILANHIP
IVEQLRPLGLEIISKNGSDQYFVSGGIAMVQPGNKLITISAIEAFKTDQIDLSAVKNLIADAQKRAESS
DEKVAEEANIELEVLDAHQHFTK

YDR099W_homolog 795bp public: 1..795 (SEQ ID NO 601)

ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA
ATGGTTGAAAACATGAAAGCCGTTGCTTCTCTGGCCAAGAATTGTCTGTTGAAGAACGTAATTTATTA
TCTGTTGCTTACAAGAATGTCATTGGTGCTCGTCTGCTTCTGGAGAATTGTTTCATCAATTGAACAA
AAAGAAGAAGCCAAAGGAAATGAGAGCCAAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT
GAATTGTCTAAAATTTGTGAAGATATTCTCTGTGTTGAGCGACCATTAAATTACATCTGCCCAAAC
GGTGAATCAAAAGTATTTTACTACAAGATGAAAGGTGATTACCACAGATACTTGGCTGAATTTGCTATC
GCTGAAAAACGTAAGGAAGCTGCTGATTTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTGCTGTG
ACCGAGTTGCCACCAACCCATCCAATCAGATTAGGTTTAGCATTGAACCTTCTCTGTTTTCTACTATGAA
ATTTTGAACCTCCCAGATAGAGCTTGTCAATTTAGCTAAACAAGCTTTTCGATGATGCTGTTGCTGATTTA
GAAACCTTATCTGAAGATTTCATACAAGGATTCAACTTTGATTATGCAATTATTGAGAGATAACTTGACT
TTATGGACCGATTTATCTGAAGCCCCAGCTGCCACTGAAGAACAACAACATCCAGTCAAGCTCCAGCT
GCTCAACCAACAGAAGGTAAGGCTGATCAAGAATAG

YDR099W_homolog 264aa (SEQ ID NO 602)

MPASREDSVYLAKLAEQAERYEEMVENMKAVASSQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ
KEEAKGNESQVALIRDYRAKIEAELSKICEDILSVLSDHLITSAQTGESKVFYKMKGDYHRYLAEPFI
AEKRKEAADLSLEAYKAASDVAVTELPPTHPIRLGLALNFSVFYIEILNSPDRACHLAKQAFDDAVADL
ETLSEDSYKDSLIMQLLRDNLTLWTDLSEAPAATEEQQSSQAPAAQPTGKADQE

YDR399W_homolog 642bp public: 1..642 (SEQ ID NO 603)

ATGCTCTGAATCTGAGAAAATGTACATTTCTGTACAATAATATACACCAGTTATGTCAAGAAATAGCCCC
AAGATCAAAGAATTTAAGCCTGACTTGATCATTGCTATTGGTGGCGGTGGTTTTATTCCAGCTAGAATG
TTGCGTTCCCTTCTTGAAAAGAACCAGGTCAACCAAACGTTAGAATTATGGCTATCATATTGTCTTTATAC
GAAGAGATTGAGAGTGAAAACGTTATTGAAAAGCCAGGTACCCAAGTTGTGCGTACTCAATGGATTGAT
TATCATCAATCTAAAATTGACTTGGTTGGTAAAAATGTGTTAATTATTGATGAGGTTGATGATACCAGA
ACCACTTTGCATTACGCAGTCAGTGAATTGAAAAAGATGTGGAAGAGCAATCAAAAGCCAAAGGTGCA
GATCCTAAAGATACCAAGTTTGGTATTTTGTGTTGCACGACAAGCAAAAGCAAAAGGAGAGCAATG
CCAGATGATATTATGAAGACTGGTAATTATTTCTGCTGCTCGTTCTGTCCCAGATAGCTGGATTGCATAC
CCATGGGAGTCTACTGACATTTTATCATCAATGAAAGCTGAAGAACAAGGAAACGATGTGTTCCCTT
CCTTCATCCACTTTAGAGTAA

YDR399W_homolog 213aa (SEQ ID NO 604)

MSESEKMYISYNNIHQLCQEIAPKIKEFKPDLLIAIGGGGFIPARMLRSFLKEPGQPNVRIMAILLSLY
EEIESENGIEKPGTQVVRTQWIDYHQSKIDLVGKQNLIIIDEVDDTRTTLHYAVSELKKDVEEQSKAKGA
DPKDTKFGIFVLHDKQKQKKAELPDDIMKTGNFYFAARSVPDSWIAYPWESTDIVYHQMKAEEQGNVFL
PSSTLE

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YDR418W_homolog 498bp public: 1..498(SEQ ID NO 605)

ATGCCTCCAAAATTTGATCCAAATGAAGTTAAATTCCTTTACTTAAGAGCTGTTGGTGGTGAAGTTGGT
GCTTCATCTGCTTTAGCTCCAAAGATTGGTCCATTAGGTTTATCCCCAAAGAAAGTTGGTGAAGATATT
GCCAAAGCCACCAAGAATACAAAGGTATTAAAGTTACTGTTCAATTGAGAAATCAAACAGACAAGCT
ACTGCTTCTGTTGTTCCATCCGCTTCATCTTTAGTCATCACCGCTTTGAAAGAACCAGTCAGAGACAGA
AAGAAGGAAAAGAAGCTCAAACACTCTGGTAACATTCCATTAGATGAAATCTTTGAAATTGCCAGAAAA
ATGCAACACAAATCATTTCGGTAAGAATTTGGCATCTGTCTCCAAGGAAATCTTGGGTACTGCTCAATCT
GTTGGTTGTAGAGTTGATGGTAAGAACCCTCATGACATCATTGACGCCATCAACGCTGGTGAATTTGAT
GTTCCAGAAAACTAG

YDR418W_homolog 165aa(SEQ ID NO 606)

MPPKFDPNEVKFLYLRAVGGEVGASSALAPKIGPLGLSPKKVGEDIAKATKEYKGIKVTVQLRIQNRQA
TASVVPSSASSLVITALKEPVRDRKKEKNVKHSGNIPLDEIFEIARKMQHKSFGKNLASVSKEILGTAQS
VGCRVDGKNPHDIIDAINAGEIDVPEN

YDR513W_homolog 360bp public: 1..360(SEQ ID NO 607)

ATGTTTCGTACATTATTAAACAAAAGACTATTCAATACATCAACAATGGTTTCATCTCAAGTTAAGAAC
AAGGTCGAACAATTGATCAAAACCAAACAGTTTTCATTGCCTCCAAATCCTATTGTCCATACTGTAAG
GCTACCAAAAGCACAATTGAAGCTATAACAAAGGATGCTTACATTCTTGAATTAGACGAAGTTGACGAC
GGTCTGAAATCCAAAGAACATTTATTGGAAATCACTGGTCAAAGAACCGTTCCAAATGTCTTTATTGGT
GGTCAACATATTGGTGGCAATTCGATGTGCAAGCTTTGAAGTCTAGTGACAAATTAGATGACAAATC
AAAGCTGCTTTATAA

YDR513W_homolog 119aa(SEQ ID NO 608)

MFRLLTKRLFNTSTMVSSQVKNKVEQLIKTPVFIASKSYCPYCKATKSTIEAITKDAYILELDEVDD
GAIEQEAALLEITGQRTVPNVFIGGQHIGGNSDVQALKSSDKLDDKIKAAAL

YEL009C_homolog 972bp public: 1..972(SEQ ID NO 609)

ATGCCGTGCTACTACTCCTATTATTTATGAAGATTCTTTATTTGAATCTCAAGATTTATTTGCTTCTCCA
GTTAAACAACAACATCAAAAGGTTGATACTGTTGCTACCAAAAACGAAATTTGGTTTGGAAATTAATTTA
GGTTTACCAGAAATGCAAAAGGCTTCAGAAAACCTGTTTCCACTCCATTTCAAATCCATTCCAGTGATTTG
GAGTCGGGTTTTCAGCACCAATTTGGATGGAGTCAATGATATTGATCATACTCCAATGTTTGATGAATTG
GATTTGATTATGGACGGAGCCAAAGTCAATTCATCAGAAGATTGGGTTGCTCTTTTTGGAGATGACAAAT
GATGATGGTGTGCTATAGCTGGTGTACTAGCAAAGAACCAATGTTATCATTTGAATGAAGATAACGAG
AACATGATGACGACGCTGATGACGCTGATGATGATGATGCTCTTGTTCAGAGAAGATACTATT
GAAGCTTTATTATTGGAACCATCAACAAATCGTACCATTCTGCTGCTACTTCTGCTTCTACTTCATCA
TTAAACAGTCCAGAAAGTACTATTGCTACCACAGTCACTGCTGGTGGTGAAGTTGTTGTTGCAAGTAAA
AAGCAATTTCAATTGGTAACACCAATCCTTCATCCACTTTACCAACACCATTATTGGATTCTAAAAAT
TCTAAAAAAGAGTTAAAGTTGATCATTTGGGTTGTGTTACCTATTTCGAAAAAACATAGATCTCAACCT
TTACAACCGATTGTTGTTGATGACATTAAAGATGCTGCTGCTTTGAAAAGAGCTAAAAATACTGAAGCT
GCTAGAAGATCCAGAGCTCGTAAATGGAAGAATGAGTCAATTGGAAGATAAAGTTGAGAATTTGATT
AATGAAAAGCAAGCTTTACAAGATCAAGTTGAAAGATTACAAGAAATTGTTAAGAGTTAATGGTATTCAA
TTTTAA

YEL009C_homolog 323aa(SEQ ID NO 610)

MPATTPIIYEDSLFESQDLFASPVKQHQKVDTVATKNEIGLELNLGLPEMQKASETVPFQIHSSVL
ESGFSTNLGDVNDIDHTPMFDELDLIMDGAKVNSSSEDWALFGDDNDDGVAIAGATSKEPMLSLNEDNE
NNDDDDADDADDLDALVPREDTIEALLLEPSPNRTISAATSASTSSLNSPESTIATTTVAGGEVVASK
KQFQLVTPNPSSLTPLPLDSKNSKKRVKVDHLGCVTYSKKHRSQPLQPIVVDDIKDAAALKRAKNTA
ARRSRARKMERMSQLEDKVENLINEKQALQDQVERLQELLRVNGIQF

YGL123W_homolog 750bp public: 1..750(SEQ ID NO 611)

ATGTCAGCTGAAGCCCCAAAAAGACAATTTGGTGATAGAAGAAGAGGTGGTAGAAGAGGTGGTAGAAGA
GATGCTGAAGAAAAGGTTGGACTCCAGTCAACCAAGTTAGGTAGATTAGTCAAAGCTGGTAAATCACC
AGTGTGTAACAAATCTACTTGCACTCTTTGCCAGTCAAGGAATACCAAAATCATTTGATTGTTATTGCCA
GACTTGAAAGATGATGTATGAAGATCAGATCTGTCCAAAAACAAACCAGAGCTGGTCAAAGAACCAGA
ATGAAGGCTGTTGTCTGTCATTGGTGACTCTAACGGTCACGTTGGTTTGGGTATCAAGACCGCTAAAGAA
GTTGCTTCTGCCATTAAAGCTGCTATTGTTATTGCCAAATTATCCATCATCCCAATCAGAAGAGGTTAC
TGGGGTTCTAATTGGGTCAACCACACTCTTTGCCATTGAAAGTCACTGGTAAATGTGGTTCCGTTGCC
GTTAGATTATCCAGCCCCAAGAGGTAAAGGTATTGTTGCTTCTCCAGTTGTCAAGAGATTAAATGCAA
TTGGCTGGTGTGAAGATGTCTATACTTCTCTTCTGTTCTACCAGAACTACCGAAAAACACTTGAAA
GCTGCTTCTGCTGCTATCGGTAACACTTACAGTTTCTTGACTCCAACTTGTGGGCTGAAACTCCATTA
GCTGCTTCTCCATTGGAAGTTTACGCTGAAGAAGCTGCTGCTGGTAAAAAGAGATACTAA

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YGL123W_homolog 249aa (SEQ ID NO 612)

MSAEAPKRQFGDRRRGGRRGGRRDGEKGWTPVTKLGRVLKAGKITSVEQIYLHSLPVKEYQIIDLLLP
DLKDDVMKIRSVQKQTRAGQRTMKAVVIGDSNGHVGLGIKTAKEVASAIKAAIIVIAKLSIIPIRRGY
WGSNLGQPHSLPCKVTGKCGSVAVRLIPAPRGKIVASPVVKRLMLAGVEDVYTSSSGSTRTTENTLK
AAFAAIGNTYSLTPNLWAETPLAASPLEVYAEBAAGKKRY

YGR209C_homolog 312bp public: 1..312 (SEQ ID NO 613)

ATGGTTCACGTTGTCACTGAAGTTAACAATTCCAAACCCCTTTTAAAGGAAAACAACCTTAGTTATTGTT
GACTTTTTTGGCACTTGGTGTGGTCCATGTAAATGATTGCTCCATTATTAGAAAAATTCAAAATGAA
TATTCTAATATTAAATTTTTGAAAATTGATGTTGATCAATTGGGTTCTTTAGCACAAGAATATAATGTT
AGTTCTATGCCAACCTTTGATTTTATTCAAAAATGGTGAAGAAGTCAATCGTGTCAATTGGTGCTAACCCA
GCTGCTATTAAACAAGCTTTGGCTTCTCTTGCTTAA

YGR209C_homolog 103aa (SEQ ID NO 614)

MVHVVEVNEFQTLLENLVIIVDFATWCGPCKMIAPLLEKFQNEYSNIKFLKIDVDQLGSLAQEYNV
SSMPTLILFKNGEEVNRVIGANPAAIKQALASLA

YHR039C-B_homolog 342bp public: 1..342 (SEQ ID NO 615)

ATGTCATCTGGTATCCAATCATTATTGAAAACCGAAAAAGAAGCTGCAGAAATTGTTAATGAAGCTAGA
AAATATAGAACACACGTTTGAAGCTCGAAAAACAAGATGCTCAAGCTGAAATTGATAACTATAAAAAAG
CAAAAGGAAGAAGATTAAAAAATTTGAAAAAGAACACGAAGGGTTAAATGAAAAGATCGATAAAGAA
GCTGATGCTGAAGTTGAAAAGGAATTGACCAGTATCAATCCACTTTTGAAAAGAAAAAGAGTGCAGTT
GTTAAATTGTTAGTTGACGCTACTGTCAAGCCAACACCAACTTTACACATAAATGCATCTCAATAA

YHR039C-B_homolog 113aa (SEQ ID NO 616)

MSSGIQSLLKTEKEAAEIVNEARKYRTTRLKSAKQDAQAEIDNYKKQKEELKNFEKEHEGLNEKIDKE
ADA EVEKELTSIKSTFEKKKSAVVKLVDATVKPTPTLHINASQ

YJL138C_homolog 1194bp public: 1..1194 (SEQ ID NO 617)

ATGGCATCCGAAGGTATTACTGAAATCGACTCTGGTTTAATTGAAACCAATTACGATAACGTCGTCTAC
AAGTTCGACGATTATAAATTGAAACCAACATTGTTAGAGGTATTTTTGGTTACGGGTATGAAACTCCA
TCCGCTATTCAACAAAGAGCCATCTTGCCAATCACTGAAGGTAGAGATGTTTTGGCTCAAGCTCAATCC
GGTACTGGTAAAACCGCTACCTTTACCATTTCTGCATTACAAAGAATCAATGAAAATGAAAAAGCCACT
CAAGCTTTAATCTTGGCCCCAACAGAGAATTGGCTTTGCAAATCAAGAATGTTATCACTGCTATTGGT
TTGTACTTGAAGGTTACTGTCCATGCTTCTATTGGTGGTACCTCAATGAGTGACGATATTGAAGCTTTC
AGATCTGGTGTTCAAATTGTCGTTGGTACTCCAGGTAGAGTCTTAGACATGATTGAAAGAAGATATTTT
AAAACCGATAAAGTCAAGATGTTCAATTTGGATGAAGCTGATGAAATGTTATCAAGTGGATTAAAGAA
CAAAATTACAACATTTTCAGATTATTACCAGAAACACCCAAATTGTCTTATTATCTGCCACCATTGCCA
CAAGACGTTTTGGAAGTCACCACCAATTCATGAACAACCCAGTCAGAATCTTAGTCAAAAAGATGAA
TTGACTTTGGAAGGTATCAAAACATTTCTATATTAAATGTTGAATTAGAAGATTACAAATTCGATTGTTTG
TGTGATTTGTACGATTCTATTTCTGTCAACCAAGCCGTCATTTTCTGTAACACTAGATCCAAGGTTGAA
TTTTTAACCAACAAATTGAGAGAACAACACTTACTGTCTCTGCCATCCACGCTGATTTGCCACAAGCC
GAAAGAGACACCATTTATGAAAGAATTGAGATCTGGTCTTCAAGAATCTTGATCTCTACTGATTGTTTA
GCTAGAGGTATTGATGTCCAACAAGTTTCTTTAGTTATCAACTACGATTTGCCAGCCAACAAGGAAAC
TACATTCATAGAATTGGTAGAGGTGGTCTGTTTGGTAGAAAGGGGGTTGCCATCAACTTTGTCACTGAC
AGAGATGTTGGTATGATGAGAGAAATTGAAAAATCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT
ATTGGTGCTTTATTTGCTTAG

YJL138C_homolog 397aa (SEQ ID NO 618)

MASEGITEIDSLIETNYDNVVKFDDLNLKPNIVRGIFGYGYETPSAIQQRAILPITEGRDVLAAQAS
GTGKTATFTISALQRINENEKATQALILAPTRELALQIKNVITAIGLYLKVTVHASIGGTSMSDDIEAF
RSGVQIVVGTGPRVLDMIERRYFKTDKVKMFLDEADEMLSSGFKEQIYNIFRLLPETTQIVLLSATMP
QDVLEVTTKFMNPNVRILVKKDELFTLEGIKQFYINVELEDYKFDCLCDLYDSISVTQAVIFCNTRSKVE
FLTNLKLRHQHFTVSAIHADLPQAERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLPANKEN
YIHRIGRGRFRGRKGVAINFVTD RDVGMREIEKFYSTQIEEMPADIGALFA

YKL060C_homolog 1080bp public: 1..1080 (SEQ ID NO 619)

ATGGCTCCTCCAGCAGTTTTAAGTAAATCCGGTGTTATCTACGGTAAAGACGTCAAAGACTTGTTTGAC
TATGCTCAAGAAAAAGGTTTTGCCATTCCAGCTATCAATGTCACTTCATCCTCAACTGTTGTTGCTGCT
TTAGAAGCTGCCAGAGACAACAAGGCTCCAATCATTTGCCAACTTCTCAAGGTGGTGCTGCTACTTT
GCCGGTAAAGGTGTCGACAACAAGATCAAGCTGCTTCCATTGCTGGTTCAATTGCTGCCGCTCACTAC
ATTAGAGCCATTGCTCCAACCTTATGGTATCCCAGTTGTTTTACACACTGATCACTGTGCCAAAAAATTA

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TTGCCATGGTTTGTATGGTATGTTGAAAGCCGATGAAGAATCTTTGCTAAGACCGGTACTCCATTGTTCTC
TATCCCCACATGTTGGATTATCTGAAGAAACCGATGACGAAACATTGCTACTTGTGCCAAATATTTC
GAAAGAATGGCTAAATGGGTCAATGGTTAGAAATGGAAATGGGTATCACTGGTGGTGAAGAAGATGGT
GTCAACAACGAACACGTTGAAAAAGATGCTTTATACACTTCTCCAGAACTGTTTTCGCTGTCTACGAA
TCTTTACACAAGATTTCTCCAACTTTTCTATTGCTGCTGCTTTTGGTAACGTCCACGGTGTTCACAA
CCAGGTAATGTGCAATTGAGACCAGAAATCTTGGGTGACCACCAAGTTTACGCTAAGAAACAAATGGGT
ACTGATGCTAAACACCCATTATACTTGGTTTTCCACGGTGGTTCTGGTTCTACTCAAGAAGAAATCAAC
ACTGCTATCAAGAATGGTGTGTGCAAGGTCAACTTGGACACTGATTGTCAATATGCTTACTTGAAGTGGT
ATCAGAGATTACGTCACCAACAAGATTGAATACTTGAAAGCACCAGTTGGTAACCCAGAAGGTGCTGAC
AAACCAAAAGAAATACTTTGACCCAAAGAGTCTGGGTTAGAGAAGGTGAAAAGACCATGTCCAAGAGA
ATTGCTGAAGCTTTGGATATTTTCCACACCAAGGACAATTGTAA

YKL060C_homolog 359aa (SEQ ID NO 620)

MAPPVLSKSGVIYKDKVDFDYAQEKGFAPAINVTSSSTVVAALEAARDNKAPIILQTSQGGAAAYF
AGKGVNDKQDAASIAGSIAAAHYIRAIAPTYGIPVVLHTDHCARKLLPWFDMGLKADEEFFAKTGTPLF
SSHMLDLSEETDDENIATCAKYFERMAKMGQWLEMEIGITGGEEDGVNNEHVEKDALYTSPEVFAVYE
SLHKISPNFSIAAFGNVHGVYKPGNVQLRPEILGDHQVYAKKQIGTDAKHPLYLVFHGGSGSTQEEFN
TAIKNGVVKVNLDTDCQYAYLTGIRDYVTNKIEYLKAPVGNPEGADKPNKKYFDPVWVREGEKTMKR
IAEALDIFHTKGQL

YKL150W_homolog 906bp public: 1..906 (SEQ ID NO 621)

ATGTTGACTCATCATTTATCGAAATTGGCTACTCCAAAATCTTAGTACCAATTCGCTGGTGCCACTGCT
TTGTCAATTGGTTTGGCATTTGCAATATCTACTTCCAACAATTACATTGCTAACGAACTGGTAAACT
TTCCTGATAGCAATGAATGGGTGGACTTGAATTTATCTAAGTCAATTGATTTGACTCATAACACCAAA
CACTTGGTTTTCAAGTTAAAAGATGAGAATGATGTTTCTGGTTTGATCACTGCTTCATGTTTGTGACC
AAATTTGTTACACCAAGGGTAACAATGTTATTCGTCCATATACCCCTGCTCTGATGTTAACCAATCT
GGTGAATTTGATTTCTGATTAAAAATACGACGGAGGTAAAATGTCAAGTCACATTTTCGATTTGAAA
GAAGGTGAACCTTATCATTTCAAAGGACCAATTGTTAAATGGAAATGGGAACCAATCAATTCAAGTCC
ATTGCTTTGATTGGTGGTGGTACTGGTATTACTCCATTATACCAATTGTTGCATCAATCACTTCTAAT
CCAAAGGACAACACCAAGTTAATTTGATTTACGGTAACCTTGACTCCAGAAGATATCTTGTAAAGAAA
GAAATCGATGCTATTGCTTCTAAACACAAGGACCAAGTTAAAGTTCATTACTTTGTTGACAAGGCAGAT
GAAAAGAAATGGGAAGGTCAAATGGTTTCAATTACTAAAGAATCTTACAAAAGAAATAGAAAACCA
GGTTCTGATTTCAAGGTTTTGTTTGTGGTCCACAGGTTTATACAAGGCTATATCAGGTCCTAAAGTT
TCCCCAAGTATCAAGGTGAATTGACTGGTGTCTTGAAAGATTGGGTTTCGAAAAGAACATGTCTTT
AAATTTTAG

YKL150W_homolog 301aa (SEQ ID NO 622)

MLTHHLSKSLATPKFLVPFAGATALSIGLALQYSTSNYYIANETGKFTFDSNEWVDLKLKSIDLTHNTK
HLVFKLDENDVSLITASCLLTKFVTPKGNVIRPYTPVSDVNQSGEIDFVIKKYDGGKMSSHIFDLK
EGETLSFKGPVWKWEPNQFKSIALIGGGTGITPLYQLLHQITSNPKDNTKVNLIYGNLTPEDILLKK
EIDALASKHKDQVKVHYFVDKADEKKWEGQIGFITKEFLQKELEKPGSDFKVFVCGPPGLYKAISGPKV
SPTDQGEELTGALKDLGFEKEHVFKF

YLR029C_homolog 615bp public: 1..615 (SEQ ID NO 623)

ATGGGTGCCTACAAATATTTAGAAGAATTGCAAGAAAGAAGCAATCTGATGTTATGAGATTCTTGTAT
CGTGTACAGATGTTGGGAATACAGACAAAAGAATGTATCCACAGAGCTTCCAGACCATCTAGACCAGAC
AAGGCTAGAAGATTAGGTTACAAAGCTAAACAAGGTTTCGTTATCTACAGAATCAGAGTTAGAAGAGGT
GGTAGAAAGAGACCAGTTCCAAAGGGTGCCACTTACGGTAAACCAACCAACCAAGGGGTTAACCAATTG
AAATACCAAAAATCATTGAGATCTACTGCTGAAGAAAGAGTTGGTCGTCGTGCTTCTAACTTGAGAGTC
TTGAACCTCATCTGGGTTAACCAAGATTCCACCTACAAATACTTTGAAGTTATTTAGTCGACCCATCT
CACAAAGCTATCAGAAGAGATGCTAGATACAACCTGGATCGTTAACCAGTTACAAAACACAGAGAAGCC
AGAGGTTTGACTTCTGCTGGTAAGAAATCCAGAGGTATTAACAAGGGTCATTTGTTCAACAAAACCAA
GCTGGTAGAAGACACACCTGGAAGAAGCACAAACACCTTATCTTTATGGAGATACAGATCTTAA

YLR029C_homolog 204aa (SEQ ID NO 624)

MGAYKYLEELQRKKQSDVMRFLYRVRCWEYRQKNVIRASRPSRPDKARRLGKAKQGFVIYRIRVRRG
GRKRPVPKQATYGKPTNQGVNQLKYQKSLRSTAEVIRVGRASNLRLVNSYWNQDSTYKYFEVILVDPS
HKAIRRDARYNWIWPNVHKHREARGLTSAGKKSRLGINKGHLFNKTKAGRRHTWKKHNTLSLWRYRS

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YNL030W_homolog 318bp public: 1..318(SEQ ID NO 625)

ATGTCAGGTACCGGTAGAGGAAAAGGTGGTAAAGGTTTAGGAAAAGGTGGTGCTAAACGTCACAGAAAA
ATTTTAAGAGATAACATTCAAGGTATTACAAAACCGCTATCAGAAGATTGGCCAGAAGAGGTGGTGT
AAACGTATTTCTGCTTTGATTTATGAAGAAGTCAGAGTTGCTTGAACAATTTTGGAAAACGTTATC
AGAGATGCTGTTACTTACACTGAACATGCTAAAAGAAAACCGTCACCTTCATTGGATGTTGTTTACGCT
TTGAAGAGACAAGGTAGAACCTTGTATGGTTTCGGTGGTTAA

YNL030W_homolog 105aa(SEQ ID NO 626)

MSGTGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISALIYEEVRVVLKQFLENNI
RDAVTTYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YOR285W_homolog 546bp public: 1..546(SEQ ID NO 627)

ATGTTTGCATTTAAAAAATCTACTACTTCAATTCTCAAACAGTGGTCGCCCCAACATCATCTCGTTAT
TTATCCACCGTCACATTAAGATCAATCCCAAGAACATTCCATAATGCCACTAAAGTTTCATTATTCAAT
GGATTAAGAACTACACCAAGATTTTATAGTGTATTGACTGAATCTCCAGAGGCAAAAGTATATAAATAT
GCCGATGTTAAGGATGTGGCCGTACACCCTGAAAACACCCTGATTCTGTTTTAGTGGATGTTAGAGAA
CCAACTGAATTTGGAGATGGTCATATACCAGGAGCTTTGAATATTCCATTAAAAGTAGTCCCGGCGCA
TTGGATTTGTCAGAAGAAGATTTCGAAGAACATTTTGGATTTCCTAAACCAAGTACTGATAAAGAATTG
ATTTTCTATTGCTTGGAGGTGTTAGATCTACTGCAGCTGAAGAATTGGCCAATACTTTTGGTTATAAG
AAAAGAGGAAATTATCTTGAAGTTGGGAAGATTGGGTAAAACATGAAAATAAAAAGAACTAA

YOR285W_homolog 181aa(SEQ ID NO 628)

MFAPKKSTTSILKTVVAPTSSRYLSTVTLRSIPRTFHNATKVSLEFNGLRITPRFYSVLTESPEAKVYKY
ADVKDVAHPENHPDSVLVDVREPTFEGDGHIPGALNIPFKSSPGALDLSEEDFQEHFGFPKPSTDKEL
IFYCLGGVRSSTAEEELANTFPGYKRGNYLGSWEDWVKHENKKN

YOR327C_homolog 603bp public: 1..603(SEQ ID NO 629)

ATGAAGATTTATTACATTGGTATTTAAGATCAAGTGGAGACAAGGCTTTAGAGTTAACTTCAGCCAGA
GATTTATCACAGTTTTCCTTTTTCGAAAGAAATGGCGGTATCCCAATTCATGACTTTTTTCGCAGAAACC
GTATCCCAAAGAACTCAACCTGGACAGAGACAAAGTGTGAAGAAGGTAATTATATTGGTCATACTTAT
ACCAGATCAGAAGGAATTTCTGGTATCATTATAACGGACAAAGATTACCCTGTAAGACCAGCATATACA
TTAATAAATAAAATCTTGAAGAATATTTATCATTCATCCTAAATCTGATTGGGAAAAACATTGATAAA
GCAAAATGAAACTTTTACAATATGGACAATTAGAAGCATATTTGAAAAAATATCAAGATCCCACTCAAGCT
GATTCATCATGAAAGTTCAACAAGAATTAGATGATACTAAGGTTGTTTTACACAAAACATTTGAAGGG
GTTTTTACAAAGAGGAGAAAATTAGATTCATTGGTTGACAAATCAGAAGCATGTCAAGTCTTCAAGA
ATGTTTTTATAACAAGCAAGAAGAAAACCAATTCCTGTTGTGTGATTATGTGA

YOR327C_homolog 200aa(SEQ ID NO 630)

MKIYYIGILRSSGDKALELTSARDLSQFSFFERNVGSQFMFFAETVSQRTQPGQRQSVEEGNYIGHTY
TRSEGISGIIITDKDYPVRPAYTLINKILEEYLSLHPKSDWENIDKANETLQYGQLEAYLKKYQDPTQA
DSIMKVQQLDDTKVVLHKTIEGVLQRGEKLDLVDKSEALSSSSSRMPYKQAKKTNSCCVIM

YPL037C_homolog 474bp public: 1..474(SEQ ID NO 631)

ATGCCAGTCGATCCAGAAAAATTAGCTAAATTGCAAAAGTCATCTGCCAAAAAAGTTGGTGGTTCAAGA
GTTAAAGCCAAGAAGAACATCAAGACTGAACAAGATGACACCAAAATGATTGAAGCTTTGGGTAAATTG
AAAGCTACCAAAATCGAAGGTGTTGAAGAAGCAATTTCTTCAGAGAAGATGGTAAAGTTTACATTTT
AACAGAGTTGGTGTTCAGGGTGTCCAGCTTCTAATACTTTTCCTTCACTGGTTACCCACAAGAAAAG
AATATTACTCAATTGATCCCAAAATTTTACCACAATTGGGTGCTGAAAACCTTGAAATCTTGAGACAA
TTGGCTGAACAAATCCAAGCTGGTAAAACCTCAAAAGACTTCAACACTGGTTCTGCTAACGCTGCTGCT
GATGCCGGTGGTGAAGATATTCCAGACTTGGTTGACCAAAATTTGACGATGTAGATAA

YPL037C_homolog 157aa(SEQ ID NO 632)

MPVDPEKLAKLQKSSAKKVGGSRVKAKKNIKTEQDDTKLIEALGKLKATKIEGVVEANFFREDGKVLHF
NRVGVGAPASNTFAFTGYFPQEKNTQLIPQILPQLGAENLEILRLAEQIQAGKTPKDFNTGSANAAA
DAGGEDIPDLVDQKFDDVE

YPL079W_homolog 330bp public: 1..330(SEQ ID NO 633)

ATGCCACACAAATACTACCACGGTAAGACTGGTATTGTTTACAACGTTACCAAAATCCTCCGTTGGTGT
ATCATTAACAAGTTGTTGGAAACAGATACATTGAAAAGAGAGTTAACTTGAGAGTTGAACATGTTAA
CACTCTGCTTGTCTGCAAGAATTCTTGAACAGAGTTAAATCTAACGCTGCTAAAAAGAGAGAAGCTAAA
GCTAACGGTGAACCGTTTACTTGAAGAGACAAGCTGCCAAGCCAAGAGGTTCAAGAATTATCTCCACT
GAAGGTAACATTCTCAAACCTTGGCTCCAGTCGCTTACGAACTTTTCATTTAA

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YPL079W_homolog 109aa (SEQ ID NO 634)

MPHKYYHGKGTGIVYNVTKSSVGVIIINKVVGNRYIEKRVNLRVEHVKHSACRQEFNLNRVKSNAAKKREAK
ANGETVYLRQAAKPRGSRIISTEGNIPQTLAPVAYETFI

YBR089C-A_homolog EMBL_entry 279bp public: 1..279 (SEQ ID NO 635)

ATGGCTCCAGGTGAAAGAAAGAGTCTCTAGAAAAGAAGGATCCAGATGCTCCAAAAAGATCCCTTA
TCTGCTTATATGTTTTTCGCTAATGAAAAACAGAGATATTGTTAGAGCTGAAAACCCAGGTATCTCTTTT
GGTCAAGTTGGTAAATTTATTAGGTGAAAAATGGAAGGCTTTAAACAGTGAAGATAAATTACCTTACGAA
AACAAGGCTGAAGCTGATAAAAAGAGATATGAAAAAGAAAAGGCTGAATACGCTAAAAAGAATTCCGCC
TAA

YBR089CA_homolog SWISS-PROT_entry 92aa (SEQ ID NO 636)

MAPGERKKSSRKKKDPDAPKRSLSAYMFFANENRDIVRAENPGISFGQVVKLLGEKWKALNSEDKLPYE
NKAEDKKRYEKEKA EYAKKNSA

YBL092W_homolog EMBL_entry 396bp public: 1..396 (SEQ ID NO 637)

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YBL092W_homolog SWISS-PROT_entry 131aa (SEQ ID NO 638)

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YDL059C_homolog 2791bp PathoSeq: 1..2791 (SEQ ID NO 639)

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YDL059C_homolog_1 67aa PathoSeq: 1..67 (SEQ ID NO 640)
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YDR377W_homolog 24076bp PathoSeq: 1..24076 (SEQ ID NO 641)
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YGR008C_YLR327C_homolog_1 79aa PathoSeq: 1..79 (SEQ ID NO 644)

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YGR034W_homolog 2004bp PathoSeq: 1..2004 (SEQ ID NO 645)

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YGR034W_homolog 120aa PathoSeq: 1..120 (SEQ ID NO 646)
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YMR273C_homolog_1 98aa PathoSeq: 1..98 (SEQ ID NO 648)
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191/251

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YPR028W_homolog 149aa PathoSeq: 1..149 (SEQ ID NO 650)

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YFR033C_homolog 24142bp PathoSeq: 1..24142 (SEQ ID NO 651)

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YJL166W_homolog_1 93aa PathoSeq: 1..93 (SEQ ID NO 656)

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YPL271W_homolog 7123bp PathoSeq: 1..7123 (SEQ ID NO 657)

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YDR064W_homolog 143aa PathoSeq: 1..143 (SEQ ID NO 664)

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YKL156W_homolog_1 81aa PathoSeq: 1..81 (SEQ ID NO 666)

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YLR038C_homolog 8469bp PathoSeq: 1..8469 (SEQ ID NO 667)

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ATGAAGTGGGATTGAAAGAAAAA AATAGTACAGAATAAACATAATGAGACACACGATTTACAGACATACTC

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ACATTACAGTGATAATCTACCTACAACATCTAGATAATCACTGAAACATATCCCTCGTTTATAGAAAGAATAAAC
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YLR038C_homolog_1 74aa PathoSeq: 1..74 (SEQ ID NO 668)

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YNL131W_homolog 15251bp PathoSeq: 1..15251 (SEQ ID NO 669)

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[illegible]

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YNL131W_homolog 150aa PathoSeq: 1..150 (SEQ ID NO 670)

MVKLTQIDDETQQQFENQSVAKNNHIIDEASSEESDDDDSDLDLDFENETLLERIVALKDIVPPEQRE
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YHR161C_homolog 4220bp PathoSeq: 1..4220 (SEQ ID NO 671)

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TCTTTAAGTCTCACAGTTAAAGTTGTAGTACCCTTCCCATAGAGCCTGATGATGTCGTGTACGAAAACCTTGTGA
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YHR161C_homolog 609aa PathoSeq: 1..609 (SEQ ID NO 672)

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YDR544C_homolog 1700bp GeneSeq: 1..1700 (SEQ ID NO 673)

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YDR544C_homolog 548aa GeneSeq: 1..548 (SEQ ID NO 674)

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FIEDLGQSKYKVNPTSITSKTLGGLKYLKPTQVPVIIQQIWKFEHQSSLMVSIIRSTTPLVLENFVVSVALNQDI
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YHR094C_homolog 1653bp public: 1..1653 (SEQ ID NO 687)

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ATTGTTGGTATTATTGTTCAAATTCCTTCTCAACATGCTTTGGTATCAAATCATGATTGGTAGAATATC
ACTGGTCTTGTCTGTTGGTATGTTATCAGTTTGTGTCCATTATTTATCTCAGAGGTTTCTCCCAAACAT
TTAAGAGGTACATTAGTTTATTGTTTCCAATTGATGATTACCTTGGGTATTTTCTTGGGTTACTGTACC
AGTTACGGTACTAAGAAATATTCTGACTCCAGACAATGGAGAATTCCATTGGGTTTATGCTTTCCTTGG
GCCTTGTGTTTGTCTGGTGGTATGGTAAGAAATGCCAGAAATCTCCACGTTACCTTGTTCGGTAAAGATAGA

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ATTGACGATGCTAAGATTTCACTTGCCAAAATAACAAGGTTTCTCCAGAGGACCCCTGCATTATACCGT
GAACTTCAATTAATCCAAGCTGGTGTGAAAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTA
ATCACTGGTAAACCAAGAAATCCTTGAAAGAGTTATTGTTGGAGGTATGTTGCAATCATTCGAAACAATTG
ACTGGTGATAACTATTTCTTCTACTACAGTACCACCATTTTCAAGTCTGTCCGTTTAAATGATTCCCTTC
GAAACATCTATTATCCTTGGTGTTCATCAACTTTGCTTCCACTTTTGTGGTATTTATGCCATTGAAAGA
TTGGGTAGAAGACTCTGTTTATTAACTGGTTCCGTTGCCATGTCCATTGTTTCTTAATTTACTCATTTG
ATTGGTACTCAACATCTTTACATTGATCAACCAGGTGGTCCAACCAGAAAACCAGATGGTAACGCTATG
ATTTTCATTACTGCACTTTATGTTTCTTCTTCCGTTCTACATGGGCTGGTGGTGTCTACTCCATTGTT
TCTGAACTTTATCCATTAAAAGTCAGAAGTAAGGCTATGGGTTTGTCTAATGCATGTAACCTGGTTGTGG
GGTTTCTTGATTTCTTCTTCACTTCATTTATCACTGATGCTATCCACTTCTATTATGGTPTTGTGTTT
ATGGGCTGTTTAGTGTTTCCATTTCTTGTGTTTACTTTATGATTTACGAACTAAAGGTCCTTACTTTT
GAGGAAATTGATGAATTATACCTACCAAGGTTGTTCCATGGAAATCAGCCGGTTGGGTTCCACCTTCT
GACGAAGAAATGGTTCGTGCAAAAGGCTATACTGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

YHR094C_homolog 550aa (SEQ ID NO 688)

MSLDNSTENRDLEEKEEIPKNEHNEQGEQNEENNEHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG
TISGFINMTDFLERFGGTKADGTLFYSNVRTGLLIGLFNVGCAIGALFLSKVGDYGRVRVIMTAMIY
IVGIIIVQIASQHWYQIMIGRIITGLAVGMLSVLCPFISEVSPKHLRGLTVYCFQLMITLGIPLGYCT
SYGTTKYSRQWRIPLGLCFAWALCLLGGMVMPESPRLVKGDRIDDAKISLAKTNKVSPEPALYR
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGGMLQSLQQLTGDNYFFYYSTTIFKSVGLNDSF
ETSIIILGVINFASTFVGIYAERLGRRLCLLTGSVAMSIICFLIYSLIGTQHLIYIDQPGGPTRKPDGNAM
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLISFPTSFIITDAIHFFYGFVF
MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVVPWKSAGWVPPSDEEMVRAKGYTGDIIHADEEQV

YBL099W_homolog 1344bp public: 1..1344 (SEQ ID NO 717)

ATGGCTTTGAACCTGGAAGCTGACCAAGTCGGGGTTGTGTTGTTCCGTTCTGATAGATTAGTCAAAGAA
GGTGAAACCGTCAAGAGAACTGGTCAAATTGTTTCCGTTTCCAAATGGTCCAGAAATTGTTAGGTAGAGTT
GTTGATGGTTTTAGGTAACCCAATTGATGGTAAAGGTCCAATCAAGGCTGCTGCTTACTCCAGAGCTCAA
GTTAAAGCTCCAGGTATTTTACCAAGAAGATCCGTCCACGAACCAATGCAAACCGGTTTGAAATCTGTT
GATGCTTTGGTTCCAATTGGTAGAGGTCAAAGAGAATTGATCATTGGTGATCGTCAAACCTGGTAAAACC
GCCGTTGCCTTGGATGCCATCTTGAACCAAAAGAGATGGAACAATGGTTCTGACGAAAAGAAGAAATTG
TACTGTGTTTACGTTGCCGTTGGTCAAAGAGATCCACTGTTGCTCAATTGGTCCAAACTTTGGAACAA
CACGACGCTCTTAAATACCTCTGTTATTGTTGCTGCTACTGCTTCTGAAGCTGCTCCATTGCAANTACATT
GCTCCATTCACTGCTTGTGCTATTGGTGAATGGTTCAGAGACAATGGTAGACACGCCTTGATTGTCTAC
GATGATTTGTCCAAACAAGCTGTTGCTTACCGTCAATTGTCATTATTGTTGAGAAGACCACCAGGTAGA
GAAGCTTACCCTGGTGATGTTTTCTACTTACATTCCAGATTATTGGAAGAGCTGCTAAGATGTCTGAT
GCTTACGGTGGTGGTTCTTTGACTGCTTTGCCAGTTATTGAAACCCAAGGTGGTGATGTCTCTGCTTAT
ATTCCAACCTAACGTTATTTCCATTACTGATGGTCAAATTTCTTGGGAAGCTGAATTATTCTACAAAGGT
ATCAGACCAGCTATTAACGTCGGTTTGTCCGCTCTCCCGTGTCCGTTCTGCTGCTCAAGTTAAAGCTATG
AAACAAGTTGCCGGTTCCTTGAAATTGTTCTTGGCCCAATACAGAGAAGTTGCTGCTTTTCGCTCAATTT
GGTTCTGATTTGGATGCTTCTACCAAAACAACTTGAACAGAGGTGAAAGATTGACCCAATTATTGAAA
CAAAAACAATAACAACCCATTGGCTGCCGAAGAACAAGTTCCATTGATTTTTCGCTGGTGTTAACGGTTTC
TTGGACAATGTTGCTCTTGACAGAATTGGTGAATTCGAAGAAGCTTCTTGGGTCACTTGAAATCTAAC
GAAACTGGTATCTTGGATGCTATTAAGACCAAGGGTGAATTATCTAAAGATGAATTAGAAAAAATTGAGA
AAAGTCACCGAAGAATTGCTTGCTTCTTTCTAA

YBL099W_homolog 447aa public: 1..447 (SEQ ID NO 718)

MALNLEADQVGVLFGSDRLVKEGETVKRTGQIVSVPIGPELLGRVVDGLGNPIDGKGP IKAAYSRQA
VKAPGILPRRSVHEPMQTGLKSVDALVPIGRGQRELIIGDRQTGKTAVALDAILNQKRWNNGSDEKKKL
YCVYVAVGQKRSTVAQLVQTLQHDALKYSVIVAATASEAAPLQYIAPFTACAIGEFWRDNGRHALIVY
DDLKQAVAYRQLSLLLRPPGREAYPGDVFLHSRLRLERAAMSDAYGGGSLTALPVIETQGGDVSA
IPTNVISITDGQIFLEAEIFYKIRPAINVGLSVSRVGSAAQVKAMKQVAGSLKFLAQYREVAFAQF
GSDLDASTKQTLNRGERLTQLLKQKQYNPLAAEEQVPLIFAGVNGFLDNVALDRIGEFEEAFLGHLKSN
ETGILDAIKTKGELSKDELEKLKRVTEEFVASF

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YEL032W_homolog 2637 bp public: 1..2637 (SEQ ID NO 719)

ATGGATGAACGATTTTGAATCCACCACCTACAGCTGATCAAGATGATACTAATCAGCCACTTGATGCC
ATCTTTGGTGATAGAGTCAGAAGATTTCAAGAGTTTTAGATAGAATTGATTCTAATACAGGTATAGAT
TACAGATCTATTATCAAAGATATGTTGATCAAGAGTAAGTTTAGATTGAGTGTTCATTTGATGAAATA
AGAGAGTTTGACAGAGAATTTGGTTGGGGTTGCTCAACCAGCCAGCTGACTATTTACCAGCTTGTGAA
AGAGCTTTGAGAGACACAGTTTTAGCTATTTACGACCCACAGGATCCAAGTTTCCACATGACAGTTAT
GACCCTAACAGCAATACTATTTATCATTCAAGGGAGCATTGGGGGACATTGCTCCTCCTAGATCG
ATTGATTCCAGCTATCTTTCCAAAATGGTTTCTATTGAAGGTATTGTGACTAGAGCTTCATTAGTTAGA
CCAAAGGTTATTAGATCGGTTTATTATGCTGAAAAAACTGGTAGATTTTATGCACGTGAATACCGAGAC
CAAACAACATCCTTTGATGCAATTGCTACTCCGGCTATATATCCAACCTGAAGATATGGAAGGTAATAAA
TTAACACACAGAGTATGGTTATTTCGACATACAGAGATTACCAGAAGATCTCTGTACAAGAAATGCCTGAA
ACAGCTCCTCCAGGTCAATTGCCAAGATCGGTTGACGTTATTTTGGATGATGATTGGTGGATTGACA
AAACCCGGTGATCGTGTACAAATTGTTGGTGTATTGCTGCTTAGGAGGTGCTGCAACAATAGTTCT
TCTTTCAAAACGGTTATCTTAAGTAATTCTGTTTACTTGTACATGCCAGATCAACAGGGGTTGCTTCA
CAAGAAAAGTTAACTGATCAAGATATTAGAAATATAAATAAACTTGCAAGGATAGAAAGATTTTGTAT
ATTTTATCCCGTTCTTTGGCCCCCTCAATTTATGGGTTTGAATATATTAAGAAAGCTGTTTACTTATG
ATGATGGGAGGTGTTGAAAAAATTTAGATAATGGTACACATTTGAGAGGTGACATTAACATTTGATG
GTGGGTGACCCATCCACTGCCAAATCTCAAGTATTACGGTTTGTGTTGAACACTGCTTCATTAGCTATT
GCCACTACTGGTAGAGGATCGTCAGGTGTAGGTTTAAACAGCTGCTGTTACTACCGACAAGGAAACAGGA
GAAAGAAGATTGGAGGCTGGTGCAATGGTATTGGCTGACAGAGGTATTGTTTGTATTGATGAATTTGAT
AAAATGTCAGATATCGACCGAGTGGCCATTACGAAGTTATGGAACAACAACTGTCACTATTGCTAAA
GCTGGTATTACACCTCATTGAATGCTCGTTGTTCTGTTATTGCTGCCGCAATCCGGTTTTTGGACAG
TACGATGTCCATAAAGATCCACATAAAAAATATTGCCCTTGCCCGATTCAATTATTGTCTCGTTTTGATTG
CTCTTTGTTGTTACAGATGATGTCAACCCAACAAGAGACAGGGTTATTTCTGAGCATGTTTAAAGATG
CACAGGTTTGTCTCTCGATTGATGGAGGGAGAGCCAATCAGAGAAAAATCAGCAGTTACATGGCT
GTCGGAGATGATGAACCAATGAACAAGAATTATTAGAACAGCCAATGTTTGA AAAAATTTAACACATTA
TTGCATGCTGGTATTCAAAAACAAAAGTCAAATATATACTTTTCGATTCCATTCTTGAAAAAATATGTC
CAGTACGCCAAGCAAGAGTGAACCAAGTGTGACCAAGGGTGCATCCGACTACATTGTTACTACATAT
TCCTCCTTAAGAAACGATTTGATAGGCAACAACCAAGAAATACAGCTCCAATAACTGCTAGAACTTTA
GAAACTTTGATTGCTTTAGCAACAGCTCATGCAAAAAGTCCGTTTATCCAAAACCTGTTGATGTGAAAGAT
GCAAAAAGTTGCCGAAGAGCTATTGAGATATGCATTATTCAAGGAAGTAGCCAAAAAGACAAAAAAGAGA
CAAAAAACTACAAGTATAGTGGACTCAGAAGAGGAGGAAGAGGATGAGTCTGATGCAGAAATGGAAAT
TCCGATAACGAAATAATGCCCAGAGAAAGTACTAGAAGAACAGAGCTACAGCACAAACACAGCCTCCA
CAACAGCAACAAGCATCTCCTTCACTAACACCCGAACCGCCACTTGGACATCGGGACGATGGAGATGAC
GATGGAGTTGGTGAAGAATTAGAACAATTCATTTGTCATCATCTCAGCAACAACAGCAACAACAATAT
TTGCAACCATTGACTGAGAGATCATCAAGTAACATTGTATCATCTACCGCCACAAATGCAATCAGCGTT
GAGAGATTGAATATTTTCAAAAAGAACTAGCCCAGGTGTCACGTTCTGCATTATTTGCCAATGATCAA
GCTGCGGCAAACTATCATGACGTTACTCGTGCTATCAATGAACAGATGGAACAAGAAGATATTTCTCA
GAGCAAGAGTTGAGTGCTGGATTGGAAGTGATGAGTTCTGAAAAACAAGTTTACCTAGAAAGTGATAAG
ATTTGGAAGATTTAA

YEL032W_homolog 878 aa public: 1..878 (SEQ ID NO 720)

MDERFLNPPPTADQDDTNQPLDAIFGDRVRRFQEFLLDRIDSNTGIDYRSIIKDMLIKSKFRLSVSIDEI
REFDREFWLGLLNQPADYLPACERALRDTVLAIYDPQDPSPHDSYDPNQYYLSFKGAFGGHSLTPRS
IDSSYLSKMSVIEGIVTRASLVRPKVIRSVHYAEKTGRFYAREYRDQTTSFDAIATPAIYPTEDMEGNK
LTTEYGYSTYRDYQKISVQEMPETAPPGQLPRSDVILDDDLVDLTKPGDRVQIVGVYRALGGAANNSS
SFKTVILSNSVYLLHARSTGVASQEKLTQDIRNINKLAKDRKIFDILSRSLAPSIYGFYIKKAVLLM
MMGGVEKNLDNGTHLRGDINILMVGDPSTAKSQVLRFLVNTASLAIATTTGRGSSGVGLTAAVTTDKETG
ERRLEAGAMVLADRGIVCIDEFDKMSDIDRVAIHEVMEQQTVTIAKAGIHTSLNARCSVIAANPVFGQ
YDVHKDPHKNIAPDSLLSRFDLLFVVTDDVNPTDRDRVISEHVLRMHFRVPPGLMEGEPIREKSAVTLA
VGDDDETNEQELLEQPMFEKNTLLHAGIQNKSNILSIPFLKKYVQYAKQRVQPVLTGKASDYIVTTY
SSLRNDLIGNNQNTAPITARTLETILRLATAHAKVRLSKTVDVKDAKVAEELLRYALFKEVAKKTKKR
QKTTSIVDSEEEEEDES DAEMENS DNEIMPRESTRRTRATAQTQPPQQQQASPSLTPEPPLGHRDDGDD
DVGVEELEQFHLSSSQQQQQQYLQPLTERSSSNIVSSTATNAISVERLNIKRI LAQVSRSA LFANDQ
AAANYHDVTRAINEDIQMEQEDIFSEQELSAGFEVMSSENKFYLESCKIWKI

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YHR135C_homolog 1488 bp public: 1..1488 (SEQ ID NO 721)

ATGACAACAAACCCCTGCTTTGGCGGCTGCTCAAGCATCTCATAATAATATTCCTACAAAGCAAATGAAT
CATTCAACTTCATCTTCAAACGGTAACGGTAGCAATAATTCATCCGTGGTTGGACTTCACTACAAGATT
GGGAAAAAAATTTGGTGAAGGTTCTTTTGGTGTCATTTTGAAGGTAATAATAATAATGGAGTACCC
GTGGCCATAAAATTTGAACCTAGAAAGACTGAAGCTCCTCAATTACGAGATGAATATAGAACCTTATAAA
CATTTACAAGGATGTGACGGAATTCCTAATGCATATTATTTGGTCAAGAAGGATTACATAATATTTTA
GTCATTGATTTATTGGGTCCTTCTTTAGAAGATTTATTTGATTGGTGTGGTAGAAGATTTAGTGTATAA
ACCGTGGTACAAGTTGCTATACAAATGTTGACTTTAGTAGAAGAAGTTTCATCGTCATGATTTAATCTAT
AGAGATATCAACCCGACAATTTTTTAATTTGGAAGAAGAGGTGCTACTGATGAAAATAATGTTTCAATTTG
ATTGATTTTGGTATGGCCAAGCAATATCGTGATCCAAGAACAAGCAACATATTCATATAGAGAGAAG
AAATCTTTGAGTGGGACAGCTAGATATATGAGTATTAACTCATTTAGGAAGAGAACAATCAAGAAGA
GATGATTTAGAAGCATTGGGTGATGATTTTTTTTTTATTTCCCTTAGAGGCCAATTACCTTGGCAAGGTTTA
AAAGCTCCCAACATAAACAAGTATGAGAAAATTTGGTGATAAAAAGAGAACTACACCAGCAGTTACA
TTATGTGATGGCTTACCTCAACAATTTGCTGAATATTTAGATTTCAGTTAGATCATTACCATTGTGATGCT
GAACCTCCATATGAAGAATATAGAATGTTATTATTGTGAGTGTGGATGATTTGGGTCAAGCTTGTGAT
GGAGATATGGATTGGATGCATCTTAATGGTGGTAGAGGTTGGGATGCTACAATTAATAAAAAACCCAAC
TTGCACGGTTATGGACATCCTAATCCACCAATGAACGTGAAAGAAGACATCGTGATCAAAGAAGAACA
AGACAACATCAACAACGTGCAACAAGTACAACAACAACAAATTACAAGCTCAAGCTCAAGCACACAATTA
CAACAATTACAACAAGCACAAACAGGCACAACAACAACAACATGCAACAACATCAACCACATCTGCA
GCCAGTTACATCAACAAAATTAACAGCATTGGTTAATCGACCATTACCACCAATTAAACAAGAATCA
CAATCAGCAATACAAAGTGGTAATGGACATCATGAACCTTTGAATAATAATTTAGGTGATCAGCATGGA
GGAAACATGAAGGATACAGTTCACGACCAGATCAATATCAACAACAACAATGGTTGCCGAAGAAGAA
GAAAACAAGGGTCTGGTCTAAATTGTGTTGTCATTAG

YHR135C_homolog 495 aa public: 1..495 (SEQ ID NO 722)

MTNPNALAAAQASHNNIPTKQMNHSTSSSNGNSNNSSVVGLHYKIGKKIGEGSFGVIFEGTNIINGVP
VAIKFEPRKTEAPQLRDEYRTYKHLQCGDGI PNAYYFQGEGHLNLI LVIDLLGPSLEDLFDWCGRRF SVK
TVVQVAIQMLTLVEEVHRDLIYRDIKPDNFLIGRRGATDENNVHLIDFGMAKQYRDPRTKQHIPYREK
KSLSGTARYMSINTHLGREQSRDDLEALGHVFFYFLRGQLPWQGLKAPTNNKQKYEKIGDKKRTT PAVT
LCDGLPQQFAEYLD SVRSLPFD AEPPEYERMLLSVLDDLQACDGDMDWMHLNGGRWDATINKKPN
LHGYPHPNPPNERERRHRDQRRTRQHQSSQQVQQQQLQAQAQAQQLQQLQAQAQAQQQQSQHQPLSA
AQLHQKLQHLVNRPLPPIKQESQSAIQSGNGHHELLNNNLGQHGKGHEGYSSRPDQYQQQQMVAEE
ENKGFWSKLCCH

YJL060W_homolog 1362 bp public: 1..1362 (SEQ ID NO 723)

ATGTTAAGACGGCTCTTTCCAATACGACAATTGTACACAACAAC TAGAGCCATGGCCAGCAAATCAACA
GACCCAAC TAGTTTGCATAATCCGTATTTTATCAAAAACCGGGGCAAAAAGATATCTGGTCGTTAATC
AACGAAACTGCGGCCAGGCACAACAAGAATCCGGCGAGCCAATTGTCAATTTGGGACAAGGGTTTTTC
TCCTACAATCCTCCTGAGTTTGCGATTAACGCTGTTGAGGAAGCATTGACCAAGCCGCAATTC AACCAA
TATGCACATGCTCGTGGAACCCAAACTTATTGAAACAAGTGGCAGAGCACTATTTCGCGATCGTATGGA
CGTGCTGTGGGGTTGACGAGGTCCAAATCACCACGGGTGCAATGAGGGAATGTTTGCCATTTTCTTT
GGTTTCTTGACCCCGGGCGATGAAGTCATTGTGTTTGAACCATTTTTTGACCAATACATCCCCAATGTT
GAAATGACAGGAGCCAAGATCAAGTACGTTGAAATCAAGTATCCCAAGAAATTTGACAACGAGGTGTGTC
ACGGGCCAGGATTGGGAGATTGACTGGGAAGGATTGAATAATGCCATTACCGACAAGACCAAGATCATC
GTGATAAATACCCACACAACCAATCGGCAAGTTTTCACCGAGAAGGAGTTGTACAAGATTGGCAAG
CTTGCCGTGGAACACAATTTAATCCTTGTCAGCGACGAGGTTTACGAGAAGCTTGATTATACTGACAAG
TTCCCTCGTCCAGCTGCATTACCACAGTTGCCTGAATTGGCTGAAAGGACGTTGACAGTGGGTTCTGCT
GGGAAATCATTTGCTGCCACTGGTTGGAGAGTAGGGTATATCCAGGGCCCTGCCAATTTGATTAAATTT
GTAACAGCGGCCACACCAGAAATTTGTTTCTCGACCCACGACCATTGCAACAGGCAGTATCTCAGGGG
TTTGAGCAGGCTGAGAAATCAAACTATTTTGAGAACTCGAAAGGAGTATGAACACAAATACAAAATA
TTCACCAAGGTATTTGACGACTTGGGGTTACCTTACACCGTTGCCGAAGGAGGTACTTTGTGTTGGTG
AACTTGCTGAAAGTTAAGATACCCGACAGATTATGAGTTTCCCGGAACCATCAGCGATAGAGGCACTTTA
GATTTCAAATTTGGCGTATTTGGTTGATCAAAGAAATTTGGGGTTGTGGGAATCCCTCCAACAGAGTTTTTA
ACCGAATCGAATAGAAAGGGGAACGGCTTAGAAAATTTGTGTCAGATTTGCTGTTTGCAAGATGATTCT
GTTTTAGAAGACGCGGTTGAGAGATTGAAAAAATTTAAAGACTATTTATAA

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YJL060W_homolog 453 aa public: 1..453 (SEQ ID NO 724)

MLRRLLFPIRQLYTTTRAMASKSTDPTSLHNPYFYQKPGQKDIWSLINETAQAQQAQESGEPIVNLGQGFF
SYNPPEFAINAVEEALTKPQFNQYAHARGNPNLLKQVAEHYSRSYGRAVGVDDEVQITTGANEQMFALFF
GFLTTPGDEVIVFEPFFDQYIPNVEMTGAKIKYVEIKYPKKFDNEVVVTGQDWEIDWEGLNNAITDKTKII
VINTPHNPIGKVFTTEKELYKIGKLAVEHNLILVSDEVYENLYYTDKFFRPAALPQLPELAERTLTGSA
GKSFAATGWRVGYIQGPANLIKVFVTAHTRICFSTPAPLQQAQVSGQFEQAESNYFENTRKEYEHKYKI
FTKVFDLGLPYTVAEGGYFVLVNLKVKIPADYEFPGTISDRGTLDFKLAYWLIKEIGVVGIPPTFL
TESNRKGNLENCVRFVAVCKDDSVLEDAVERLKKLKDYL

YML028W_homolog 591 bp public: 1..591 (SEQ ID NO 725)

ATGGCTCCAGTCGTTCAACAACAGCTCCAAGTTTCAAGAAAACCGCCGTCGTTGATGGTGTCTTTGAA
GAAGTCACTTTAGAACAAATACAAAGGTAAATGGGTCTTGTGTCCTTTATTCCATTGGCCTTCACATTC
GTCTGCCCATCAGAAATTATTGCTTATCCGAAGCTGTAAAGAAATTTGCCGAAAAGGATGCTCAAGTT
TTGTTTGCCTCTACTGACTCCGAATACACCTGGTTGGCTTGGACCAATGTCGCCAGAAAAGACGGTGGT
ATTGGCAAAGTCGACTTCCAGTCTTGGCTGACACCAACCCTCTTGTCCAGAGACTACGGTGTCTTA
ATTGAAGAAGAAGGTGTTGCCTTGAGAGGTATTTCTTGATTGATCCAAAGGGTGTCTTGAGACAAATC
ACCATCAATGACTTGCCAGTCGGTAGATCTGTTGAAGAATCCTTGAGATTGTTGGAGGCTTTCCAATTC
ACTGAAAAATACGGTGAAGTTTGTCCAGCTAACTGGCACCCAGGTGATGAAACCATCAAGCCAAGCCCA
GAAGCATCCAAGGAATACTTCAACAAAGTCAACAAATAA

YML028W_homolog 196 aa public: 1..196 (SEQ ID NO 726)

MAPVVQQPAPSEFKKTAVVDGVFEVTLQYKQKWLAFIPLAFTFVCPSEIIAYSEAVKKFAEKDAQV
LFASTDSEYTWLAWTNVARKDGGIGKVDFPVLADTNHSLSRDYGVLIEEGVALRGIFLIDPKGVLRQI
TINDLPVGRSVEESLRLLEAFQFTEKYGEVCPANWHPGDETIKPSPEASKEYFNKVNK

YOL100W_homolog 2835 bp public: 1..2835 (SEQ ID NO 727)

ATGCATAAATTTAGATATTTCTTTCACCAACACTATAGCAAACGCAATTCAAGTGACAAAATCCAAAGAC
AGTCCAATTAGCCAAAACAGCAATGAAGAAAATGATTGCGACTAAATTAAGTTCAAGTAGTCTTCAAGAC
TTACATGATGATCTCGATGATATTTATAACAACCTATACTTTAGCACAGGGTACCAATAACAACAGTGTA
GATACATTGGATTCTGAAAATAATCAAGCTATAAATAAGTTTATTGATAAACCTCCAGCAATTCATGGT
ATGGAACCACAACCTACCGGTGATGCACGTTTCTTCACGATTATCTTCTTAGGTAATACCACCAATGAA
ACCGGTGAAAGCATCGCCAAAAGTGCACCAGGAACCTCCGTATCTTCACATTCATTTGATTTTCAGACCG
CATCATCTCTCGTCAGTAACAACTCATCCCTCAATGTATTTGTTAGACACCCCTAATGTCAGTTCCGAA
TTCAATCATTTAGTGGATCAAACACCACCAATGAGTCGGTAGAAAGGTTTGACGACAGTAATAATACT
GTGGACAATACAGAAGAGGAAGAAAATAATGATGATACAGACGAAATACCAAAATCCGAAACATTTGAAA
CAAAACGAGGAGAAATTTGGGAAAAAAGGGTGCTGCAAGTTAAACTATCAAGACTATGGATGGAGAAATG
AAAACATTTCCGCGAAATGTTACTGATTTCAAATTTGGTAAAGAATTTGGGTGAAGGTTTCATATTCCACG
GTGATTTTAGCCACTGATAAGATTACTGGTAAACAATATGCTGTAAAGTACTTGATAAGCGACATATT
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GGGGTTATTTTCATTATATTTACCTTCCAGGATAAAGATTGCTTTATTTTGTGTTTGGATTATGCTTCA
AATGGTGAATTTATGACATTGATCAAGAGATACAATACTTTAAATGAGGAATGTACTAGACATTTTGGT
GCACAAATATTAGATGCTATTAATATATGTCATGATAATGGTGTATACATCGAGACCTAAACCAGAG
AATATATTATTAGATGACAAAATGAGAATTCAAATTTACAGATTTTGGTACTGCAAGATTATTAGAGAAA
AAGAATGATGAAAGTGAAGAATACCCAGTGGATGTAAGAGCAAAATCATTGTTGGAACCGCTGAATAT
GTATCCCCGTAATTATTAGAAAATAAGTATTGTTGGTAAACCTGGAGATGTTTGGGCTTTTGGTTGCATC
ATATATCAAATGATTGCTGGGAAACCACCAATTAAGGCAACTAATGAATATTTAACGTTTCAAAAAATT
ACGAAATTGCAATTTGCGTTTAGTGACAGATTCCCTACAATTTATTAGAGATTTAATAAAGAAGATTCTT
GTGTTGCAACCTTCACGACGTGCCACCAATCCAGAAATACAAAAACATTACTTTTCCAATCGGTGAC
TTTAAAGATTTTGATCTGATTTGGTTGTCTGATCCTCCTGAAATAGGACCTTATAAAATGACAGCAAAA
TCCATGATGAAAGTACCGGAATTGAATAAGGCACCTATAACCACAGTCATTAAAGAAGATGTGAAGAAA
TCCACAACTCAAATTCAAATACCAACAATGTCGCCACTGCTGTTGGTGGTAGTAGTAGTAACGGACAT
AAAGGGTCATCACCGACTCCTGAGAAAGAGCCGAGCCAGCTACTATTAAATAACAAGTCCACAGAAAAA
GTTAGTGCCGCTAGTGTAGCTGCATATGTTTTAAACAAACCAGCTACAAACCAAAATTCAGTACATCC
GAGGATTTCATCTAAGCGTAGCAGCAACTCCAATGAAACTCGAAACTTTTCATATTCACAACAGGATTAT
ATTCCGGGAACAAATATTTTACGTCCACAGATTAGTACTAGACCGTCAGTAGGATCTTATGTGAAACC
ACACCATCAAAGGATAGAAAAACATTAACCAAGGTCCCACTGAATATCCATCAACAACAAGAAAAAGTG

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AAACCGAAAAGTAATGGAAGTGAAGCCAGCAACTACATTGGAAGCAGCATGGGAACCATATTTAACCCAT
CCAGATGAAAGAATACCTTCGTATTGGTCCAGTTATTGCTCATAAAGAACCAACAGAACCATTGTGAAAAG
AAGAATAAAGCATCTTTACATATATCACCTTTGGATATAAATAAAGAACAAAGAAGTAGATCCAATACT
AGTTTACTTTACACAAATTGTAATGAAGTAAACAATAACACCAGCGAATTGAAAAAAGTGGAATAATGCT
GATGAATCACTTGCCATTATTGAACCACAATATAATATGAAGAGAAGTCCAACCTCTGATAGTAAGAAA
AGTATGGATATTGAAAGATCTGCATCTACTTCTGGAAGTAGAATTAGTAAGAAGGCAATTTTCAAAAAA
TTGGGGTTTGTATCATTTAGAAAAAATGATAGTGAAGAATCAAATGGTCCTAGTTTAACGGAAAAACCA
CAAACCTGTACATTGGTTGTTACAACCTCATGGTCGAGCATTACTTTTCATTAGAAATGATATAGAAATCC
AATTATCTTTTAATTGCTGAAATCAAATTGAAATATCCATTTATTCATTTCGAAGAAATAGTTATATCA
CAAACATAAATTTCTAAATTAGTACCATCAGTCGGAGTATTTGTCATTAGTTCAATTGATAAATTCATTA
ATTTTTGAAGTAGAAAAATTTGAAGTGAATCAATGGACTGAAGCATTAGCTAAATCTAAATATAATGAA
ATATAA

YOL100W_homolog 944 aa public: 1..944 (SEQ ID NO 728)

MHKFRYSLHQHYSKRNSDKSKDSPISQNSNEENDSTKLSSSSLQDLHDDLDDIYNNYTLAQGTNNNSV
DTLDSENNQAINKFIDKPPAIHGMEPQLPVMHVSSRLSSLGNTTNETGESIAKSAPGTPLSHSPDFRP
HHPRAVTNSSLNLVLLDTPNVSSSEFNHLVDQTPPNESVERFDDSNNTVDNTEEEENNDTDEIPKSETLK
QNEENWEKKGAAVKTIKTMDGEMKTIIRNVTDFFKFGKELGEGSYSTVILATDKITGKQYAVKVLDRHI
IKEKKVKYVNIKHALNRLSNRLGVISLYFTFQDKDSLYFVLDYASNGELLTLIKRYNTLNEECTRHFG
AQILDAIKYMHNGVHIRDLKPENILLDDKMRIQITDFGTARLLEKKNDESEYYPVDVRAKSFVGTAEY
VSPellenKYCGKPGDVWAFGCIITYQMIAGKPPFKATNEYLTFFQKITKLQFAFSAGFPTIIRDLIKIL
VLQPSRRATIPEIQHYFFQSVDFKDFDSIWLSDPPEIGPYKMTAKSMMKVPELNKAPITTVIKKNVKK
STNSNSNTNNVATAVGGSSSNHGKSSPTPEKEPSPATINNKSSTEKVSAASVAAYVLNKPATNQNSSTS
EDSSKRSSNSNETRKLSSYSQDYIPGTNILRPQISTRPSVGSYVKTTPSKDRKTLTKVPSNIHQQEKV
KPKVMEVKPATTLAAWEPLYLTHPDERILRIGPVIAHKEPTEPFKKNKASLHISPLDINKEQRSRSNT
SLLTQIVNEVNNNTSELKKVENADESLAIEPQYNMKRSPTSDSKKSMDIERSASTSGSRI SKKAIFFK
LGFSHLEKNDSEESNGPSLTEKPQTCTLVVTTTHRALLFIRNDIESNYLLIAEIKLKYPFIFHQELVIS
QTKFSKLVPSGVFVISSIDNSLIFEVEKFEVNVQWTEALAKSKYNEI

YJL166W_homolog 288bp Pathoseq: 1..288 (SEQ ID NO 729)

ATGGCAGGTGCACCACATCCACATACTTATATGGGCTGGTGGGGTAGTTTAGGCTCCCCAAAGCAAAAA
TATATTACTCAATATACTATTTCTCCATATGCTGCTAAACCATTAAAGGGGGCTGCTTATAATGCTGTT
TTCAATACTTTTAGAAGAACCAAGAATCAATTTCTTTATGTTGCCATTCCATTGTTGTTGTTTGGAGT
ATTTGGACTAGAGCTAGAGATTATAATGAATACTTGTACACTAAAGAAGGTAGAGAAGAATTGGAAGA
GTTAATGTTTAA

YJL166W_homolog 95aa PathoSeq: 1..95 (SEQ ID NO 730)

MAGAPHPHTYMGWWSLGSPKQKYITQYITISPYAAKPLKGAAYNAVFNTRRTKNQFLYVAIPFVVVWS
IWTRARDYNEYLYTKEGREELERVNV

YLR038C_homolog 252bp PathoSeq: 1..252 (SEQ ID NO 731)

ATGCCAGTCGATCCAGCTACTTTTAAATTCGAAACTCCACAATTTGACCCAAGATTCCTCAAACCAAAAC
CAATCCAAACATTGTGCTCAAGCCTACGTGATTACCACAAATGTGTCAATGTGAAAGGTGAAGAATTT
GAACCATGCAAAATCTTTTCAAAACTTTCACTTCATTATGTCTTTGGATTGGGTCGAAAAATGGGAT
GATCAAAGAGCTGCTGGTAAATTTCCAGTCAACATGGACGCTTAG

YLR038C_homolog 83aa PathoSeq: 1..83 (SEQ ID NO 732)

MPVDPATFKFETPQFDPRFPNQNSKHCAQAYVDYHKCVNVKGEEFEPCKIFFKTFTSLCPLDWVEKWD
DQRAAGKFPVNMDA

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Human homologues

>YGL080W_homolog, CDS: 1-330 bp (SEQ ID NO 675)

ATGGCGGGCGCGTTGGTGCGGAAAGCGGCGGACTATGTCCGAAGCAAGGATTTCCGGGACTACCTCATG
AGTACGCACTTCTGGGGCCCAGTAGCCAACTGGGGTCTTCCCATTGCTGCCATCAATGATATGAAAAAG
TCTCCAGAGATTATCAGTGGGCGGATGACATTTGCCCTCTGTTGCTATTCTTTGACATTTCATGAGATTT
GCCTACAAGGTACAGCCTCGGAAGTGGCTTCTGTTTGCATGCCACGCAACAAATGAAGTAGCCAGCTC
ATCCAGGGAGGGCGGCTTATCAAACACGAGATGACTAAAACGGCATCTGCATAA

>YGL080W_homolog, 109 aa (SEQ ID NO 676)

MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGRMTFALCCYSLTFMRP
AYKVQPRNWLLFACHATNEVAQLIQGGRLIKHEMTKTASA

>YGR243W_homolog, CDS: 1-384 bp (SEQ ID NO 677)

ATGTCGGCCGCCGGTGCCCGAGGCCTGCGGGCCACCTACCACCGGCTCCTCGATAAAGTGGAGCTGATG
CTGCCCAGAAATTGAGGCCGTGTACAAACCATCCAGCAGGTCCAGAACAGTTTTCTTCTGGGCTCCA
ATTATGAAATGGGGGTTGGTGTGTGCTGGATTGGCTGATATGGCCAGACCTGCAGAAAACTTAGCACA
GCTCAATCTGCTGTTTTGATGGCTACAGGGTTTATTTGGTCAAGATACTCACTTGTAATTATTCCAAAA
AATTGGAGTCTGTTTGCTGTFAATTTCTTTGTGGGGGCAGCAGGAGCCTCTCAGCTTTTTCGTATTG
AGATATAACCAAGAACTAAAAGCTAAAGCACACAAATAA

>YGR243W_homolog, 127 aa (SEQ ID NO 678)

MSAAGARGLRATYHRLLDKVELMLPEKLRLPLYNHPAGPRTVFFWAPIMKWGLVCAGLADMARPAEKLST
AQSAVLMATGFIWSRYSLVIIIPKNWSLFAVNFFVGAAGASQLFRIWRYNQELKAKAHK

>YGR183C_homolog, CDS: 1-399 bp (SEQ ID NO 679)

ATGGCGGCCGCGACGTTGACTTCGAAATTGTACTCCCTGCTGTTCCGCAGACCTCCACCTTCGCCCTCA
CCATCATCTTGGCGTCATGTTCTTCGAGCGCGCCTTCTCAAGGCGCGGACGCTATCTACGACCACA
TCAACGAGGSAAGCTGTGGAAACACATCAAGCACAAAGATGAGAACAAGTAGTTCCCTGGAGGCCCCC
ATCCAGGCCAGAAGGACCAGGTCCACCCAGCAGCTGTTTCCCCAGAGCTGGAGCCTCAGCTTGAAGATG
ATGCTCAAGGTACTCTTCATGGACCACCATTCGCTGTTGGCAAGAAACGGCTTTACTTACAAAACAGAC
TCTTTACCTTCTGCTGTGTTTGAAGTATGTTTAGTCAGCATGCTCAGGAAATAA

>YGR183C_homolog, 132 aa (SEQ ID NO 680)

MAAATLTSKLYSLFRPPPPSPSSWASCSSSAPSIKARTLSTTTSTRGSCGNTSSTSMRTSSSLEAP
IQARRTRSTQQLFAQSWSLSLKMMLKVLMDHHSLLARNGFTYKTDSLPSAVFEVCLVSMRLK

>YBR009C_homolog, CDS: 1-312 bp (SEQ ID NO 681)

ATGTCGCGCCGCGCAAAGGCGGGAAGGGTCTTGGCAAAGGCGGCGCTAAGCGCCACCGTAAAGTACTG
CGCGACAAATATCCAGGGCATACCAAGCCGGCCATCCGGCGCCTTGCTCGCCGCGGCGGCGTGAAGCGC
ATCTCCGGCCTCATCTACGAGGAGACTCGCGGGTGTGTAAGGTGTTCTGGAGAACGTGATCCGGGAC
GCCGTGACCTATACAGAGCACGCCAAGCGCAAGACGGTCACCGCCATGGATGTGGTCTACGCGCTCAAG
CGCCAGGGCCGACCCCTCTACGGTTTCCGTGGTTGA

>YBR009C_homolog, 103 aa (SEQ ID NO 682)

MSGRGKGGKGLGKGGAKRHRKVLDRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRD
AVTYTEHAKRKTVTAMDVVYALKRQGRITLYGFGG

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>YGR209C_homolog, CDS: 1-318 bp (SEQ ID NO 683)

ATGGTGAAGCAGATCGAGAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAACTTGTA
GTAGTTGACTTCTCAGCCACGTGGTGTGGGCCTTGCAAAATGATCAACCCCTTCTTTTCATTCCCTCTCT
GAAAAGTATTCCAACGTGATATTCCCTTGAAGTAGATGTGGATGACTGTCAGGATGTTGCTTCAGAGTGT
GAAGTCAAATGCACGCCAACATTCCAGTTTTTTAAGAAGGGACAAAAGGTGGGTGAATTTTCTGGAGCC
AATAAGGAAAAGCTTGAAGCCACCATTAATGAATTAGTCTAA

>YGR209C_homolog, 105 aa (SEQ ID NO 684)

MVKQIESKTAFQEALDAAGDKLVVVDVSATWCGPCKMINPFFHSLSEKYSNVIFLEVDVDDCQDVASEC
EVKCTPTFQFFKKGQKVGEFSGANKEKLEATINELV

>YPR028W_homolog, CDS: 1-594 bp (SEQ ID NO 685)

CCGAGCGGCGAGACGGTCCCCGCCATGTCTGCGGCCATGAGGGAGAGGTTGACCGGTTCTGACGAG
AAGAACTGCATGACTGACCTTCTGGCCAAGCTCGAGGCCAAAACCGGCGTGAACAGGAGCTTCATCGCT
CTTGGTGTGATCGGACTGGTGGCCTTGTAACCTGGTGTTCGGTTATGGAGCCTCTCTCCTCTGCAACCTG
ATAGGATTTGGCTACCCAGCCTACATCTCAATTAAAGCTATAGAGAGTCCCAACAAAGAAGATGATACC
CAGTGGCTGACCTACTGGGTAGTGTATGGTGTGTTGAGCATTGCTGAATTCCTCTCTGATATCTTCCTG
TCATGGTTCCCTTCTACTACATACTGAAGTGTGGCTTCCTGTTGTGGTGCATGGCCCCGAGCCCTTCT
AATGGGGCTGAACTGCTCTACAAGCGCATCATCCGTCCTTTCTTCCTGAAGCACGAGTCCCAGATGGAC
AGTGTGGTCAAGGACCTTAAAGACAAGGCCAAAGAGACTGCAGATGCCATCACTAAAGAAGCGAAGAAA
GCTACCGTGAATTTACTGGGTGAAGAAAAGAAGAGCACCTAA

>YPR028W_homolog, 197 aa (SEQ ID NO 686)

PSGETVPAMSAAMRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFYGYASLLCNL
IGFGYPAYISIKAIESPKNEDDTQWLTYWVVYGVFSIAEFFSDIFLSWFPFYIILKCGFLLWCMAPSPS
NGAELLYKRIIRPFFLKHESQMDSVVKDLKDKAKETADAITKEAKKATVNLLGEEKKST

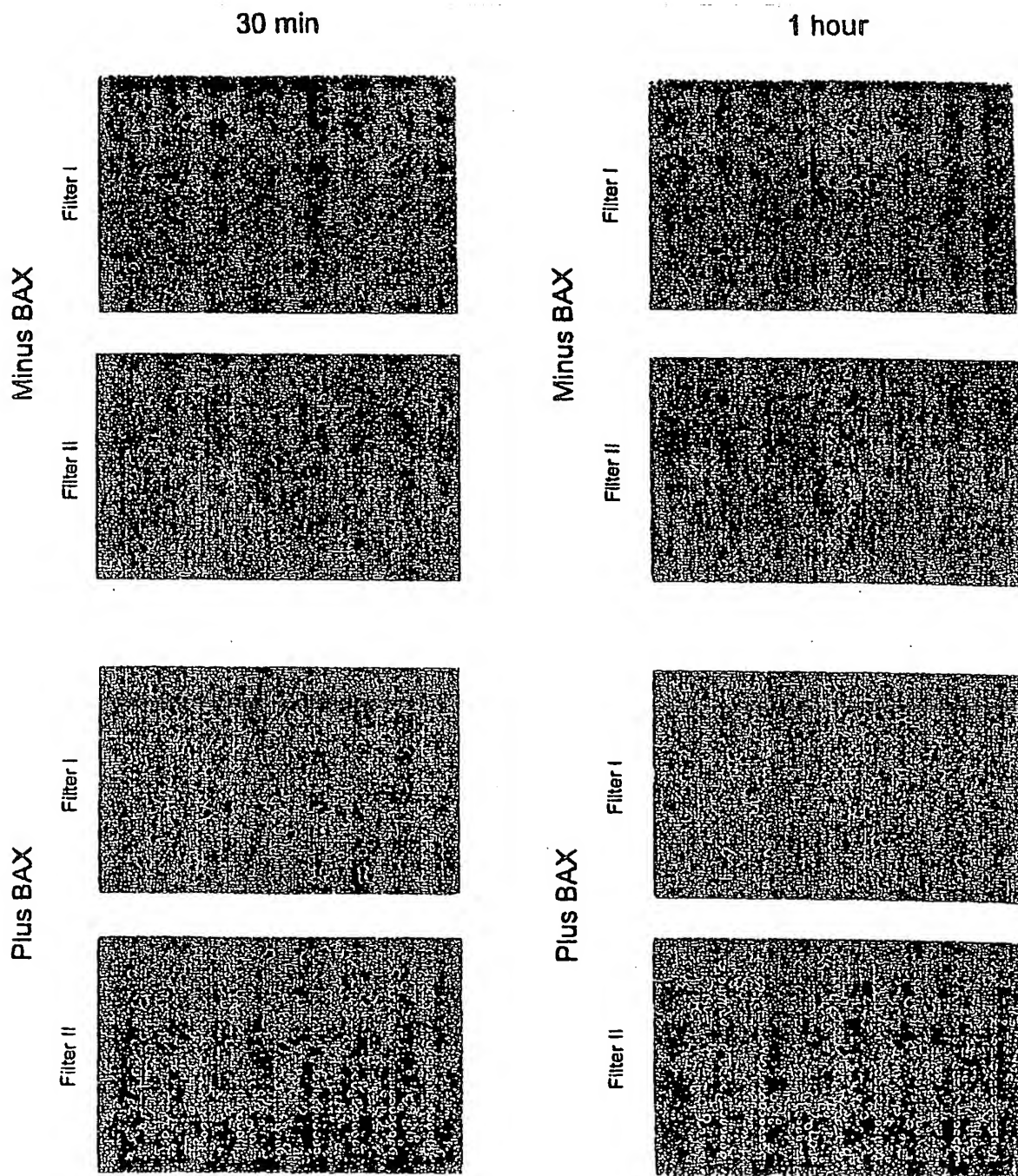
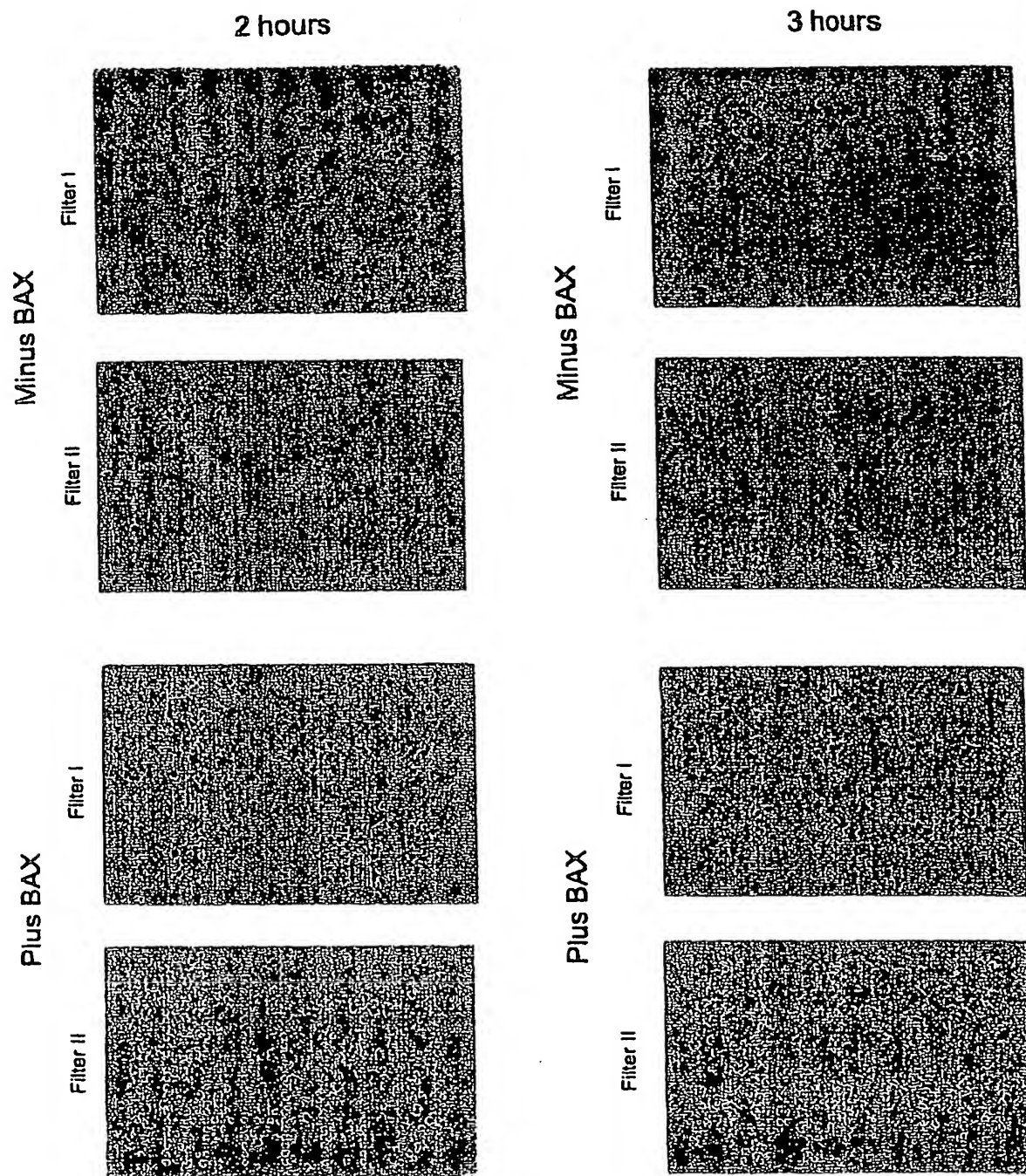


Figure 3 - 1



Figuur 3 - 2

6 hours

Minus BAX

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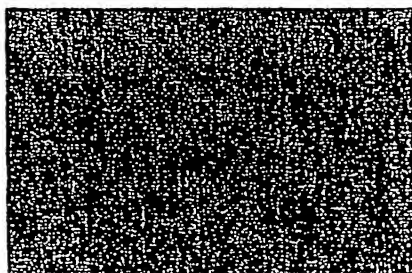


Filter II



Plus BAX

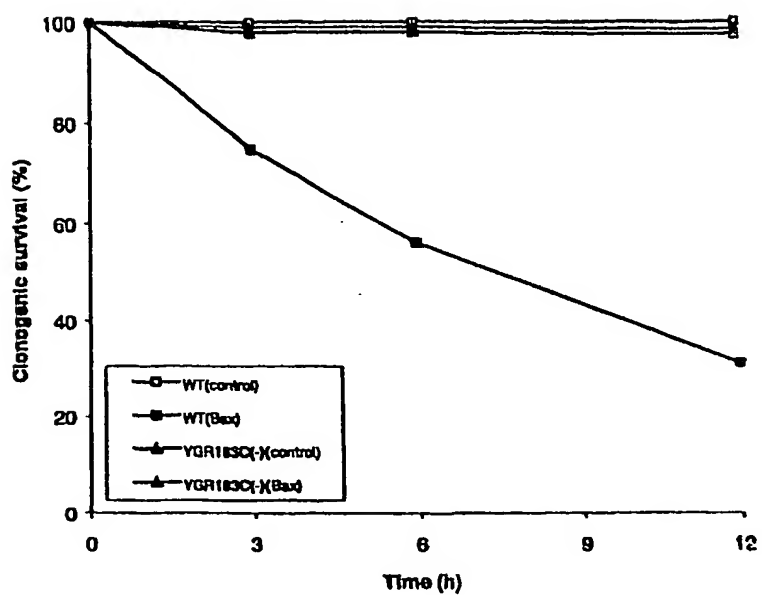
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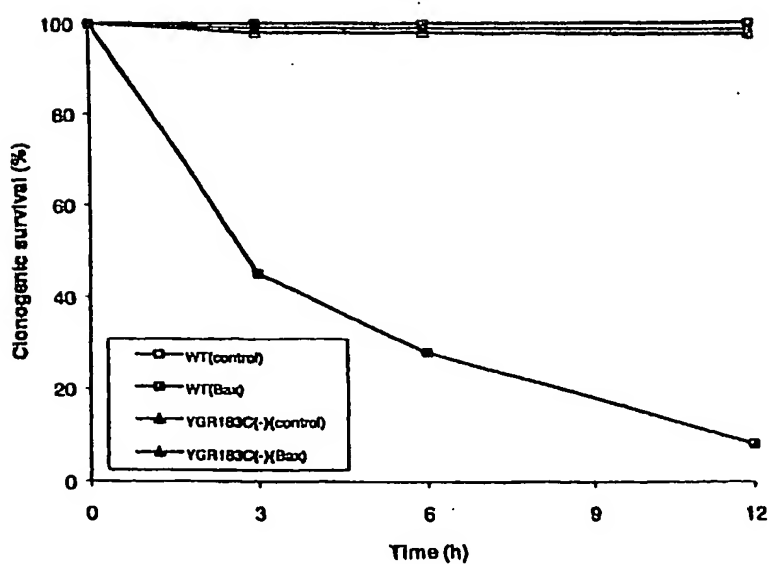
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Figuur 3 - 3



(A)



(B)

Figure 4

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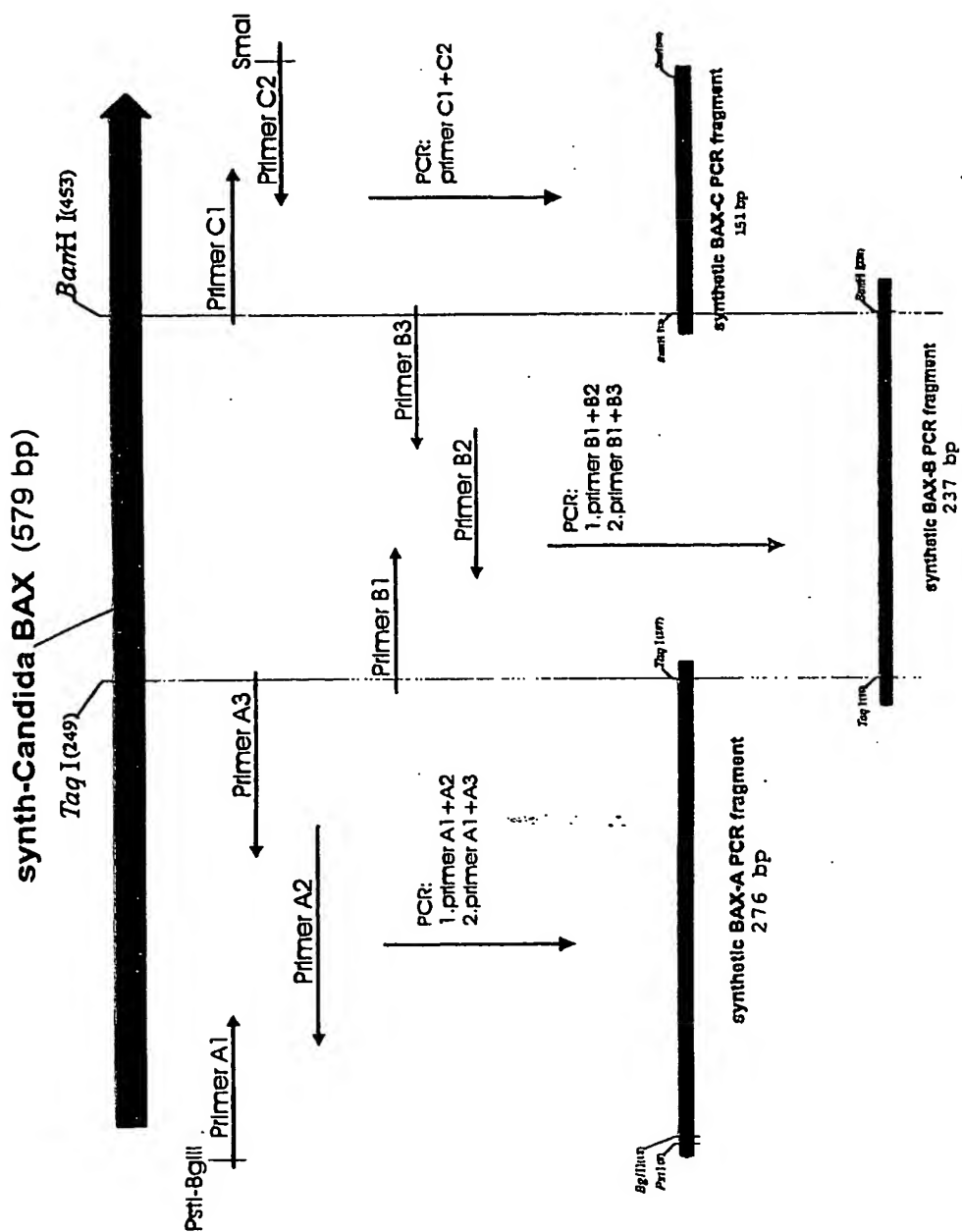


Fig. 5

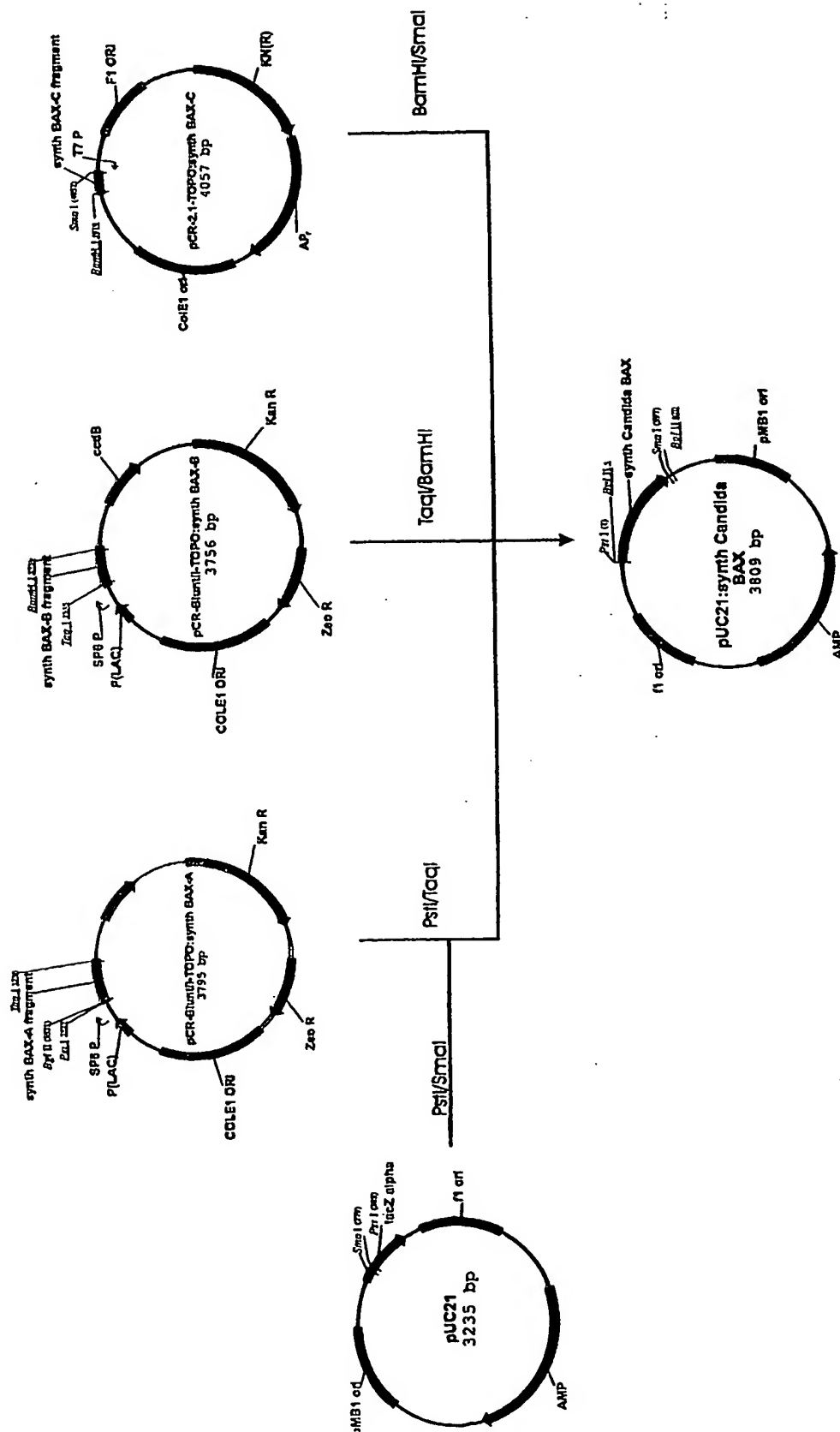


Fig. 5. Continued

Met Asp Gly Ser Gly Glu Gln Leu Gly Ser Gly Gly Pro Thr Ser Ser Glu Gln Ile Met
1 ATG GAT GGT TCT GGT GAA CAA TTG GGT TCT GGT GGT CCA ACC TCT TCT GAA CAA ATC ATG

Lys Thr Gly Ala Phe Leu Leu Gln Gly Phe Ile Gln Asp Arg Ala Gly Arg Met Ala Gly
61 AAA ACC GGT GCT TTC TTG TTG CAA GGT TTC ATC CAA GAT AGA GCT GGT AGA ATG GCT GGT

Glu Thr Pro Glu Leu Thr Leu Glu Gln Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser
121 GAA ACC CCA GAA TTG ACC TTG GAA CAA CCA CCA CAA GAT GCT TCT ACC AAA AAA TTG TCT

Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
181 GAA TGT TTG AGA AGA ATC GGT GAT GAA TTG GAT TCT AAC ATG GAA TTG CAA AGA ATG ATC

Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala Ala Asp Met Phe
241 GCT GAT GTC GAT ACC GAT TCT CCA AGA GAA GTC TTC TTC AGA GTC GCT GCT GAT ATG TTC

Ala Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala Leu Phe Tyr Phe Ala Ser Lys Leu
301 GCT GAT GGT AAC TTC AAC TGG GGT AGA GTC GTC GCT TTG TTC TAC TTC GCT TCT AAA TTG

Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr
361 GTC TTG AAA GCT TTG TGT ACC AAA GTC CCA GAA TTG ATC AGA ACC ATC ATG GGT TGG ACC

Leu Asp Phe Leu Arg Glu Arg Leu Leu Val Trp Ile Gln Asp Gln Gly Gly Trp Glu Gly
421 TTG GAT TTC TTG AGA GAA AGA TTG TTG GTC TGG ATC CAA GAT CAA GGT GGT TGG GAA GGT

Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val
481 TTG TTG TCT TAC TTC GGT ACC CCA ACC TGG CAA ACC GTC ACC ATC TTC GTC GCT GGT GTC

Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly (SEQ ID NO 2)
541 TTG ACC GCT TCT TTG ACC ATC TGG AAA AAA ATG GGT TAA (SEQ ID NO 1)

Fig. 6

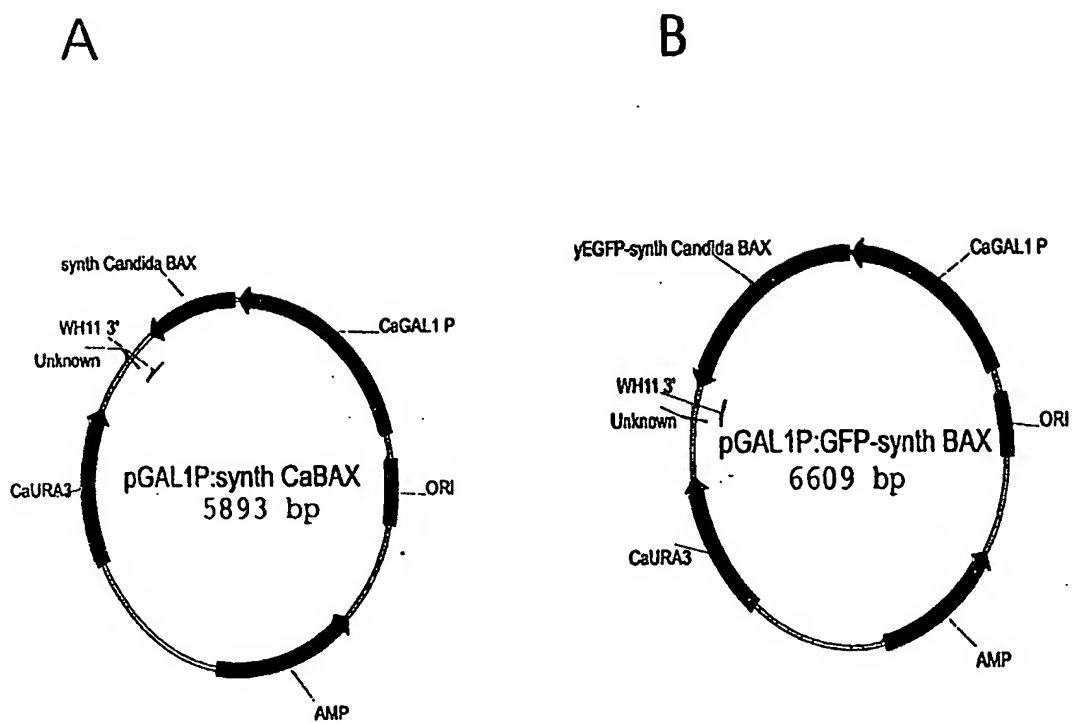


Fig. 7.

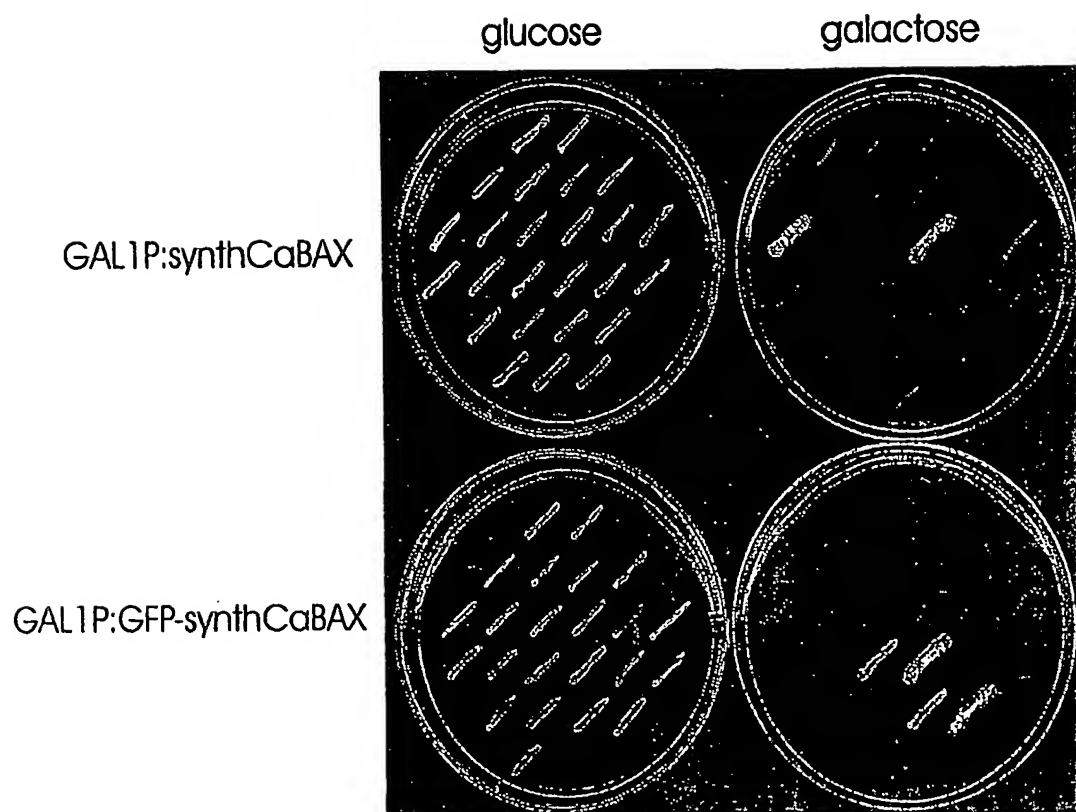


Fig. 8.

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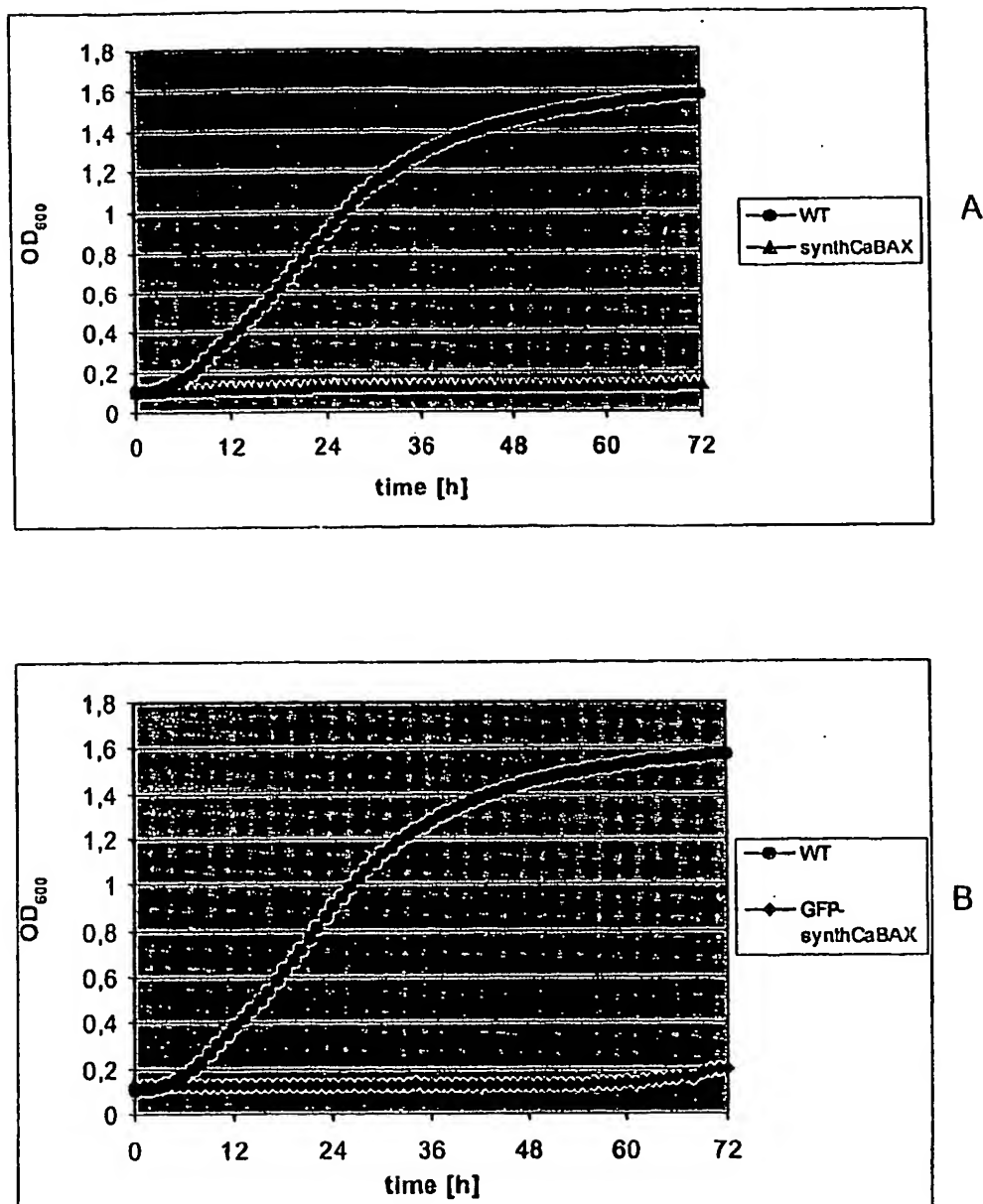


Fig. 9.

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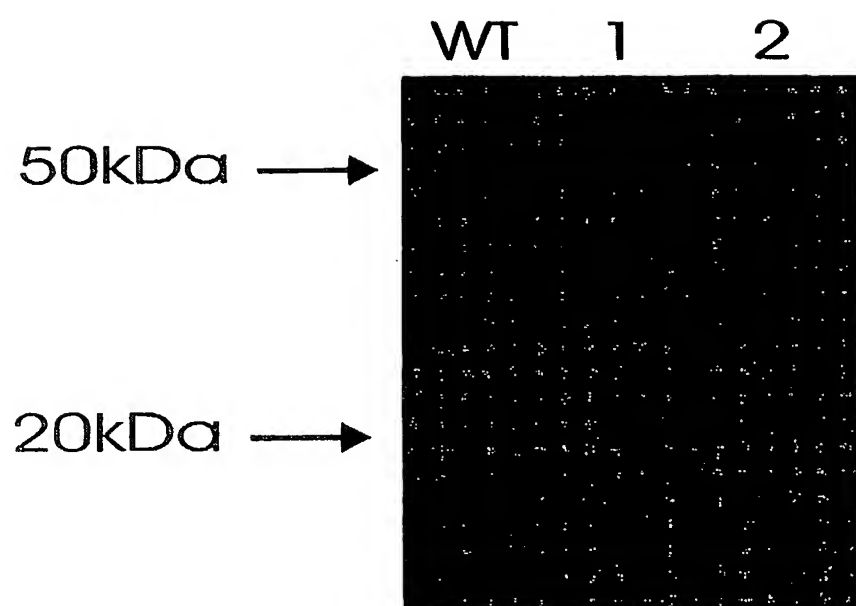


Fig. 10.

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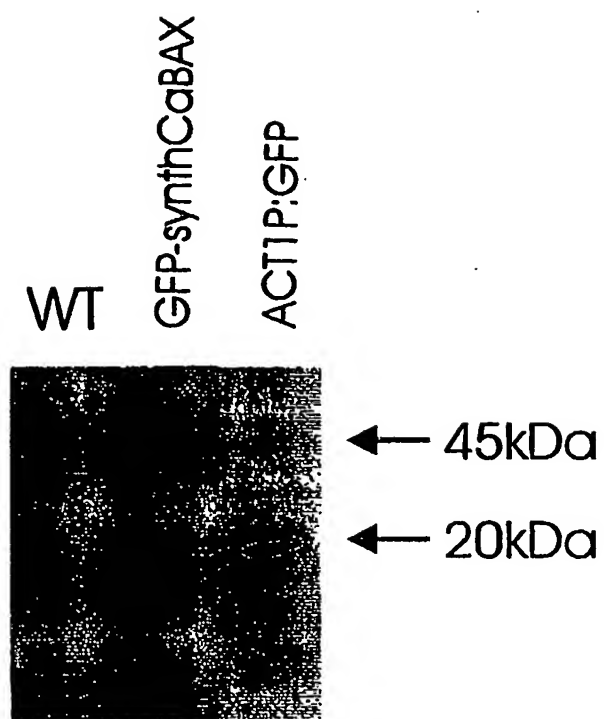


Fig. 11.

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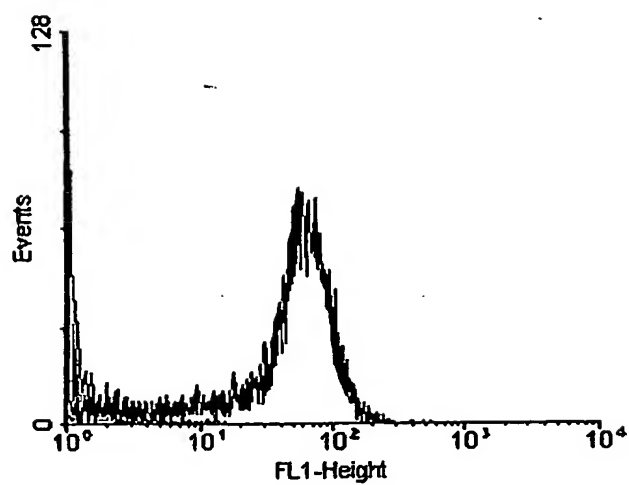
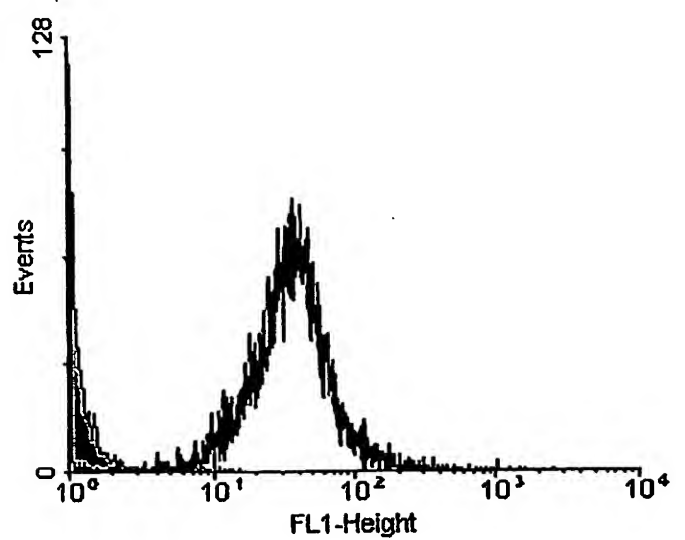


Fig.12.

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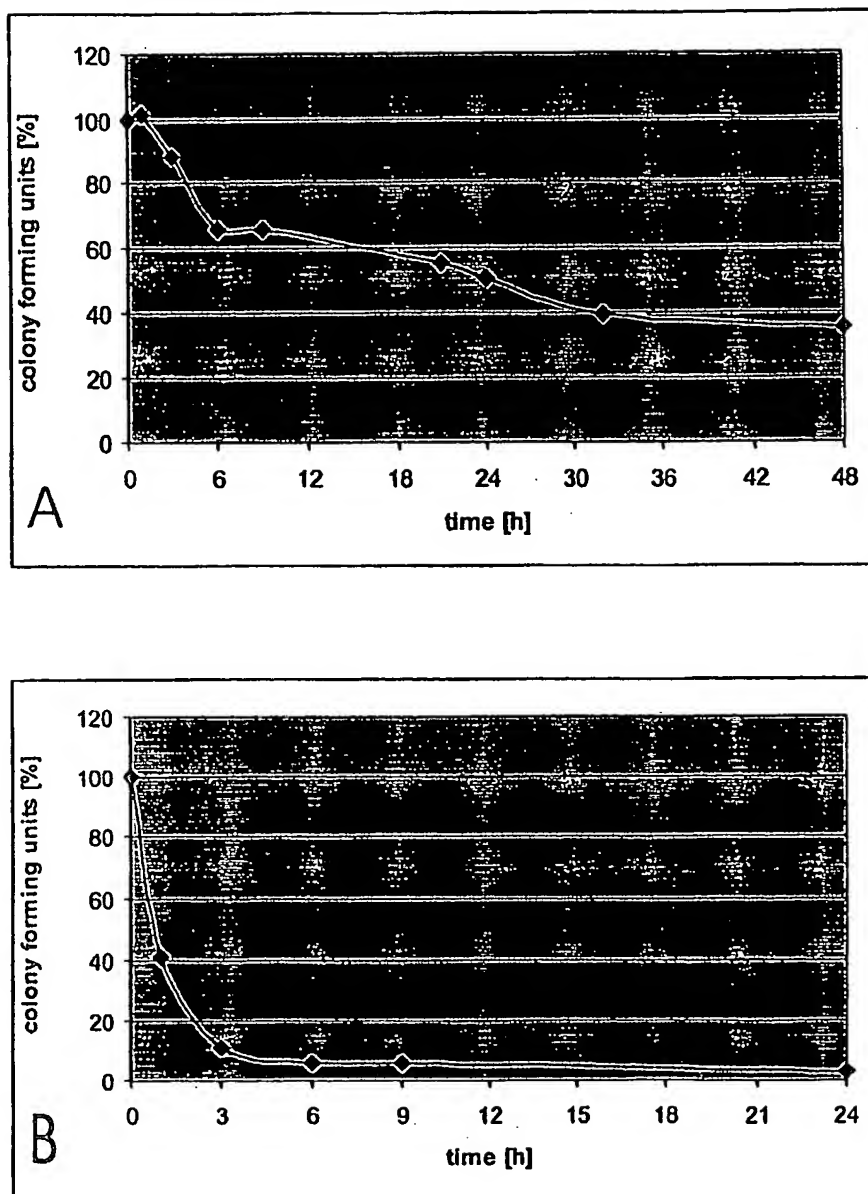


Fig. 13.